```
Glycine max
Seq. No.
Contig ID
                   0 1.R1040
5'-most EST
                   CPR2866 700213140 FL
Method
                   BLASTX
NCBI GI
                   q4262236
BLAST score
                   405
E value
                   4.0e-64
Match length
                   214
% identity
                   63
                   (AC006200) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1 1.R1040
5'-most EST
                   sat701014721.hl
Method
                   BLASTX
NCBI GI
                   g2980802
BLAST score
                   400
E value
                   2.0e-38
Match length
                   189
% identity
                   46
NCBI Description (AL022197) transcriptional activator CBF1 - like protein
                   [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1 2.R1040
5'-most EST
                   CPR6130_700750838_FL
Method
                   BLASTX
NCBI GI
                   g3660548
BLAST score
                   207
E value
                   5.0e-16
Match length
                   145
% identity
NCBI Description
                   (AB013815) DREB1A [Arabidopsis thaliana]
Seq. No.
Contig ID
                  1 3.R1040
5'-most EST
                  uC-gmropic021g01b1
Seq. No.
Contig ID
                   2 1.R1040
5'-most EST
                  rlr700897446.h1
Method
                  BLASTX
NCBI GI
                  q2980802
BLAST score
                   326
E value
                  8.0e-30
Match length
                  212
% identity
NCBI Description
                   (AL022197) transcriptional activator CBF1 - like protein
                   [Arabidopsis thaliana]
```

Seq. No.

Contig ID 3 1.R1040

Method BLASTX

```
g4105772
NCBI GI
BLAST score
                   804
E value
                   6.0e-86
Match length
                   183
                   53
% identity
                   (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
Seq. No.
Contig ID
                   4 1.R1040
                   ssr700556639.hl
5'-most EST
                   BLASTX
Method
                   g2655008
NCBI GI
BLAST score
                   867
E value
                   5.0e-93
Match length
                   374
% identity
                   45
                   (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   4 2.R1040
Contig ID
5'-most EST
                   jC-qmle01810053b07a1
Method
                   BLASTX
'NCBI GI
                   g2642640
BLAST score
                   1554
E value
                   1.0e-173
Match length
                   339
% identity
                   85
                   (AF032473) ADP-glucose pyrophosphorylase large subunit 2
NCBI Description
                   [Citrullus lanatus]
Seq. No.
                   4 3.R1040
Contig ID
5'-most EST
                   jC-gmf102220050f03d1
                   10
Seq. No.
                   4 4.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy075b06b1
                   BLASTX
Method
NCBI GI
                   g2655008
BLAST score
                   313
                   1.0e-28
E value
Match length
                  . 101 .
% identity
                   54
                   (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   11
                   5 1.R1040
Contig ID
5'-most EST
                   LIB3106-062-Q1-K1-E6
Method
                   BLASTN
NCBI GI
                   g1663540
BLAST score
                   277
E value
                   1.0e-154
Match length
                   461
                   90
% identity
                  Glycine max clone RLG3 disease resistance protein homolog
NCBI Description
```

## gene, partial cds Seq. No. 12

Contig ID 6 1.R1040

5'-most EST ASG32442DA-001-B5 FL

Method BLASTX NCBI GI g1709127 BLAST score 2023 0.0e+00E value Match length 409 % identity 93

GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-1 NCBI Description

> >gi 481020 pir S37644 protein kinase MSK-1 (EC 2.7.1.-) alfalfa >gi 313144 emb CAA48474 (X68411) protein kinase

[Medicago sativa]

Seq. No. 13

6 2.R1040 Contig ID

jC-gmro02910008h06a1 5'-most EST

Method BLASTN NCBI GI q1431621 BLAST score 178 E value 4.0e-95 Match length 527 % identity

NCBI Description T.repens mRNA for protein kinase

Seq. No.

Contig ID 6 4.R1040

5'-most EST ncj700980733.hl

Method BLASTN NCBI GI g313143 BLAST score 109 5.0e-54 E value Match length 485 % identity 86

NCBI Description A.medicago MSK-1 mRNA for protein kinase

Seq. No. 15

6 5.R1040 Contig ID

5'-most EST jC-qmf102220050g09a1

Method BLASTN NCBI GI g313143 BLAST score 109 3.0e-54E value 153 Match length 93 % identity

NCBI Description A.medicago MSK-1 mRNA for protein kinase

Seq. No.

6 6.R1040 Contig ID

5'-most EST uC-gmrominsoy213e03b1

Method BLASTN g313143 NCBI GI BLAST score 216 E value 1.0e-118

Match length 359

Method

NCBI GI

BLASTX

q2673906

```
% identity
NCBI Description
                  A.medicago MSK-1 mRNA for protein kinase
Seq. No.
Contig ID
                  6 9.R1040
5'-most EST
                  leu701150045.h1
                  BLASTN
Method
NCBI GI
                  q313143
BLAST score
                  169
                  5.0e-90
E value
Match length
                  224
                  94
% identity
                  A.medicago MSK-1 mRNA for protein kinase
NCBI Description
Seq. No.
Contig ID
                  7 1.R1040
5'-most EST
                  LIB3106-035-Q1-K1-G4
Method
                  BLASTX
                  q1345977
NCBI GI
                  1965
BLAST score
                  0.0e+00
E value
Match length
                  383
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  ISOZYME 2 >gi 904154 (L43921) microsomal omega-6 desaturase
                  [Glycine max]
Seq. No.
                  7 2.R1040
Contig ID
5'-most EST
                  LIB3053-001-Q1-B1-H3
                  BLASTX
Method
NCBI GI
                  g1345977
BLAST score
                  1939
                  0.0e + 00
E value
Match length
                  383
% identity
                  93
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  ISOZYME 2 >gi 904154 (L43921) microsomal omega-6 desaturase
                  [Glycine max]
                  20
Seq. No.
Contig ID
                  7 3.R1040
5'-most EST
                  zhf700958467.h1
Method
                  BLASTX
NCBI GI
                  q2673906
BLAST score
                  525
E value
                  1.0e-53
Match length
                  139
% identity
                  (AC002561) putative DNA polymerase delta small subunit
NCBI Description
                  [Arabidopsis thaliana]
                  21
Seq. No.
Contig ID
                  7 4.R1040
5'-most EST
                  uC-gmrominsoy162c08b1
```

Method

NCBI GI

BLASTN

q4210834

```
BLAST score
E value
                   3.0e-35
Match length
                   97
% identity
                   84
NCBI Description
                   (AC002561) putative DNA polymerase delta small subunit
                   [Arabidopsis thaliana]
Seq. No.
Contig ID
                   7 5.R1040
5'-most EST
                   kl1701211444.h1
Method
                   BLASTN
NCBI GI
                   q904153
BLAST score
                   97
E value
                   3.0e-47
Match length
                   158
% identity
                   93
NCBI Description
                  Glycine max FAD2-2 microsomal omega-6 desaturase mRNA,
                  complete cds
Seq. No.
Contig ID
                   8 1.R1040
5'-most EST
                  uC-qmrominsoy222b04b1
Method
                  BLASTX
NCBI GI
                  q3452497
BLAST score
                  2296
E value
                  0.0e + 00
Match length
                   566
                  79
% identity
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]
Seq. No.
Contig ID
                  8 2.R1040
5'-most EST
                  jC-gmro02910060h03a1
Method
                  BLASTN
NCBI GI
                  g4210834
BLAST score
                  71
E value
                   2.0e-31
Match length
                  115
% identity
                   90
NCBI Description Pisum sativum mRNA for ketol-acid reductoisomerase
Seq. No.
Contig ID
                  8 3.R1040
5'-most EST
                  LIB3049-016-Q1-E1-E11
Method
                  BLASTN
NCBI GI
                  q4210834
BLAST score
                  213
E value
                  1.0e-116
Match length
                  569
% identity
                  84
NCBI Description Pisum sativum mRNA for ketol-acid reductoisomerase
Seq. No.
                  26
                  8 5.R1040
Contig ID
                  jC-gmro02910073g04d1
5'-most EST
```

E value

```
BLAST score
                   64
                   2.0e-27
 E value
 Match length
                   116
                   89
 % identity
 NCBI Description Pisum sativum mRNA for ketol-acid reductoisomerase
 Seq. No.
                   27
 Contig ID
                   8 6.R1040
 5'-most EST
                   g4304571
                   BLASTN
 Method
 NCBI GI
                   g4210834
 BLAST score
                   157
                   7.0e-83
 E value
                   376
 Match length
                   88
 % identity
                   Pisum sativum mRNA for ketol-acid reductoisomerase
 NCBI Description
 Seq. No.
 Contig ID
                   9 1.R1040
 5'-most EST
                   leu701146904.hl
                   BLASTX
 Method
 NCBI GI
                   g2842490
BLAST score
                   791
E value
                   1.0e-106
Match length
                   337
                   62
 % identity
 NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
                   29
 Seq. No.
 Contig ID
                   9 2.R1040
                   LIB3049-020-Q1-E1-E8
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g2842490
 BLAST score
                   244
                   7.0e-27
 E value
 Match length
                   76
 % identity
                   (AL021749) heat-shock protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   9 3.R1040
 Contig ID
 5'-most EST
                   jC-gmst02400068a04d1
 Method
                   BLASTX
 NCBI GI
                   q2842490
 BLAST score
                   151
                   8.0e-10
 E value
Match length
                   38
 % identity
 NCBI Description
                   (AL021749) heat-shock protein [Arabidopsis thaliana]
 Seq. No.
 Contig ID
                   10 1.R1040
 5'-most EST
                   LIB3139-004-P1-N1-H2
Method
                   BLASTX
 NCBI GI
                   q3243234
 BLAST score .
                   1356
```

1.0e-150

NCBI GI

```
306
Match length
% identity
                  (AF071477) isoflavone reductase related protein [Pyrus
NCBI Description
                  communis]
Seq. No.
                  11 1.R1040
Contig ID
                  uC-gmrominsoy081c11b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q166421
BLAST score
                  287
E value
                  1.0e-160
Match length
                  475
                  90
% identity
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                  33
Seq. No.
                  11 2.R1040
Contig ID
5'-most EST
                  LIB3139-094-P1-N1-A2
                  BLASTN
Method
NCBI GI
                  g166421
BLAST score
                  282
E value
                  1.0e-157
Match length
                  630
                  89
% identity
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
Seq. No.
                  11 3.R1040
Contig ID
                  wvk700684812.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q136636
BLAST score
                  222
                  4.0e-36
E value
Match length
                  84.
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                  >gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -
                  Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin
                  Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894 pdb 2AAK
                  Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                  >qi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                  thaliana] >qi 431260 (L19351) ubiquitin conjugating enzyme
                  [Arabidopsis thaliana]
Seq. No.
                  35
Contig ID
                  11 4.R1040
5'-most EST
                  LIB3106-009-Q1-K1-G1
Seq. No.
                  36
Contig ID
                  11 5.R1040
5'-most EST
                  LIB3087-001-Q1-K1-E4
Method
                  BLASTN
```

q166421

Seq. No.

```
BLAST score
                  172
                  8.0e-92
E value
Match length
                  248
% identity
                  92
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
Seq. No.
                  37
                  11 6.R1040
Contig ID
                  LIB3092-033-Q1-K1-A7
5'-most EST
Method
                  BLASTN
NCBI GI
                  g166421
                  77
BLAST score
E value
                  3.0e-35
Match length
                  125
% identity
                  90
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                   38
Seq. No.
                  11 8.R1040
Contig ID
                  LIB3051-088-Q1-K1-B12
5'-most EST
                  BLASTN
Method
                  g166421
NCBI GI
BLAST score
                  108
                   2.0e-53
E value
                   148
Match length
                   93
% identity
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                   39
Seq. No.
                   11 9.R1040
Contig ID
                  LIB3106-105-Q1-K1-F5
5'-most EST
Method
                   BLASTN
NCBI GI
                   g166421
BLAST score
                   164
                   4.0e-87
E value
Match length
                   320
% identity
                   88
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                   cds
                   40
Seq. No.
Contig ID
                   12 1.R1040
                   leu701146018.h1
5'-most EST
Method
                   BLASTX
                   g1717950
NCBI GI
BLAST score
                   1036
                   1.0e-113
E value
                   242
Match length
                   81
% identity
                   UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 2
NCBI Description
                   PRECURSOR (RIESKE IRON-SULFUR PROTEIN 2) (RISP2) >gi_530052
                   (L16810) Rieske iron-sulfur protein [Nicotiana tabacum]
```

Match length

```
Contig ID
                   12 2.R1040
5'-most EST
                  LIB3106-095-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                   g1717950
BLAST score
                   397
E value
                   2.0e-38
Match length
                   118
% identity
                   68
                   UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 2
NCBI Description
                   PRECURSOR (RIESKE IRON-SULFUR PROTEIN 2) (RISP2) >gi 530052
                   (L16810) Rieske iron-sulfur protein [Nicotiana tabacum]
                   42
Seq. No.
                   12 3.R1040
Contig ID
5'-most EST
                   leu701151219.hl
Seq. No.
                   43
                   13 1.R1040
Contig ID
5'-most EST
                  CPR2864_700208152_FL
Method
                   BLASTN
NCBI GI
                   g1673455
BLAST score
                   443
E value
                   0.0e+00
Match length
                   882
% identity
                   98
NCBI Description
                  Z.mays rubisco small subunit gene
Seq. No.
                   14 1.R1040
Contig ID
5'-most EST
                  CPR6566_700985454_FL
Method
                  BLASTX
NCBI GI
                  g2618686
BLAST score
                  1213
E value
                   1.0e-134
Match length
                   319
% identity
                   70
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45
                   14 2.R1040
Contig ID
                  CPR6559 700731265_FL
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2618686
BLAST score
                  1017
E value
                   1.0e-121
Match length
                  310
% identity
NCBI Description
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  14 3.R1040
Contig ID
5'-most EST
                  LIB3170-072-Q1-J1-E12
Method
                  BLASTX
NCBI GI
                  g2618686
BLAST score
                  309
E value
                   4.0e-28
```

Match length

```
% identity
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47
Seq. No.
                   15 1.R1040
Contig ID
5'-most EST
                   fC-gmle7000742678f1
Method
                   BLASTX
NCBI GI
                   g2618686
BLAST score
                   989
E value
                   1.0e-107
Match length
                   389
                   48
% identity
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   48
Seq. No.
                   15 2.R1040
Contig ID
                   CPR6560 700742678_FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3882018
BLAST score
                   416
E value
                   5.0e-66
Match length
                   324
                   47
% identity
NCBI Description
                   (Y18377) cytokinin oxidase [Zea mays]
Seq. No.
                   16 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir010b05b1
Method
                   BLASTN
                   g1663536
NCBI GI
BLAST score
                   219
                   1.0e-119
E value
Match length
                   287
                   94
% identity
                   Glycine max clone RLG1 disease resistance protein homolog
NCBI Description
                   gene, partial cds
Seq. No.
                   16 2.R1040
Contig ID
                   sat701011581.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1663536
BLAST score
                   346
E value
                   0.0e+00
Match length
                   446
% identity
                   94
                  Glycine max clone RLG1 disease resistance protein homolog
NCBI Description
                   gene, partial cds
Seq. No.
                   17 1.R1040
Contig ID
5'-most EST
                   LIB3051-054-Q1-K2-C3
                   BLASTX
Method
NCBI GI
                   g4262226
BLAST score
                   277
E value
                   5.0e-24
```

```
% identity
NCBI Description
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   17 2.R1040
Contig ID
5'-most EST
                   LIB3139-085-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   g4262226
BLAST score
                   197
                   5.0e-15
E value
Match length
                   128
% identity
                   45
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   17 3.R1040
Contig ID
5'-most EST
                   lus701015877.hl
Seq. No.
                   54
                   19 1.R1040
Contig ID
5'-most EST
                   LIB3030-011-Q1-B1-D10
Method
                   BLASTX
NCBI GI
                   g4325041
BLAST score
                   2609
                   0.0e+00
E value
Match length
                   668
% identity
                   80
NCBI Description
                   (AF117339) FtsH-like protein Pftf precursor [Nicotiana
                   tabacum]
Seq. No.
                   55
                   19 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810022f02d1
Method
                   BLASTN
                   g3808100
NCBI GI
BLAST score
                   80
E value
                   6.0e-37
Match length
                   244
                   83
% identity
                   Capsicum annuum mRNA for chloroplast protease (CACP) from
NCBI Description
                   the AAA atpase family
Seq. No.
                   56
Contig ID
                   19 3.R1040
5'-most EST
                   ssr700559811.hl
                   BLASTX
Method
NCBI GI
                   q3808101
BLAST score
                   392
E value
                   7.0e-38
Match length
                   165
% identity
NCBI Description
                   (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
Contig ID
                   19 4.R1040
```

jC-gmf102220072h01a1

```
58
Seq. No.
                   20 1.R1040
Contig ID
5'-most EST
                   CPR3447_700959152_FL
Method
                   BLASTX
NCBI GI
                   g1935000
BLAST score
                   404
E value
                   1.0e-38
Match length
                   238
% identity
                   35
NCBI Description
                   (Y12314) GTPase [Schizosaccharomyces pombe]
Seq. No.
Contig ID
                   21 1.R1040
5'-most EST
                   LIB3109-017-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   g3493172
BLAST score
                   1329
E value
                   1.0e-147
Match length
                   313
% identity
NCBI Description
                   (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                   21 2.R1040
Contig ID
5'-most EST
                   fC-qmse700660534z1
Method
                   BLASTX
NCBI GI
                   g3493172
BLAST score
                   383
E value
                   1.0e-36
Match length
                   108
% identity
                   (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
Seq. No.
Contig ID
                   21 4.R1040
5'-most EST
                   LIB3107-060-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g3493172
BLAST score
                   424
E value
                   8.0e-42
                   108
Match length
% identity
                   (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
Seq. No.
                   62
                   22 1.R1040
Contig ID
5'-most EST
                   CPR3456 700739290 FL
                   BLASTX
Method
NCBI GI
                   g2213598
BLAST score
                   436
                   2.0e-42
E value
Match length
                   332
% identity
NCBI Description
                   (AC000348) T7N9.18 [Arabidopsis thaliana]
Seq. No.
```

23 1.R1040

Contig ID

```
5'-most EST
                    CPR3463 700797953 FL
 Method
                    BLASTX
                    g3947733
 NCBI GI
 BLAST score
                    378
 E value
                    4.0e-36
 Match length
                    155
 % identity
                    (AJ009719) NL25 [Solanum tuberosum]
 NCBI Description
 Seq. No.
                    24 1.R1040
 Contig ID
 5'-most EST
                    je\bar{x}700908154.h1
 Method
                    BLASTX
 NCBI GI
                    g2088653
 BLAST score
                    1230
                    1.0e-135
 E value
 Match length
                    443
 % identity
                    54
 NCBI Description
                    (AF002109) Hs1pro-1 related protein isolog [Arabidopsis
                    thaliana]
 Seq. No.
                    24 2.R1040
 Contig ID
5'-most EST
                    uC-gmrominsoy256f04b1
Method
                    BLASTX
 NCBI GI
                    g2088653
 BLAST score
                    390
 E value
                    2.0e-37
                    130
 Match length
                    59
 % identity .
                    (AF002109) Hs1pro-1 related protein isolog (Arabidopsís
 NCBI Description
                    thaliana]
 Seq. No.
                    66
 Contig ID
                    24 3.R1040
 5'-most EST
                    fC-gmle700557849f3
 Method
                    BLASTX
 NCBI GI
                    g2088653
 BLAST score
                    413
 E value
                    4.0e-40
 Match length
                    123
 % identity
 NCBI Description
                    (AF002109) Hs1pro-1 related protein isolog [Arabidopsis
                    thaliana]
                    67 ·
 Seq. No.
                    24 5.R1040
 Contig ID
 5'-most EST
                    fua701040369.hl
 Method
                    BLASTX
                    g2088653
 NCBI GI
 BLAST score
                    352
                    3.0e-33
 E value
                    134
 Match length
 % identity
                    52
 NCBI Description
                    (AF002109) Hslpro-1 related protein isolog [Arabidopsis
```

thaliana]

Match length

```
Seq. No.
.Contig ID
                   25 1.R1040
5'-most EST
                   CPR3468 700835511 FL
Method
                   BLASTX
NCBI GI
                   g3947735
BLAST score
                   499
E value
                   1.0e-49
Match length
                   480
% identity
NCBI Description
                   (AJ009720) NL27 [Solanum tuberosum]
Seq. No.
Contig ID
                   26 1.R1040
5'-most EST
                   fC-gmro700562665z1
Method
                   BLASTX
NCBI GI
                   g3947735
BLAST score
                   670
E value
                   5.0e-70
Match length
                   358
% identity
                   41
                   (AJ009720) NL27 [Solanum tuberosum]
NCBI Description
Seq. No.
Contig ID
                   26 2.R1040
                   CPR3475_700870127 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3860167
BLAST score
                   322
E value
                   6.0e-29
                   358
Match length
% identity
                   (AF098964) disease resistance protein RPP1-WsC [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   71
Contig ID
                   26 3.R1040
5'-most EST
                   CPR10175 FL
Method
                   BLASTX
NCBI GI ...
                   g3947735
BLAST score
                   442
                  .3<u>.</u>0e-43
E value
Match length
                   360
% identity
NCBI Description
                   (AJ009720) NL27 [Solanum tuberosum]
Seq. No.
Contig ID
                   26 4.R1040
5'-most EST
                   pcp700990320.hl
Seq. No.
Contig ID
                   26 5.R1040
5'-most EST
                   LIB3028-048-Q1-B1-A10
Method
                   BLASTX
NCBI GI
                   g4204265
BLAST score
                   158
E value
                   2.0e-10
```

NCBI Description

```
% identity
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
Contig ID
                   26 6.R1040
5'-most EST
                   LIB3053-011-Q1-N1-A10
Method
                   BLASTX
NCBI GI
                   g4388834
BLAST score
                  .333
E value
                   7.0e-31
Match length
                   199
% identity
                   18
                   (ACO06528) putative disease resistance protein RPP1, 3'
NCBI Description
                   partial [Arabidopsis thaliana]
Seq. No.
Contig ID
                   26 11.R1040
5'-most EST
                   dp\overline{v}701099972.h1
Seq. No.
                   26 14.R1040
Contig ID
5'-most EST
                   zsq701118496.h1
Seq. No.
                  27 1.R1040
Contig ID
5'-most EST
                   CPR3479 700891859 FL
Method
                   BLASTX
NCBI GI
                   g1086263
BLAST score
                   384
E value
                   2.0e-36
Match length
                   412
% identity
                   32
NCBI Description
                   TMV resistance protein N - tobacco (Nicotiana glutinosa)
                   >gi 558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                   28 1.R1040 -
Contig ID
5'-most EST
                   leu701154138.h1
Method
                   BLASTX
NCBI GI
                   g2213598
BLAST score
                   403
                   1.0e-38
E value
Match length
                   342
% identity
                  (AC000348) T7N9.18 [Arabidopsis thaliana]
NCBI Description
                   79
Seq. No.
Contig ID
                   30 1.R1040
5'-most EST
                   gsv701053417.h1
Method
                   BLASTX
NCBI GI
                   q2316016
BLAST score
                   704
E value
                   3.0e-74
Match length
                   225
% identity
```

(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

```
80
Seq. No.
                   30 2.R1040
Contig ID
                   LIB3138-032-Q1-N1-B2
5'-most EST
                   BLASTX
Method
                   g2316016
NCBI GI
BLAST score
                   353
E value
                   2.0e-33
Match length
                   114
                   61
% identity
                   (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   34 1.R1040
Contig ID
                   CPR6213 700991711 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2088653
BLAST score
                   1154
E value
                   1.0e-126
Match length
                   434
% identity
                   53
                   (AF002109) Hs1pro-1 related protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   82
Seq. No.
                   34 2.R1040
Contig ID
                  LIB3049-052-Q1-E1-C5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2088653
BLAST score
                   586
E value
                   1.0e-121
Match length
                   435
% identity
                   53
                   (AF002109) Hs1pro-1 related protein isolog [Arabidopsis
NCBI Description
                   thaliana)
Seq. No.
Contig ID
                   37 1.R1040
                  CPR6212 700968464 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4490297
                   605
BLAST score
E value
                   1.0e-86
Match length
                   617
% identity
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                   84
                   37 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir032h02b1
Seq. No.
                   85
                   37 3.R1040
Contig ID
5'-most EST
                   uC-gmropic011e09b1
Seq. No.
                   39 1.R1040
Contig ID
```

CPR6214 701001301 FL

Seq. No.

```
Method
                  BLASTX
NCBI GI
                  g3600040
BLAST score
                  479
E value
                  3.0e-47
Match length
                  402
                  36
% identity
NCBI Description
                  (AF080119) similar to Arabidopsis thaliana disease
                  resistance protein RPS2 (GB:U14158) [Arabidopsis thaliana]
Seq. No.
                  41_1.R1040
Contig ID
5'-most EST
                  CPR6217 701068966 FL
Method
                  BLASTX
NCBI GI
                  g2213598
BLAST score
                  408
E value
                  1.0e-39
Match length
                  158
                  28
% identity
NCBI Description
                  (AC000348) T7N9.18 [Arabidopsis thaliana]
                  88
Seq. No.
                  42 1.R1040
Contig ID
5'-most EST.
                  LIB3051-038-Q1-K1-E12
Method
                 BLASTX
                  g4580460
NCBI GI
BLAST score
                  2010
                  0.0e+00
E value
Match length
                  446
% identity
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
                  89
Seq. No.
Contig ID
                  42 2.R1040
5'-most EST
                  gsv701051332.h1
                  BLASTX
Method
NCBI GI
                  q4580460
BLAST score
                  622
E value
                  6.0e-65
Match length
                  127
% identity
NCBI Description
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                  thaliana]
                  90
Seq. No.
Contig ID
                  42 3.R1040
5'-most EST
                  LIB3051-047-Q1-K1-D7
Method
                  BLASTN
NCBI GI
                  g556557
BLAST score
                  122
                  6.0e-62
E value
                  302
Match length
                  85
% identity
NCBI Description
                  Rice mRNA for homologue of Tat binding protein, complete
```

```
45 1.R1040
Contig ID
                    zsg701117822.h2
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3947735
BLAST score
                    424
                    5.0e-41
E value
Match length
                    435
% identity
                    40
NCBI Description
                    (AJ009720) NL27 [Solanum tuberosum]
                    92
Seq. No.
Contig ID
                    45 2.R1040
5'-most EST
                    LIB3139-050-P1-N1-E6
Method
                    BLASTX
NCBI GI
                    g730125
BLAST score
                    1929
                    0.0e + 00
E value
Match length
                    488
                    73
% identity
NCBI Description
                    NADPH-CYTOCHROME P450 REDUCTASE >gi_322739_pir__S31502
                    NADPH--ferrihemoprotein reductase (\overline{EC} 1.6.\overline{2}.4) - Madagascar
                    periwinkle >gi_18139_emb_CAA49446_ (X69791)
NADPH--ferrihemoprotein reductase [Catharanthus roseus]
Seq. No.
                    93
Contig ID
                    45 3.R1040
5'-most EST
                    jC-gmro02910024d12a1
Method
                    BLASTX
NCBI GI
                    g2580499
BLAST score
                    609
E value
                    1.0e-112
Match length
                    323
% identity
                    66
NCBI Description
                    (U67186) NADPH: ferrihemoprotein oxidoreductase
                    [Eschscholzia californica]
                    94
Seq. No.
Contig ID
                    45 4.R1040
5'-most EST
                    g5058215
Method
                    BLASTX
NCBI GI
                    g2580499
BLAST score
                    220
E value
                    1.0e-17
Match length
                    98
% identity
                    45
                    (U67186) NADPH:ferrihemoprotein oxidoreductase
NCBI Description
                    [Eschscholzia californica]
Seq. No.
                    95
Contig ID
                    45 5.R1040
5'-most EST
                    LIB3051-067-Q1-K1-H3
Method
                    BLASTX
NCBI GI
                    g480669
BLAST score
                    366
E value
                    5.0e-35
Match length
                    106
% identity
                    68
```

```
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem
                   artichoke (fragment) >gi_1359894_emb_CAA81210_ (Z26251)
                  NADPH-ferrihemoprotein reductase [Helianthus tuberosus]
                   96
Seq. No.
Contig ID
                   45 6.R1040
5'-most EST
                  LIB3170-037-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g730125
BLAST score
                   312
                   3.0e-28
E value
Match length
                  176
                  73
% identity
                  NADPH-CYTOCHROME P450 REDUCTASE >gi 322739 pir S31502
NCBI Description
                  NADPH--ferrihemoprotein reductase (\overline{EC}\ 1.6.\overline{2}.4)^{-} Madagascar
                  periwinkle >gi 18139_emb_CAA49446_ (X69791)
                  NADPH--ferrihemoprotein reductase [Catharanthus roseus]
                   97
Seq. No.
                   45 7.R1040
Contig ID
5'-most EST
                  vzy700755269.h1
                  BLASTX
Method
NCBI GI
                  g99737
BLAST score
                  542
                  1.0e-55
E value
                  150
Match length
                   67
% identity
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
                  Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                   46 1.R1040
Contig ID
5'-most EST
                  uC-gmropic067a07b1
Method
                  BLASTX
NCBI GI
                  q322752
BLAST score
                  1146
                  0.0e+00
E value
Match length
                   427
% identity
                  auxin-independent growth promoter - Nicotiana tabacum
NCBI Description
                  >gi 559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]
Seq. No.
                  99 :
Contig ID
                   48 1.R1040
                  CPR6563 700945759 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2618686
BLAST score
                  671
                  3.0e-70
E value
                  220
Match length
% identity
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  100
                  49 1.R1040
Contig ID
```

CPR6564\_700953259\_FL

```
BLASTX
Method
NCBI GI
                   q4191780
BLAST score
                   281
                   9.0e-25
E value
                   95
Match length
                   54
% identity
                   (AC005917) putative cytokinin oxidase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   101
Contig ID
                   51 1.R1040
5'-most EST
                   CPR6639_700684235_FL
Method
                   BLASTX
NCBI GI
                   g2258317
BLAST score
                   172
E value
                   6.0e-12
Match length
                   132
% identity
                   37
NCBI Description
                   (AF004879) resistance complex protein I2C-2 [Lycopersicon
                   esculentum]
Seq. No.
                   102
Contig ID
                   52 1.R1040
5'-most EST
                   CPR6640_700942632_FL
Method
                   BLASTX
NCBI GI
                   q3947733
BLAST score
                   218
E value
                   4.0e-17
Match length
                   98
% identity
                   (AJ009719) NL25 [Solanum tuberosum]
NCBI Description
Seq. No.
                   103
Contig ID
                   54 1.R1040
5'-most EST
                   zsq701118302.hl
Method
                   BLASTN
NCBI GI
                   q310562
BLAST score
                   89
E value
                   7.0e-42
Match length
                   336
% identity
                   88
                   Glycine max calmodulin (SCaM-5) mRNA, complete cds
NCBI Description
Seq. No.
                   54 2.R1040
Contig ID
5'-most EST
                   g310562 FL
Method
                   BLASTN
NCBI GI
                   g310562
BLAST score
                   873
E value
                   0.0e + 00
Match length
                   873
% identity
                   100
                   Glycine max calmodulin (SCaM-5) mRNA, complete cds
NCBI Description
                   105
Seq. No.
                   54 3.R1040
Contig ID
```

zzp700831855.hl



```
BLASTN
Method
NCBI GI
                   g310562
BLAST score
                   115
E value
                   4.0e-58
                   123
Match length
                   98
% identity
NCBI Description
                  Glycine max calmodulin (SCaM-5) mRNA, complete cds
Seq. No.
                   106
                   55 1.R1040
Contig ID
5'-most EST
                  .fC-gmle700560625a1
Method
                   BLASTX
NCBI GI
                   g2853078
BLAST score
                   393
                   7.0e-77
E value
Match length
                   594
                   34
% identity
NCBI Description
                   (AL021768) TMV resistance protein N-like [Arabidopsis
                   thaliana]
                   107
Seq. No.
                   55 2.R1040
Contig ID
5'-most EST
                   fC-gmle700560625i1
                   BLASTX
Method
                   q2853078
NCBI GI
BLAST score
                   317
E value
                   6.0e-29
Match length
                   201
% identity
                   33
                   (AL021768) TMV resistance protein N-like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   108
                   56 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy185f08b1
                   BLASTX
Method
NCBI GI
                   g3947735
BLAST score
                  .638
                   4.0e-66
E value
Match length
                   402
% identity
                   (AJ009720) NL27 [Solanum tuberosum]
NCBI Description
Seq. No.
Contig ID
                   57 1.R1040
5'-most EST
                   LIB3051-041-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3947733
BLAST score
                   162
                   1.0e-10
E value
Match length
                   112
% identity
                  (AJ009719) NL25 [Solanum tuberosum]
NCBI Description
Seq. No.
                   110
Contig ID
                   58 1.R1040
```

CPR6648a 700993771\_FL

```
BLASTX
Method
NCBI GI
                   g4092774
BLAST score
                   669
                   1.0e-69
E value
Match length
                   604
                   31
% identity
NCBI Description
                   (AF105140) disease resistance gene homolog 9N [Brassica
                   napus]
                  · 111
Seq. No.
                  59 1.R1040
Contig ID
5'-most EST
                   CPR6649 700999286 FL
Method
                   BLASTX
NCBI GI
                   q3947735
                   373
BLAST score
                   3.0e-35
E value
                   301
Match length
                   42.
% identity
                   (AJ009720) NL27 [Solanum tuberosum]
NCBI Description
Seq. No.
                   112
                   60 1.R1040
Contig ID
5'-most EST
                   zhf700962285.h1
Method
                  BLASTX
                  q1652057
NCBI GI
BLAST score
                  1192
                   1.0e-131
E value
Match length
                   535
% identity
                   51
                  (D90902) hypothetical protein [Synechocystis sp.]
NCBI Description
                  113
Seq. No.
                   60 2.R1040
Contig ID
5'-most EST
                   sat701012774.h1
Seq. No.
                   114
                   65 1.R1040
Contig ID
5'-most EST
                   g5606563
Method
                   BLASTX
                   g3080405
NCBI GI
BLAST score
                   353
                   4.0e-33
E value
                   83
Match length
% identity
                   (AL022603) Lsd1 like protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4455269_emb_CAB36805.1_ (AL035527) Lsd1 like protein
                   [Arabidopsis thaliana]
                   115
Seq. No.
Contig ID
                   66 1.R1040
5'-most EST
                  LIB3106-074-Q1-K1-G6
Method
                  BLASTX
                  g2738248
NCBI GI
BLAST score
                   3400
E value
                  0.0e + 00
                   762
Match length
                  85
% identity
```

% identity

```
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
                   116
Seq. No.
                   66 2.R1040
Contig ID
5'-most EST
                   epx701108427.h1
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  294
                   3.0e-26
E value
                  74
Match length
                   77
% identity
                   (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
Seq. No.
                   117
                   66 3.R1040
Contig ID
5'-most EST
                  LIB3092-020-Q1-K1-C11
                  BLASTX
Method
NCBI GI
                  g1914683
BLAST score
                  325
E value
                   4.0e-30
Match length
                  109
% identity
                   61
                   (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
Seq. No.
                  66 6.R1040
Contig ID
5'-most EST
                  crh700854007.hl
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  194
                   6.0e-15
E value
Match length
                  52
                   75
% identity
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                  119
Seq. No.
                   66 7.R1040
Contig ID
5'-most EST
                  pxt700943841.hl
Method
                  BLASTX
NCBI GI
                  g974782
BLAST score
                   418
                  3.0e-46
E value
Match length
                  111
% identity
                  86
                   (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                  120
Seq. No.
Contig ID
                  66 9.R1040
5'-most EST
                  LIB3050-019-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  g974781
BLAST score
                  125
E value
                  8.0e-64
Match length
                  313
```

```
NCBI Description C.blumei kinetoplast met gene for cobalamine-independent
                   methionine synthase
Seq. No.
                   121
                   66 16.R1040
Contig ID
                   wvk700682724.hl
5'-most EST
Method
                   BLASTX
                   q2738248
NCBI GI
BLAST score
                   201
                   1.0e-31
E value
Match length
                   82
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   122
                   67 1.R1040
Contig ID
                   zsg701118017.h2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4376158
BLAST score
                   1940
                   0.0e + 00
E value
Match length
                   472
% identity
                   82
NCBI Description
                   (X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.
                   123
                   67 2.R1040
Contig ID
5'-most EST
                   CPR9211 700959057 FL
Method
                   BLASTX
NCBI GI
                   q4376158
BLAST score
                   1866
E value
                   0.0e + 00
Match length
                   458
% identity
NCBI Description
                   (X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.
                   67 3.R1040
Contig ID
5'-most EST
                   uC-qmropic064c02b1
Method
                   BLASTN
NCBI GI
                   g2257742
BLAST score
                   115
                   1.0e-57
E value
Match length
                   375
% identity
                   83
                  Arabidopsis thaliana lysine-sensitive aspartate kinase
NCBI Description
                   mRNA, complete cds
Seq. No.
                   69 1.R1040
Contig ID
                   CPR9215 701060142 FL
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2970446
BLAST score
                   905
E value
                   0.0e+00
```

1341

Match length

```
% identity
                   Glycine max aspartokinase-homoserine dehydrogenase
NCBI Description
                   (AK-HSDH) mRNA, complete cds
                   126
Seq. No.
Contig ID
                   69 2.R1040
5'-most EST
                   dpv701100440.hl
Method
                   BLASTX
                   g2970447
NCBI GI
BLAST score
                   2096
                   0.0e + 00
E value
Match length
                   417
                   99
% identity
NCBI Description
                   (AF049706) aspartokinase-homoserine dehydrogenase [Glycine
                   max}
                   127
Seq. No.
                   69 3.R1040
Contig ID
5'-most EST
                   fC-gmro700865466a2
Method
                   BLASTN
                   g2104674
NCBI GI
                   169
BLAST score
                   1.0e-89
E value
                  477
Match length
                   84
% identity
                  V. faba mRNA for transcription factor containing bZIP
NCBI Description
Seq. No.
                   69 4.R1040
Contig ID
5'-most EST
                   fC-gmro700798021b2
Method
                   BLASTN
NCBI GI
                   g2970446
BLAST score
                   648
E value
                   0.0e + 00
Match length
                   656
                   100
% identity
                  Glycine max aspartokinase-homoserine dehydrogenase
NCBI Description
                   (AK-HSDH) mRNA, complete cds
                   129
Seq. No.
                   69 5.R1040
Contig ID
5'-most EST
                   fC-gmle700557507r2
Method
                   BLASTN
NCBI GI
                   g2970446
BLAST score
                   519
E value
                   0.0e+00
Match length
                   535
                   99
% identity
                   Glycine max aspartokinase-homoserine dehydrogenase
NCBI Description
                   (AK-HSDH) mRNA, complete cds
                   130
Seq. No.
Contig ID
                   71 1.R1040
5'-most EST
                   uxk700672773.h1
Method
                   BLASTX
```

q1762933

485

NCBI GI

BLAST score

Contig ID

```
E value
                   2.0e-48
Match length
                   186
% identity
                   53
NCBI Description
                   (U66263) tumor-related protein [Nicotiana tabacum]
Seq. No.
                   72 1.R1040
Contig ID
                   CPR9004 701042534 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2754816
BLAST score
                   374
E value
                   2.0e-35
Match length
                   176
                   43
% identity
                   (AF021346) non-race specific disease resistance protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   74 1.R1040
Contig ID
                   LIB3051-114-Q1-K1-H12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1742961
BLAST score
                   1892
E value
                   0.0e+00
Match length
                   505
% identity
                   73
NCBI Description
                   (X94756) cystathionine gamma-synthase [Arabidopsis
                   thaliana]
                   133
Seq. No.
Contig ID
                   74 2.R1040
                   fC-gmse7000751425d1
5'-most EST
Method
                   BLASTX
                   q1791309
NCBI GI
BLAST score
                   380
                   2.0e-36
E value
                   83
Match length
% identity
                   (U83500) cystathionine gamma-synthase [Arabidopsis
NCBI Description
                   thaliana] >gi 2852454 dbj BAA24699 (AB010888)
                   cystathionine gamma-synthase [Arabidopsis thaliana]
Seq. No.
                   134
Contig ID
                   74 3.R1040
5'-most EST
                   LIB3051-006-Q1-E1-G10
Method
                   BLASTX
NCBI GI
                   q1791309
BLAST score
                   424
E value
                   9.0e-42
Match length
                   146
% identity
                   61
                   (U83500) cystathionine gamma-synthase [Arabidopsis
NCBI Description
                   thaliana] >gi 2852454 dbj BAA24699 (AB010888)
                   cystathionine gamma-synthase [Arabidopsis thaliana]
Seq. No.
```

74 10.R1040

```
5'-most EST
                  eep700867801.h1
Method
                  BLASTX
NCBI GI
                  g3202028
BLAST score
                  395
                  3.0e-38
E value
Match length
                  96
% identity
NCBI Description
                  (AF069317) cystathionine gamma-synthase [Mesembryanthemum
                  crystallinum]
                  136
Seq. No.
Contig ID
                  75 1.R1040
5'-most EST
                  CPR9221 700567374 FL
Method
                  BLASTX
NCBI GI
                  g100728
BLAST score
                  1351
E value
                  1.0e-149
                  407
Match length
                  61
% identity
                  aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso
NCBI Description
                  millet >gi_1084464_pir__S53304 aspartate aminotransferase -
                  proso millet >gi 20601 emb CAA45024 (X63430) aspartate
                  aminotransferase [Panicum miliaceum]
                  >gi 435459 dbj BAA04993 (D25323) aspartate
                  aminotransferase [Panicum miliaceum]
Seq. No.
                  137
Contig ID
                  75 2.R1040
5'-most EST
                  uC-gmropic106a04b1
Method
                  BLASTX
NCBI GI
                  g100728
BLAST score
                  573
                  6.0e-59
E value
Match length
                  128
                  77
% identity
                  aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso
NCBI Description
                  millet >gi 1084464 pir S53304 aspartate aminotransferase -
                  proso millet >gi 20601 emb CAA45024 (X63430) aspartate
                  aminotransferase [Panicum miliaceum]
                  >gi_435459 dbj_BAA04993_ (D25323) aspartate
                  aminotransferase [Panicum miliaceum]
                  138
Seq. No.
Contig ID
                  78 1.R1040
5'-most EST
                  CPR9214 LIB3039-051-A2 FL
                  BLASTX
Method
NCBI GI
                  g2984139
BLAST score
                  789
E value
                  7.0e-84
Match length
                  338
% identity
NCBI Description
                  (AE000760) aspartate-semialdehyde dehydrogenase [Aquifex
                  aeolicus]
Seq. No.
                  139
Contig ID
                  78 2.R1040
```

hrw701060760.hl

5'-most EST

Match length

% identity

382

```
Method
                  BLASTX
NCBI GI
                  g416901
BLAST score
                  341
                  7.0e-32
E value
Match length
                  111
% identity
                  59
NCBI Description
                  ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (ASA DEHYDROGENASE)
                  >gi 142828 (L08471) aspartate semialdehyde dehydrogenase
                  [Bacillus subtilis] >gi 2634047 emb CAB13548 (Z99112)
                  aspartate-semialdehyde dehydrogenase [Bacillus subtilis]
Seq. No.
                  79 1.R1040
Contig ID
5'-most EST
                  ssr700556460.hl
Method
                  BLASTX
NCBI GI
                  g1705463
BLAST score
                  1460
E value
                  1.0e-162
Match length
                  373
                  75
% identity
                  BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi 2129547 pir S71201
NCBI Description
                  biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147)
                  biotin sythase [Arabidopsis thaliana] >gi 1403662 (U31806)
                  BIO2 protein [Arabidopsis thaliana] >gi 1769457 (L34413)
                  biotin synthase [Arabidopsis thaliana] >gi 2288983
                  (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                  >gi 1589016 prf 2209438A biotin synthase [Arabidopsis ]
                  thaliana]
Seq. No.
                  141
Contig ID
                  79 2.R1040
5'-most EST
                  LIB3170-010-Q1-K1-G7
Seq. No.
Contig ID
                  79 3.R1040
                  wvk700685486.h1
5'-most EST
Seq. No.
                  143
Contig ID
                  82 1.R1040
                  ssr700555656.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4098966
BLAST score
                  335
E value
                  0.0e + 00
Match length
                  602
                  96
% identity
NCBI Description Glycine max putative reistance gene analog genomic sequence
                  144
Seq. No.
Contig ID
                  82 2.R1040
5'-most EST
                  LIB3093-028-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1086263
BLAST score
                  346
E value
                  4.0e-32
```

Method

```
NCBI Description
                  TMV resistance protein N - tobacco (Nicotiana glutinosa)
                   >gi_558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                   83 1.R1040
Contig ID
5'-most EST
                   CPR9217 701001147 FL
Method
                   BLASTX
NCBI GI
                   g1708993
BLAST score
                   863
E value
                   7.0e-93
Match length
                  195
                   86
% identity
NCBI Description
                  CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
                   (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
                  >gi 2129567 pir S61429 cystathionine beta-lyase (EC
                   4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511)
                  cystathionine beta-lyase [Arabidopsis thaliana]
                   146
Seq. No.
                   84 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir063g05b1
                  BLASTX
Method
NCBI GI
                  g2129753
BLAST score
                   1559
                  0.0e + 00
E value
Match length
                   466
                  85
% identity
NCBI Description
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
                   thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                   [Arabidopsis thaliana]
Seq. No.
                  147
Contig ID
                  85 1.R1040
5'-most EST
                  ssr700556066.h1
Method
                  BLASTX
NCBI GI
                  g4490297
BLAST score
                  717
                  3.0e-75
E value
Match length
                   656
% identity
                  34
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  148
Contig ID
                  85 2.R1040
5'-most EST
                  g5688438
Method
                  BLASTX
NCBI GI
                  g4490297
BLAST score
                  270
E value
                  1.0e-23
Match length
                  129
% identity
                  41
NCBI Description
                  (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  86_1.R1040
5'-most EST
```

epx701108161.hl

BLASTX

NCBI Description

```
g1709205
NCBI GI
BLAST score
                  1051
E value
                   1.0e-115
Match length
                  268
                  74
% identity
                  MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL
NCBI Description
                  MONOPHOSPHATASE 3) >gi_1098971 (U39059) myo-inositol
                  monophosphatase 3 [Lycopersicon esculentum]
Seq. No.
                  86 2.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy001g09b1
Method
                  BLASTX
NCBI GI
                  g1709205
BLAST score
                  1092
E value
                  1.0e-119
Match length
                  268
                  77
% identity
                  MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL
NCBI Description
                  MONOPHOSPHATASE 3) >gi 1098971 (U39059) myo-inositol
                  monophosphatase 3 [Lycopersicon esculentum]
                  151
Seq. No.
                  86 3.R1040
Contig ID
5'-most EST
                  LIB3092-041-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3914097
                  208
BLAST score
E value
                  5.0e-31
Match length
                  102
                  70
% identity
                  MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL
NCBI Description
                  MONOPHOSPHATASE) >gi 2708322 (AF037220) inositol
                  monophosphatase [Mesembryanthemum crystallinum]
Seq. No.
                  87 1.R1040
Contig ID
5'-most EST
                  CPR9728:2F701150047 FL
Method
                  BLASTX
NCBI GI
                  g2245036
BLAST score
                  1287
                  1.0e-142
E value
Match length
                  391
% identity
NCBI Description
                   (Z97342) triacylglycerol lipase homolog [Arabidopsis
                  thaliana]
                  153
Seq. No.
                  87 2.R1040
Contig ID
5'-most EST
                  CPR9727 FL
Method
                  BLASTX
NCBI GI
                  g2245036
BLAST score
                  1289
                  1.0e-142
E value
Match length
                  381
% identity
```

(Z97342) triacylglycerol lipase homolog [Arabidopsis

NCBI GI

E value

. .

BLAST score

Match length

## thaliana]

```
154
Seq. No.
                   88 1.R1040
Contig ID
                   CPR10281:2F700737217_FL
5'-most EST
Method
                   BLASTN
NCBI GI
                   g476215
                   912
BLAST score
                   0.0e + 00
E value
                   1756
Match length
                   91
% identity
                   Glycine max Century 84 p24 oleosin isoform B gene, complete
NCBI Description
                   155
Seq. No.
                   88 2.R1040
Contig ID
                   g5688194
5'-most EST
                   BLASTN
Method
                   g944829
NCBI GI
                   856
BLAST score
E value
                   0.0e + 00
                   860
Match length
                   100
% identity
                   G.max mRNA for 24 kDa oleosin isoform (clone P24/91)
NCBI Description
Seq. No.
                   88 3.R1040
Contig ID
5'-most EST
                   CPR10278:2F700678725_FL
Method
                   BLASTN
NCBI GI
                   g476213
BLAST score
                   907
                   0.0e + 00
E value
Match length
                   1025
                   97
% identity
                   Glycine max Century 84 p24 oleosin isoform A gene, complete
NCBI Description
                   cds
                   157
Seq. No.
                   88 8.R1040
Contig ID
                   zpv700759006.h1
5'-most EST
Method
                   BLASTN '
NCBI GI
                   g476213
BLAST score
                   172
                   4.0e-92
E value
Match length
                   276
% identity
                   91
                   Glycine max Century 84 p24 oleosin isoform A gene, complete
NCBI Description
                   cds
                   158
Seq. No.
                   91 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy089b10b1
Method
                   BLASTX
```

g4126401

1.0e-178

1596

Method

```
% identity
                  (AB011795) flavanone 3-hydroxylase [Citrus sinensis]
NCBI Description
                  159
Seq. No.
                  92 1.R1040
Contig ID
5'-most EST
                  fC-gmse700669702f4
Seq. No.
                  160
                  92 2.R1040
Contig ID
5'-most EST
                  CPR10713 FL
Method
                  BLASTX
NCBI GI
                  g1332411
BLAST score
                  1410
                  1.0e-157
E value
                  331
Match length
                  78
% identity
NCBI Description (D85102) dihydroflavonol 4-reductase [Rosa hybrida]
Seq. No.
                  161
                  92 3.R1040
Contig ID
5'-most EST
                  jC-gmst02400075d12d1
                  BLASTX
Method
NCBI GI
                  g1706377
                  250
BLAST score
                  4.0e-21
E value
                  79
Match length
                  66
% identity
NCBI Description
                  DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
                  4-REDUCTASE) >gi 499018 emb CAA53578 (X75964)
                  dihydroflavonol reductase [Vitis vinifera]
Seq. No.
                  162
                  92 4.R1040
Contig ID
                  k11701212272.h1
5'-most EST
Method
                  BLASTX
                  g1888485
NCBI GI
BLAST score
                  657
                  6.0e-69
E value
Match length
                  164
                  76
% identity
                 (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
NCBI Description
Seq. No.
                  163
Contig ID
                  92 5.R1040
5'-most EST
                  jsh701065818.hl
                  BLASTX
Method
NCBI GI
                  q1888485
BLAST score
                  312
E value
                  7.0e-29
Match length
                  71
                  83
% identity
                  (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
NCBI Description
Seq. No.
Contig ID
                  93 1.R1040
5'-most EST
                  CPR10721 FL
```

BLASTX

E value

```
NCBI GI
                  q1488255
BLAST score
                  1899
                  0.0e+00
E value
Match length
                  483
                  74
% identity
NCBI Description
                   (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
                  >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase
                   (FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)
                  ferulate-5-hydroxylase [Arabidopsis thaliana]
                  165
Seq. No.
Contig ID
                  93 2.R1040
5'-most EST
                  LIB3170-046-Q1-J1-B7
Method
                  BLASTX
NCBI GI
                  g1488255
BLAST score
                  553
E value
                  1.0e-56
Match length
                  125
                  82
% identity
NCBI Description
                   (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
                  >gi 2961381 emb CAA18128_ (AL022141) ferulate-5-hydroxylase
                  (FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)
                  ferulate-5-hydroxylase [Arabidopsis thaliana]
Seq. No.
                  166
Contig ID
                  93 3.R1040
5'-most EST
                  uC-gmflminsoy082h04b1
Method
                  BLASTX
NCBI GI
                  g1488255
BLAST score
                  726
E value
                  4.0e-77
Match length
                  174
                  76
% identity
NCBI Description
                  (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
                  >gi 2961381 emb CAA18128 (AL022141) ferulate-5-hydroxylase
                  (FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)
                  ferulate-5-hydroxylase [Arabidopsis thaliana]
Seq. No.
                  167
Contig ID
                  94 1.R1040
5'-most EST
                  CPR10745 FL
Method
                  BLASTX
NCBI GI
                  q3660465
BLAST score
                  563
                  1.0e-57
E value
Match length
                  191
% identity
                  (AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  168
Contig ID
                  95 1.R1040
5'-most EST
                  LIB3052-012-Q1-N1-D4
Method
                  BLASTX
NCBI GI
                  q3097321
BLAST score
                  1840
```

0.0e + 00

```
379
Match length
                   90
% identity
NCBI Description
                   (AB013289) Bd 30K [Glycine max]
Seq. No.
                   169
                   95 6.R1040
Contig ID
                   tx<del>t</del>700733563.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3097320
BLAST score
                   264
E value
                   1.0e-147
Match length
                   357
                   97
% identity
NCBI Description
                   Glycine max gene for Bd 30K, complete cds
Seq. No.
Contig ID
                   96 1.R1040
                   CPR10171 FL
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3452139
BLAST score
                   124
E value
                   2.0e-62
Match length
                   312
% identity
                   88
NCBI Description
                   Glycine max mRNA for resistance protein, partial
Seq. No.
                   171
                   98 1.R1040
Contig ID
5'-most EST
                   k1\overline{1}701215045.h1
Method
                   BLASTX
NCBI GI
                   g1213629
BLAST score
                   1711
                   0.0e + 00
E value
Match length
                   480
% identity
                   68
NCBI Description
                   (X95991) pectinesterase [Prunus persica]
Seq. No.
                   98 2.R1040
Contig ID
5'-most EST
                   kl1701204315.h2
Method
                   BLASTX
NCBI GI
                   g1213629
BLAST score
                   220
                   7.0e-18
E value
Match length
                   91
% identity
                   52
                   (X95991) pectinesterase [Prunus persica]
NCBI Description
Seq. No.
                   173
                   99 1.R1040
Contig ID
5'-most EST
                   CPR10679:2F701202691H1 FL
Method
                   BLASTX
                   g2832625
NCBI GI
BLAST score
                   742
E value
                   2.0e-78
Match length
                   329
                   46
% identity
```

```
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                   174
                   101 1.R1040
Contig ID
5'-most EST
                   cpr9972_FL
Method
                   BLASTX
NCBI GI
                   g4100321
BLAST score
                   434
E value
                   1.0e-42
Match length
                   203
% identity
                   45
                   (U96642) A sunflower resistance gene homolog, partial cds
NCBI Description
                   [Helianthus annuus]
                   175
Seq. No.
                   102 1.R1040
Contig ID
                   CPR2854 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g120663
BLAST score
                   1673
                   0.0e+00
E value
Match length
                   429
                   78
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,
NCBI Description
                   CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -
                   garden pea >gi 309671 (M55147) glyceraldehyde-3-phosphate
                   dehydrogenase \overline{B} subunit [Pisum sativum]
                   176
Seq. No.
                   104 1.R1040
Contig ID
5'-most EST
                   cpr6672:2F701214276 FL
Method
                   BLASTX
NCBI GI
                   g2258315
BLAST score
                   174
                   6.0e-12
E value
Match length
                   193
                   39
% identity
                   (AF004878) resistance complex protein I2C-1 [Lycopersicon
NCBI Description
                   esculentum]
                   177
Seq. No.
                   105 1.R1040
Contig ID
5'-most EST
                   CPR10672:2F701213889H1 FL
Method
                   BLASTX
NCBI GI
                   q543616
BLAST score
                   344
                   6.0e-32
E value
Match length
                   213
% identity
                   40
                   kunitz type subtilisin inhibitor, CLSI-II - Canavalia
NCBI Description
                   lineata
Seq. No.
                   178
Contig ID
                   106 4.R1040
```

leu701154480.h1

Seq. No.

```
Method
                   BLASTX
NCBI GI
                   q541849
BLAST score
                   740
E value
                   2.0e-96
                   253
Match length
% identity
                   69
                   anthranilate synthase (EC 4.1.3.27) beta chain -
NCBI Description
                   Arabidopsis thaliana >gi 403434 (L22585) anthranilate
                   synthase beta subunit [Arabidopsis thaliana]
                   179
Seq. No.
                   106 5.R1040
Contig ID
5'-most EST
                   LIB3028-047-Q1-B1-C9
Method
                   BLASTN
NCBI GI
                   q1173641
BLAST score
                   837
E value
                   0.0e+00
Match length
                   1175
% identity
                   96
                   Glycine max lipoxygenase (lox7) mRNA, complete cds
NCBI Description
Seq. No.
                   106 6.R1040
Contig ID
                   kl1701202328.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1928991
BLAST score
                   306
E value
                   8.0e-28
                   90
Match length
% identity
                   73
                   (U92815) heat shock protein 70 precursor [Citrullus
NCBI Description
                   lanatus]
Seq. No.
                   181
                   106 7.R1040
Contig ID
5'-most EST
                   epx701108350.hl
Method
                   BLASTX
NCBI GI
                   q1236949
BLAST score
                   964
E value
                   0.0e+00
                   858
Match length
                   63
% identity
                   (U50075) lipoxygenase L-5 [Glycine max]
NCBI Description
Seq. No.
                   182
                   106 8.R1040
Contig ID
                   g1173641_FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1173642
BLAST score
                   1190
E value
                   0.0e+00
                   854
Match length
                   47
% identity
                   (U36191) lipoxygenase [Glycine max]
NCBI Description
                   >gi 1588566 prf 2208476A lipoxygenase [Glycine max]
```

```
106 9.R1040
Contig ID
5'-most EST
                  LIB3106-026-Q1-K1-H7
Method
                  BLASTX
                  g585418
NCBI GI
BLAST score
                  758
                  0.0e + 00
E value
Match length
                  855
% identity
                  38
                  LIPOXYGENASE-4 (L-4) (VSP94) >gi 2160320 dbj BAA03101
NCBI Description
                   (D13999) lipxygenase L-4 [Glycine max]
Seq. No.
                  108_1.R1040
Contig ID
                  jC-gmro02910022e06d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g115608
BLAST score
                  1619
                  0.0e+00
E value
Match length
                  314
                  98
% identity
                  PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE)
NCBI Description
                  >gi_22563_emb_CAA33316_ (X15238) phosphoenolpyruvate
                  carboxylase (AA 1 - 970) [Zea mays]
                  185
Seq. No.
                  109 1.R1040
Contig ID-
5'-most EST
                  CPR10669:2F701207222H1 FL
Seq. No.
                  186
                  110 1.R1040
Contig ID
                  CPR10386 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2529678
BLAST score
                  402
                  1.0e-38
E value
                  190
Match length
                  31
% identity
                  (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  112 1.R1040
Contig ID
5'-most EST
                  k11701212463.h1
                  BLASTX
Method
NCBI GI
                  g1619602
BLAST score
                  602
                   4.0e-62
E value
Match length
                  215
% identity
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                  188
Seq. No.
Contig ID
                  112 3.R1040
                  k11701205638.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1619602
BLAST score
                  234
```

1.0e-19

E value

NCBI GI

```
96
Match length
                  52
% identity
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                  189
Seq. No.
                  113 1.R1040
Contig ID
5'-most EST
                  701060596H1.SEQ FL
Method
                  BLASTX
NCBI GI
                  q134151
BLAST score
                  218
                  2.0e-17
E value
                  109
Match length
                  41
% identity
                  3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID
NCBI Description
                  5-ALPHA-REDUCTASE 1) (SR TYPE 1) >gi_1079480_pir__A55274
                  3-oxo-5alpha-steroid 4-dehydrogenase (EC 1.3.99.5) - human
                  >gi_177767 (M32313) steroid 5-alpha-reductase (EC 1.3.99.5)
                  [Homo sapiens] > gi_338476 (M68886) steroid
                  5-alpha-reductase [Homo sapiens] >gi_3360435 (AF052126)
                  steroid 5-alpha-reductase [Homo sapiens]
                  >gi 4507201 ref NP_001038.1_pSRD5A1
                  steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5
                  alpha-steroid delta 4-dehydrogenase alpha 1)
                  190
Seq. No.
                  117 1.R1040
Contig ID
                  CPR9734 FL
5'-most EST
                  BLASTX
Method
                  g3135672
NCBI GI
                  161
BLAST score
                  3.0e-10
E value
Match length
                  118
                  39
% identity
NCBI Description
                  (AF064070) putative 1-acyl-sn-glycerol-3-phosphate
                  acyltransferase [Burkholderia pseudomallei]
                  191
Seq. No.
                  117 2.R1040
Contiq ID
5'-most EST
                  leu701157888.h1
                  192
Seq. No.
                  118 1.R1040
Contig ID
5'-most EST
                  700732879H1.SEQ FL
                  BLASTX
Method
NCBI GI
                  g3873678
                  162
BLAST score
                  7.0e-11
E value
                  79
Match length
                  42
% identity
                  (Z71178) Similarity with yeast hypothetical protein (Swiss
NCBI Description
                  prot accession number P40526) [Caenorhabditis elegans]
                  193
Seq. No.
                  119 1.R1040
Contig ID
5'-most EST
                  asn701132823.h1
Method
                  BLASTX
```

g3738284

```
BLAST score
                   448
E value
                   8.0e-44
Match length
                   239
% identity
                   46
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   194
Seq. No.
Contig ID
                   119 2.R1040
5'-most EST
                   jC-gmle01810049d01d1
                  195
Seq. No.
                   119 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy049e04b1
                   196
Seq. No.
                   119 4.R1040
Contig ID
5'-most EST
                   zhf700964040.hl
Method
                   BLASTX
NCBI GI
                   g3738284
BLAST score
                   303
E value
                   2.0e-27
Match length
                  78
                  71
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120 2.R1040
Contig ID
5'-most EST
                  g5510071
Method
                  BLASTX
NCBI GI
                   g1255954
BLAST score
                   239
E value
                   3.0e-26
Match length
                   110
% identity
                   59
NCBI Description
                  (Z70677) thioredoxin [Ricinus communis]
Seq. No.
                   198
                  120 3.R1040
Contig ID
5'-most EST
                  g5687937
Method
                  BLASTN
NCBI GI
                   g169972
BLAST score
                   1204
E value
                   0.0e + 00
Match length
                   1744
% identity
                   96
                  Soybean glycinin A-la-B-x subunit mRNA, complete cds
NCBI Description
Seq. No.
                  120 4.R1040
Contig ID
5'-most EST
                  LIB3072-059-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  g218264
BLAST score
                  1281
                  0.0e+00
E value
Match length
                  1751
% identity
                   95
```

NCBI Description Glycine max mRNA for glycinin A2Bla subunit, complete cds

```
200
Seq. No.
                   122 1.R1040
Contig ID
                   LIB3050-003-Q1-E1-G6
5'-most EST
                   BLASTX
Method
                   g2511541
NCBI GI
BLAST score
                   1505
E value
                   1.0e-168
Match length
                   392
% identity >
                   76
                   (AF020787) DNA-binding protein GBP16 [Oryza sativa]
NCBI Description
                   201
Seq. No.
                   122 2.R1040
Contig ID
                   jC-gmle01810085c10d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4539457
BLAST score
                   613
E value
                   3.0e-63
Match length
                   308
                   49
% identity
                   (AL049500) heat shock transcription factor-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   202
Seq. No.
                   122 3.R1040
Contig ID
                   fC-gmro700846171a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2511541
BLAST score
                   909
                   2.0e-98
E value
Match length
                   251
                   77
% identity
                   (AF020787) DNA-binding protein GBP16 [Oryza sativa]
NCBI Description
Seq. No.
                   122 4.R1040
Contig ID
5'-most EST
                   awf700837002.hl
Method
                   BLASTX
NCBI GI
                   g4539457
BLAST score
                   586
                   3.0e-60
E value
Match length
                   255
% identity
NCBI Description
                   (AL049500) heat shock transcription factor-like protein
                   [Arabidopsis thaliana]
                   204
Seq. No.
                   122 6.R1040
Contig ID
                   fC-\overline{g}mro700864991g1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2511541
BLAST score
                   331
E value
                   2.0e-30
Match length
                   77
% identity
NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]
```

```
205
Seq. No.
                  122 7.R1040
Contig ID
                  LIB3170-029-Q1-J1-G11
5'-most EST
                  BLASTX
Method
                  g3645985
NCBI GI
BLAST score
                  482
                  3.0e-48
E value
                  84
Match length
                  96
% identity
                   (AL031581) 1-evidence=predicted by content;
NCBI Description
                  1-method=genefinder;084; 1-method score=23.36;
                  1-evidence end; 2-evidence=predicted by match;
                  2-match accession=AA141041;
                  2-match description=CK01110.3prime CK Drosophila
                  melanogaster
                  206
Seq. No.
                  122 8.R1040
Contig ID
                  g4396625
5'-most EST
Method
                  BLASTX
                  g3645985
NCBI GI
BLAST score
                  479
E value
                  4.0e-48
                  84
Match length
% identity
                   (AL031581) 1-evidence=predicted by content;
NCBI Description
                  1-method=genefinder;084; 1-method_score=23.36;
                  1-evidence_end; 2-evidence=predicted by match;
                  2-match accession=AA141041;
                  2-match description=CK01110.3prime CK Drosophila
                  melanogaster
                  207
Seq. No.
                  122 9.R1040
Contig ID
                  2DC-01-Q1-B1-H1
5'-most EST
Method
                  BLASTX
                  g3645985
NCBI GI
BLAST score
                  428
                  3.0e-42
E value
                  74
Match length
% identity
                   (AL031581) 1-evidence=predicted by content;
NCBI Description
                  1-method=genefinder;084; 1-method_score=23.36;
                  1-evidence_end; 2-evidence=predicted by match;
                  2-match accession=AA141041;
                  2-match_description=CK01110.3prime CK Drosophila
                  melanogaster
                  208
Seq. No.
                  122 11.R1040
Contig ID
5'-most EST
                  LIB3028-028-Q1-B1-B8
                  BLASTX
Method
NCBI GI
                  g3645985
BLAST score
                  245
E value
                  7.0e-21
Match length
                   41
```

```
% identity
                   (AL031581) 1-evidence=predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-method_score=23.36;
                  1-evidence_end; 2-evidence=predicted by match;
                  2-match accession=AA141041;
                  2-match description=CK01110.3prime CK Drosophila
                  melanogaster
                  209
Seq. No.
                  124 1.R1040
Contig ID
                  CPR10667:2F701214015H1 FL
5'-most EST
                  BLASTX
Method
                  q535454
NCBI GI
                  962
BLAST score
                   1.0e-104
E value
                  309
Match length
                  59
% identity
                   (U13940) cysteine proteinase [Alnus glutinosa]
NCBI Description
                  210
Seq. No.
                  124 2.R1040
Contig ID
                  LIB3050-026-Q1-K1-D9 :
5'-most EST
                  BLASTX
Method
NCBI GI
                  q535454
BLAST score
                  238
                  5.0e-20
E value
                  94
Match length
                   51
% identity
                  (U13940) cysteine proteinase [Alnus glutinosa]
NCBI Description
                  211
Seq. No.
                  124 3.R1040
Contig ID
                  k11701211192.hl
5'-most EST
                  BLASTX
Method
                  g2944446
NCBI GI
BLAST score
                  177
                   3.0e-13
E value
Match length
                  51
% identity
                   (AF050756) cysteine endopeptidase precursor [Ricinus
NCBI Description
                  communis]
                  212
Seq. No.
Contig ID
                  125 1.R1040
                  CPR10665:2F701213140H1 FL
5'-most EST
                  BLASTX
Method
                  q3688284
NCBI GI
                  1204
BLAST score
                   1.0e-132
E value
Match length
                   371
% identity
                   (AJ011567) lanatoside 15'-O-acetylesterase [Digitalis
NCBI Description
                  lanata]
Seq. No.
                   213
```

126 1.R1040

LIB3051-042-Q1-K1-H5

Contig ID

5'-most EST

Method

BLASTX

```
Method
                  BLASTX
NCBI GI
                  g1946364
BLAST score
                  1416
                  1.0e-157
E value
Match length
                   420
                   64
% identity
                  (U93215) lipase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  214
                  127 1.R1040
Contig ID
                  CPR6969:2F700980490 FL
5'-most EST
Method
                  BLASTX
                  q4165132
NCBI GI
BLAST score
                  1783
                  0.0e+00
E value
                   483
Match length
% identity
                   69
                   (AF098292) endo-beta-1,4-D-glucanase [Lycopersicon
NCBI Description
                  esculentum]
                  215
Seq. No.
                  127 2.R1040
Contig ID
                  LIB3109-002-Q1-K2-H3
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3170524
BLAST score
                  104
                  3.0e-51
E value
                  224
Match length
                  87
% identity
                  Fragaria x ananassa cellulase (Cel2) mRNA, complete cds
NCBI Description
                  216
Seq. No.
                  130 1.R1040
Contig ID
5'-most EST
                  k11701211539.h1
Method
                  BLASTX
NCBI GI
                  g2367431
BLAST score
                  1358
                  1.0e-150
E value
Match length
                  467
% identity
                  56
                  (AF000403) putative cytochrome P450 [Lotus japonicus]
NCBI Description
                  217
Seq. No.
                  131 1.R1040
Contig ID
5'-most EST
                  CPR9001:2F700903466 FL
Method
                  BLASTX
NCBI GI
                  g3212880
BLAST score
                  1185
                  1.0e-159
E value
                  455
Match length
% identity
                   (AC004005) putative Mlo protein [Arabidopsis thaliana]
NCBI Description
                  218
Seq. No.
                  131 2.R1040
Contig ID
5'-most EST
                  pcp700989120.hl
```

```
NCBI GI
                   g2765817
BLAST score
                   404
                   2.0e-39
E value
Match length
                   135
                   67
% identity
                   (Z95352) AtMlo-h1 [Arabidopsis thaliana]
NCBI Description
                   >gi 3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
Seq. No.
                   219
                   131 4.R1040
Contig ID
5'-most EST
                   fua701038423.hl
Method
                   BLASTX
NCBI GI
                   q2765817
BLAST score
                   291
                   3.0e-26
E value
Match length
                   88
                   62
% identity
NCBI Description
                   (Z95352) AtMlo-h1 [Arabidopsis thaliana]
                   >gi 3892049 gb AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
                   220
Seq. No.
                   132 1.R1040
Contig ID
5'-most EST
                   leu701150403.h1
Method
                   BLASTX
NCBI GI
                   g2213598
BLAST score
                   389
E value
                   5.0e-37
Match length
                   312
                   16
% identity
                   (AC000348) T7N9.18 [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   133 1.R1040
5'-most EST
                   fC-zmf1700343886 FL
Method
                   BLASTX
NCBI GI
                   q4580398
BLAST score
                   746
E value
                   6.0e-79
Match length
                   198
                   71
% identity
                   (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   222
                   134 1.R1040
Contig ID
5'-most EST
                   fC-zmf1700344343 FL
Method
                   BLASTX
NCBI GI
                   q3482921
BLAST score
                   264
E value
                   2.0e-22
                   79
Match length
                   62
% identity
                   (AC003970) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

% identity

```
Contig ID
                   135 1.R1040
5'-most EST
                   fC-zmf1700352002_FL
Method
                   BLASTX
NCBI GI
                   g585593
BLAST score
                   220
E value
                   3.0e-17
Match length
                  188
% identity
                   27
NCBI Description
                  NUCLEAR PORE GLYCOPROTEIN P62 (NUCLEOPORIN P62)
                  >gi 432654 emb CAA41411 (X58521) nucleoporin p62 [Homo
                  sapiens]
                  224
Seq. No.
Contig ID
                  136 1.R1040
5'-most EST
                  fC-zmle700422033_FL
Seq. No.
                  225
                   137 1.R1040
Contig ID
5'-most EST
                  fC-zmf1700351889 FL
Seq. No.
                  226
                  138 1.R1040
Contig ID
5'-most EST
                  LIB3093-038-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g4126473
BLAST score
                  876
E value
                  3.0e-94
Match length
                  211
% identity
NCBI Description
                   (AB014884) adenylyl cyclase associated protein [Gossypium
                  hirsutum]
                  227
Seq. No.
Contig ID
                  139 1.R1040
5'-most EST
                  fC-gmst700790741 FL
Method
                  BLASTN
NCBI GI
                  q1785614
BLAST score
                  49
E value
                  5.0e-18
Match length
                  126
% identity
                  85
NCBI Description
                  Pisum sativum protein kinase homolog PsPK4 mRNA, complete
Seq. No.
                  228
Contig ID
                  139 2.R1040
5'-most EST
                  uC-gmflminsoy058f07b1
Seq. No.
                  229
Contig ID
                  139 3.R1040
5'-most EST
                  LIB3094-030-Q1-K1-D3
Method
                  BLASTN
NCBI GI
                  g1480927
BLAST score
                  170
E value
                  2.0e-90
Match length
                  301
```

```
NCBI Description Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed
                  pseudogene
Seq. No.
                  230
                  139 4.R1040
Contig ID
5'-most EST
                  LIB3094-072-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  g1480927
BLAST score
                  97
                  7.0e-47
E value
Match length
                  211
                  91
% identity
NCBI Description
                  Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed
                  pseudogene
Seq. No.
                  231
                  139 5.R1040
Contig ID
                  jsh701064823.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g1480927
BLAST score
                  93
                  1.0e-44
E value
Match length
                  137
% identity
                  92
                  Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed
NCBI Description
                  pseudogene
                  232
Seq. No.
                  140 1.R1040
Contig ID
5'-most EST
                  fC-zmf1700344725 FL
Method
                  BLASTX
NCBI GI
                  g3786005
BLAST score
                  1535
                  1.0e-171
E value
Match length
                  365
% identity
                   (AC005499) putative phosphoethanolamine
NCBI Description
                  cytidylyltransferase [Arabidopsis thaliana]
Seq. No.
                  233
                  141 1.R1040
Contig ID
5'-most EST
                  fC-zmf1700352293 FL
Method
                  BLASTX
NCBI GI
                  g127112
BLAST score
                  450
E value
                  4.0e-44
Match length
                  175
                  51
% identity
                  MAK16 PROTEIN >qi 73269 pir BVBYK6 MAK16 protein - yeast
NCBI Description
                  (Saccharomyces cerevisiae) >gi 171880 (J03852) MAK16
                  protein [Saccharomyces cerevisiae] >qi 595561 (U12980)
                  Mak16p: putative nuclear protein [Saccharomyces cerevisiae]
                  234
Seq. No.
Contig ID
                  142 1.R1040
5'-most EST
                  fC-gmse700645507 FL
Method
                  BLASTN
```

```
g791097
NCBI GI
BLAST score
                   258
E value
                   1.0e-143
                   773
Match length
                   90
% identity
                   P.vulgaris plsB mRNA
NCBI Description
Seq. No.
                   143 1.R1040
Contig ID
5'-most EST
                  LIB3107-017-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                   g1666096
BLAST score
                   1108
E value
                   1.0e-121
Match length
                   308
                   69
% identity
                   (Y09113) dioxygenase [Marah macrocarpus]
NCBI Description
Seq. No.
                   236
                   144 1.R1040
Contig ID
5'-most EST
                   fC-gmse700667947f1
                  BLASTX
Method
                   g3128225
NCBI GI
BLAST score
                   1076
E value
                   1.0e-117
Match length
                   322
                   68
% identity
                   (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   144 2.R1040
Contig ID
5'-most EST
                   fC-gmse700674467a2
Method
                  BLASTX
NCBI GI
                  g3128225
                  170
BLAST score
                   8.0e-12
E value
                   45
Match length
% identity
                   (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                   238
Seq. No.
                   145 1.R1040
Contig ID
5'-most EST
                   fC-zmse700838611 FL
                  BLASTX
Method
NCBI GI
                  g2252846
                   681
BLAST score
                   7.0e-90
E value
                  310
Match length
                   64
% identity
NCBI Description
                   (AF013293) Similar to phospholipase D [Arabidopsis
                  thaliana]
                  239
Seq. No.
                  146 1.R1040
Contig ID
5'-most EST
                  fC-zmse700838837 FL
```

```
147 1.R1040
Contig ID
5'-most EST
                   kl1701210137.hl
Method
                   BLASTX
NCBI GI
                   g4510395
BLAST score
                   1198
E value
                   1.0e-146
                   394
Match length
% identity
                   66
NCBI Description
                   (AC006587) putative beta-galactosidase precursor
                   [Arabidopsis thaliana]
Seq. No.
                   148 1.R1040
Contig ID
                   zhf700960184.h1
5'-most EST
                  BLASTX
Method
                   g3914394
NCBI GI
BLAST score
                   2455
                   0.0e+00
E value
Match length
                   559
                   83
% identity
                   2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                   >gi_2118335_pir__S60473 phosphoglycerate mutase (EC
                   5.4.2.1) - common ice plant >gi 602426 (U16021)
                  phosphoglyceromutase [Mesembryanthemum crystallinum]
                   242
Seq. No.
                   149 1.R1040
Contig ID
5'-most EST
                   uaw700661032.h1
Method
                  BLASTX
                   g2244744
NCBI GI
BLAST score
                   347
                   3.0e-32
E value
Match length
                  122
% identity
                   57
                   (Y13676) bZIP DNA-binding protein [Antirrhinum majus]
NCBI Description
                   243
Seq. No.
                   149 2.R1040
Contig ID
5'-most EST
                  LIB3049-016-Q1-E1-B3
Method
                  BLASTN
                  g394735
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   52
% identity
                   92
                  Rice lip19 mRNA for basic/leucine zipper protein
NCBI Description
                   244
Seq. No.
                   149 3.R1040
Contig ID
5'-most EST
                   zzp700836073.h1
                  245
Seq. No.
                  149 4.R1040
Contig ID
5'-most EST
                  LIB3028-008-Q1-B1-A1
```

```
150 1.R1040
Contig ID
5'-most EST
                   zsg701120848.hl
Method ·
                  BLASTX
NCBI GI ·
                  g1362002
BLAST score
                   990
                  1.0e-107
E value
Match length
                  242
% identity
                  77
NCBI Description
                  protein kinase 1 - Arabidopsis thaliana >gi 166817 (L05561)
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                  150 2.R1040
Contig ID
5'-most EST
                  uC-qmropic058h06b1
                  BLASTX
Method
NCBI GI
                  g1362002
BLAST score
                  256
                   9.0e-30
E value
Match length
                  130
% identity
                  60
                  protein kinase 1 - Arabidopsis thaliana >gi_166817 (L05561)
NCBI Description
                  protein kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                  151 1.R1040
                  k11701214918.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2459435
BLAST score
                  1494
E value
                  1.0e-166
Match length
                  452
% identity
                  63
                   (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  249
                  152 1.R1040
Contig ID
5'-most EST
                  fC-gmro700562302 FL
Method
                  BLASTX
NCBI GI
                  q1888359
BLAST score
                  294
E value
                  6.0e-33
Match length
                  179
% identity
                   69
NCBI Description
                   (Y11689) 3-ketoacyl-acyl carrier protein synthase III
                   [Arabidopsis thaliana]
                  250
Seq. No.
                  152 2.R1040
Contig ID
                  fC-gmse700854533a1
5'-most EST
Method
                  BLASTX
                  g1706757
NCBI GI
BLAST score
                  1048
                  1.0e-114
E value
                  232
Match length
% identity
                  86
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III A PRECURSOR
NCBI Description
```

251

257

Seq. No.

(BETA-KETOACYL-ACP SYNTHASE III A) (KAS III A) >gi\_1276434 (U15935) beta-ketoacyl-ACP synthase III [Cuphea wrightii]

```
Contig ID
                   153 1.R1040
5'-most EST
                   xpa700793632.hl
Method
                  BLASTX
NCBI GI
                   g2346978
BLAST score
                   344
E value
                   7.0e-32
Match length
                   167
% identity
                   49
NCBI Description
                   (AB006601) ZPT2-14 [Petunia x hybrida]
Seq. No.
                   252
                   153 2.R1040
Contig ID
5'-most EST
                  LIB3049-032-Q1-E1-B4
Method
                  BLASTX
NCBI GI
                   g2346976
BLAST score
                   356
E value
                   2.0e-33
Match length
                   152
% identity
NCBI Description
                   (AB006600) ZPT2-13 [Petunia x hybrida]
Seq. No.
Contig ID
                  154 1.R1040
                  awf700836660.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2664214
BLAST score
                  189
E value
                   2.0e-13
Match length
                  171
% identity
NCBI Description
                   (AJ222646) G2484-1 [Arabidopsis thaliana]
                  254
Seq. No.
                  154 2.R1040
Contig ID
5'-most EST
                  LIB3170-039-Q1-J1-H5
Seq. No.
                  255
                  155 1.R1040
Contig ID
5'-most EST
                   fC-gmro700566983 FL
                  256
Seq. No.
Contig ID
                  156 1.R1040
5'-most EST
                   fC-gmro700567081 FL
                  BLASTX
Method
                  g1346729
NCBI GI
BLAST score
                  192
E value
                   4.0e-14
Match length
                  198
% identity
                   16
                  PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA >gi_886024
NCBI Description
                   (U23820) protein kinase PkwA [Thermomonospora curvata]
```

Method

NCBI GI

BLASTX

g4115914

```
157 1.R1040
Contig ID
                    q5752858
5'-most EST
Method
                    BLASTX
NCBI GI
                    g2811029
BLAST score
                    385
E value
                    6.0e-37
                    107
Match length
% identity
                    72
NCBI Description
                    ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)
                    (ACETYLORNITHINE TRANSAMINASE) (AOTA)
                    >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine
aminotransferase [Alnus glutinosa]
Seq. No.
                    158 1.R1040
Contig ID
                    fua701037507.hl
5'-most EST
Method
                    BLASTX
                    g1076318
NCBI GI
BLAST score
                    383
E value
                    2.0e-36
Match length
                    109
% identity
NCBI Description
                    dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)
                    precursor - Arabidopsis thaliana (fragment)
>gi_559395_emb_CAA86300_ (Z46230) dihydrolipoamide
                    acetyltransferase (E2) subunit of PDC [Arabidopsis
                    thaliana]
                    259
Seq. No.
                    158 2.R1040
Contig ID
5'-most EST
                    zzp700833589.hl
Method
                    BLASTX
                    g2129473
NCBI GI
BLAST score
                    375
E value
                    1.0e-35
Match length
                    161
                    47
% identity
                    arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                    (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                    260
                    158 3.R1040
Contig ID
5'-most EST
                    fua701041084.hl
                    BLASTX
Method
NCBI GI
                    g2129473
BLAST score
                    325
E value
                    5.0e-30
                    136
Match length
                    49
% identity
                    arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                    (U09556) arabinogalactan-like protein [Pinus taeda]
                    261
Seq. No.
                    159 1.R1040
Contig ID
5'-most EST
                    LIB3049-021-Q1-E1-A2
```

Contig ID 5'-most EST

```
BLAST score
                   524
E value
                    7.0e-53
Match length
                   324
% identity
                   38
NCBI Description
                    (AF118222) contains similarity to Iron/Ascorbate family of
                   oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1_
                    (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis
                   thaliana]
Seq. No.
                   262 ·
                   159 2.R1040
Contig ID
5'-most EST
                   leu701153539.hl
Seq. No.
                   263
Contig ID
                   160 1.R1040
5'-most EST
                   LIB3028-040-Q1-B1-E7
Method
                   BLASTX
NCBI GI
                   q2780955
BLAST score
                   238
E value
                   3.0e-19
Match length
                   214
% identity
                   35
NCBI Description
                   Phosphatidylinositol Transfer Protein Sec14p From
                   Saccharomyces Cerevisiae
Seq. No.
                   264
Contig ID
                   160 2.R1040
5'-most EST
                   LIB3049-026-Q1-E1-A3
Seq. No.
                   265
                   161_1.R1040
Contig ID
5'-most EST
                   jC-qmf102220098b09d1
Method
                   BLASTX
NCBI GI
                   q1352186
BLAST score
                   1271
E value
                   1.0e-140
Match length
                   473
% identity
                   51
                   ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
NCBI Description
                    (CYTOCHROME P450 74) >gi 404866 (U00428) allene oxide
                   synthase [Linum usitatissimum]
Seq. No.
                   161 2.R1040
Contig ID
5'-most EST
                   fC-gmse700751003d2
Method
                   BLASTN
NCBI GI
                   g18662
BLAST score
                   903
                   0.0e + 00
E value
                   974
Match length
% identity
                   98
                   Glycine max hsp 70 gene
NCBI Description
                   267
Seq. No.
                   161 3.R1040
```

jC-gmst02400030e01d1

Contig ID

```
Method
                   BLASTX
NCBI GI
                   q4263779
BLAST score
                  ·540
E value
                   4.0e-55
Match length
                   147
                   67
% identity
                   (AC006068) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   268
                   161 4.R1040
Contig ID
5'-most EST
                   fC-qmro700793925r1
                   BLASTX
Method
NCBI GI
                   q4262242
BLAST score
                   305
E value
                   1.0e-27
Match length
                   129
                   55
% identity
                   (AC006200) NADC homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   161 5.R1040
Contig ID
5'-most EST
                   zpv700760758.h1
Method
                   BLASTN
NCBI GI
                   q18662
BLAST score
                   541
E value
                   0.0e + 00
Match length
                   729
% identity
NCBI Description
                   Glycine max hsp 70 gene
                   270
Seq. No.
                   161 8.R1040
Contig ID
5'-most EST
                   zsg701123403.h1
Method
                   BLASTN
NCBI GI
                   g18662
BLAST score
                   150
E value
                   6.0e-79
Match length
                   202
% identity
                   94
                   Glycine max hsp 70 gene
NCBI Description
Seq. No.
                   162 1.R1040
Contig ID
                   LIB3107-040-Q1-K1-F3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2493494
BLAST score
                   1567
                   1.0e-175
E value
                   428
Match length
% identity
                   SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)
NCBI Description
                   >gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase
                   [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
                   aa]
                   272
Seq. No.
```

163 1.R1040

```
fC-zmst700621904 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q113029
BLAST score
                   1716
E value
                    0.0e+00
Match length
                    452
                    74
% identity
NCBI Description
                   ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                   >gi_68209_pir__WZCNIU isocitrate lyase (EC 4.1.3.1) -
upland cotton >gi_18486_emb_CAA36381_ (X52136) isocitrate
                    lyase (AA 1-576) [Gossypium hirsutum]
                    273
Seq. No.
Contig ID
                    164 1.R1040
5'-most EST
                    fC-qmle700786490 FL
                   BLASTX
Method
NCBI GI
                    g4204849
BLAST score
                   948
E value
                    1.0e-102
Match length
                    223
% identity
                    78
                    (U55875) protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                    165 1.R1040
                    LIB3109-022-Q1-K1-G3
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3688123
                    2069
BLAST score
E value
                    0.0e+00
Match length
                    619
% identity
                    66
                    (AJ006293) granule-bound starch synthase [Antirrhinum
NCBI Description
                   majus]
Seq. No.
                    275
                    165 5.R1040
Contig ID
                    LIB\overline{3}092-018-Q1-K1-G2
5'-most EST
Seq. No.
                    166 1.R1040
Contig ID
                    fC-zmro700835672 FL
5'-most EST
                    BLASTX
Method
                    g3450842
NCBI GI
BLAST score
                    894
E value
                    3.0e-96
Match length
                    269
                    62
% identity
                    (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                    sativa]
Seq. No.
                    277
                    167 1.R1040
Contig ID
5'-most EST
                    fC-zmro700835718 FL
Method
                    BLASTX
NCBI GI
                    g2829275
```

837

BLAST score

BLAST score

E value

514 4.0e-52

```
1.0e-89
E value
Match length
                  236
% identity
                  70
                  (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
NCBI Description
                  thaliana] >gi_3513740 (AF080118) contains similarity to
                  nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
                  301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
                   (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                  [Arabidopsis thaliana]
Seq. No.
                  278
                  167 2.R1040
Contig ID
5'-most EST
                  LIB3093-031-Q1-K1-H3
                  BLASTX
Method
NCBI GI
                  q2829275
BLAST score
                  125
E value
                  6.0e-09
Match length
                  70
% identity
                  (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
NCBI Description
                  thaliana] >gi_3513740 (AF080118) contains similarity to
                  nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
                  301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1
                   (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                  [Arabidopsis thaliana]
                                        279
Seq. No.
                  168 1.R1040
Contig ID
                  fC-zmro700835944 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3901012
BLAST score
                  1162
                  1.0e-128
E value
Match length
                  274
% identity
                  75
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                  sylvatica]
                  280
Seq. No.
                  168 2.R1040
Contig ID
5'-most EST
                  uC-gmropic070h06b1
Method
                  BLASTX
NCBI GI
                  g3901012
BLAST score
                  1197
E value
                  1.0e-132
Match length
                  278
% identity
                  78
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                  sylvatica]
Seq. No.
                  281
                  168 3.R1040
Contig ID
5'-most EST
                  fC-gmse700670426g2
Method
                  BLASTX
NCBI GI
                  g3901012
```

```
127
Match length
                   69
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   282
Seq. No.
                   168 4.R1040
Contig ID
5'-most EST
                   zzp700832650.hl
Method
                   BLASTX
NCBI GI
                   g3901012
BLAST score
                  1119.
                   1.0e-123
E value
                   249
Match length
% identity
                   80
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   283
Seq. No.
Contig ID
                   168 5.R1040
                   dpv701097331.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3901012
                   327
BLAST score
E value
                   2.0e-30
Match length
                  71
                   87
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
Seq. No.
                   284
                  169 ·1.R1040
Contig ID
5'-most EST
                   fua701039647.hl
Method
                  BLASTX
                  q1915974
NCBI GI
BLAST score
                  1420
E value
                  1.0e-158
Match length
                   319
% identity
                   (U62329) fructokinase [Lycopersicon esculentum] >gi 2102693
NCBI Description
                   (U64818) fructokinase [Lycopersicon esculentum]
                  285
Seq. No.
                  169 2.R1040
Contig ID
5'-most EST
                  uC-gmronoir063d06b1
Method
                  BLASTX
NCBI GI
                  g585973
BLAST score
                  756
                  2.0e-80
E value
Match length
                  182
                  77
% identity
                  FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC
NCBI Description
                  2.7.1.4) - potato >gi 297015 emb CAA78283 (Z12823)
                  fructokinase [Solanum tuberosum] >gi 1095321 prf 2108342A
                  fructokinase [Solanum tuberosum]
Seq. No.
                  286
```

169 3.R1040

Contig ID

E value

```
LIB3055-004-Q1-N1-H3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q585973
BLAST score
                   353
E value
                   4.0e-53
Match length
                   127
% identity
                   89
                   FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823)
NCBI Description
                   fructokinase [Solanum tuberosum] >gi 1095321 prf 2108342A
                   fructokinase [Solanum tuberosum]
                   287
Seq. No.
                   170 1.R1040
Contig ID
                   fC-zmle700426440 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2736286
BLAST score
                   322
E value
                   1.0e-51
Match length
                   125
% identity
                   80
NCBI Description
                   (AF031079) isopentenyl diphosphate isomerase I [Camptotheca
                   acuminata]
Seq. No.
                   288
                   171 5.R1040
Contig ID
5'-most EST
                   LIB3106-113-Q1-K1-C5
Method
                   BLASTN
                   g18730
NCBI GI
BLAST score
                   85
                   7.0e-40
E value
Match length
                   89
                   99
% identity
                   Soybean 4.5 - 5S rRNA intergenic region
NCBI Description
Seq. No.
                   171 6.R1040
Contig ID
                   wvk700685569.h1
5'-most EST
Method
                   BLASTN
                   g18730
NCBI GI
BLAST score
                   72
                   3.0e-32
E value
                   72
Match length
                   100
% identity
                   Soybean 4.5 - 5S rRNA intergenic region
NCBI Description
                   290
Seq. No.
                   171 7.R1040
Contig ID
5'-most EST
                   wrg700791869.hl
Seq. No.
                   291
                   171 8.R1040
Contig ID
5'-most EST
                   LIB3092-010-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g1173218
BLAST score
                   237
```

1.0e-19

BLAST score

```
46
Match length
% identity
                  96
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  292
Seq. No.
                  171 9.R1040
Contig ID
                  LIB3107-079-Q1-K1-G11
5'-most EST
Method
                  BLASTN
NCBI GI
                  g18730
BLAST score
                  85
E value
                  7.0e-40
                  97
Match length
                  97
% identity
                  Soybean 4.5 - 5S rRNA intergenic region
NCBI Description
Seq. No.
                  171 10.R1040
Contig ID
5'-most EST
                  LIB3049-047-Q1-E1-C11
Seq. No.
                  171 11.R1040
Contig ID
5'-most EST
                  uC-gmronoir004f06b1
Seq. No.
                  171 12.R1040
Contig ID
5'-most EST
                  LIB3093-004-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2780192
BLAST score
                  338
E value
                  2.0e-41
Match length
                  178
% identity
                  48
                  (AJ222713) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  296
Seq. No.
                  171 13.R1040
Contig ID
5'-most EST
                  kmv700739214.h1
                  297
Seq. No.
                  171 14.R1040
Contig ID
5'-most EST
                  LIB3049-016-Q1-E1-A4
                  BLASTX
Method
NCBI GI
                  g4140398
BLAST score
                  375
E value
                  6.0e-36
Match length
                  105
                  63
% identity
NCBI Description
                  (AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]
Seq. No.
                  171 15.R1040
Contig ID
5'-most EST
                  jC-gmro02910059f03d1
Method
                  BLASTX
NCBI GI
                  g3152559
```

```
E value
                   1.0e-48
Match length
                   333
% identity
                   40
                   (AC002986) Similarity to A. thaliana gene product
NCBI Description
                   F21M12.20, gb AC000132. EST gb Z25651 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   171 16.R1040
Contig ID
                   zvj700605110.h2
5'-most EST
Method
                   BLASTX
                   g3800878
NCBI GI
BLAST score
                   664
E value
                   4.0e-86
                   201
Match length
% identity
                   63
                   (AF096281) threonine dehydratase/deaminase [Arabidopsis
NCBI Description
                   thaliana]
                   300
Seq. No.
                   171 17.R1040
Contig ID
5'-most EST
                  LIB3087-010-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                   g1432083
BLAST score
                   349
                   7.0e-51
E value
                   155
Match length
                   70
% identity
                   (U60981) homolog to Skplp, an evolutionarily conserved
NCBI Description
                   kinetochore protein in budding yeast [Arabidopsis thaliana]
                   >gi 3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana]
                   >gi 3719209 (U97020) UIP1 [Arabidopsis thaliana]
Seq. No.
                   171 18.R1040
Contig ID
5'-most EST
                   uC-gmropic010a05b1
Seq. No.
                   171 19.R1040
Contig ID
5'-most EST
                   wvk700683133.hl
Method
                   BLASTN
NCBI GI
                   g2150129
BLAST score
                  104
E value
                   5.0e-51
Match length
                   344
% identity
                   83
                  Arabidopsis thaliana cytoplasmic ribosomal protein S15a
NCBI Description
                  mRNA, complete cds
Seq. No.
                   171 20.R1040
Contig ID
                   jC-gmst02400027h04d1
5'-most EST
Method
                   BLASTX
                  g3800878
NCBI GI
BLAST score
                  376
E value
                   1.0e-35
```

136

Match length

Match length

```
% identity
                  (AF096281) threonine dehydratase/deaminase [Arabidopsis
NCBI Description
                  thaliana]
                  304
Seq. No.
                  171 21.R1040
Contig ID
                  LIB3040-043-Q1-E1-A11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1173218
                  382
BLAST score
E value
                  2.0e-41
Match length
                  110
% identity
                  90
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  171 22.R1040
Contig ID
5'-most EST
                  uC-gmropic104d08b1
Method
                  BLASTX
NCBI GI
                  g2760606
BLAST score
                  302
E value
                  1.0e-68
Match length
                  165
% identity
                  (AB001568) phospholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Arabidopsis thaliana] >gi_3004869
                  (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                  thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500)
                  phospholipid hydroperoxide glutathione peroxidase
                  [Arabidopsis thaliana]
                  306
Seq. No.
                  171_23.R1040
Contig ID
5'-most EST
                  jC-gmle01810010g10a1
Method
                  BLASTN
NCBI GI
                  q20740
BLAST score
                  258
E value
                  1.0e-142
Match length
                  813
% identity
NCBI Description
                  Pisum sativum mRNA for P protein, a part of glycine
                  cleavage complex
Seq. No.
Contig ID
                  171 24.R1040
                  vzy700754515.h1
5'-most EST
Seq. No.
Contig ID
                  171 25.R1040
5'-most EST
                  LIB3050-018-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  g480618
BLAST score
                  629
E value
                  2.0e-73
```

```
% identity
                  ATAF1 protein - Arabidopsis thaliana (fragment)
NCBI Description
                  >qi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis
                  thaliana]
                   309
Seq. No.
                   171 26.R1040
Contig ID
                  LIB3072-021-Q1-E1-C1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3551838
                   331
BLAST score
E value
                   4.0e-49
                  151
Match length
% identity
                   75
NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]
Seq. No.
                   310
                   171 27.R1040
Contig ID
5'-most EST
                  LIB3138-085-P1-N1-A12
Method
                  BLASTN
NCBI GI
                   g210811
BLAST score
                   163
E value
                   4.0e∸86
                   704
Match length
% identity
                   85
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   311
                   171 28.R1040
Contig ID
                   awf700838388.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g480618
BLAST score
                   423
E value
                   6.0e-41
Match length
                   233
% identity
                   48
                   ATAF1 protein - Arabidopsis thaliana (fragment)
NCBI Description
                   >gi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis
                   thaliana]
Seq. No.
                   312
                   171 29.R1040
Contig ID
                   LIB3107-010-Q1-K1-B8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1350954
BLAST score
                   148
                   5.0e-23
E value
                   129
Match length
                   62
% identity
                   40S RIBOSOMAL PROTEIN S15A >gi 422493_pir__S33498 ribosomal
NCBI Description
                   protein DS15a - fruit fly (Drosophila melanogaster)
                   >gi 311606 emb CAA79771 (Z21673) ribosomal protein 15a
                   (40\overline{S} subunit) [Drosophila melanogaster]
Seq. No.
```

171 30.R1040

Contig ID

```
5'-most EST
                   LIB3049-047-Q1-E1-H10
Method
                   BLASTN
NCBI GI
                   g296357
BLAST score
                    67
                   8.0e-29
E value
Match length
                    403
                   80
% identity
~NCBI Description
                   C.sinensis mRNA csa for salt-associated protein
Seq. No.
                   171 31.R1040
Contig ID
                   LIB3107-049-Q1-K1-D4
5'-most EST
Method
                   BLASTN
NCBI GI
                   q940048
BLAST score
                   79
E value
                    5.0e-36
Match length
                   127
% identity
                   91
NCBI Description
                   Phaseolus vulgaris clone XZT-205 mRNA, partial cds
Seq. No.
                   315
                   171 32.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy304f08b1
Method
                   BLASTX
NCBI GI
                   q4097880
BLAST score
                   2146
E value
                   0.0e + 00
Match length
                   1521
% identity
                   25
NCBI Description
                    (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   172 1.R1040
Contig ID
                   fC-gmf1700905758 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2129855
BLAST score
                   1745
                   0.0e + 00
E value
Match length
                   372
                   87
% identity
NCBI Description
                   mitogen-activated protein kinase MMK2 (EC 2.7.1.-) -
                   alfalfa
                   317
Seq. No.:
                   172 2.R1040
Contig ID
5'-most EST
                   g5127047
Method
                   BLASTN
NCBI GI
                   g1204128
BLAST score
                   272
                   1.0e-151
E value
                   456
Match length
% identity
                   90
                   M.sativa MMK2 mRNA for protein kinase
NCBI Description
Seq. No.
                   318
                   172 3.R1040
Contig ID
5'-most EST
```

uC-gmronoir049d11b1

```
Method
                   BLASTN
NCBI GI
                   g1204128
BLAST score
                   169
                   8.0e-90
E value
Match length
                   325
% identity
                   88
NCBI Description
                  M.sativa MMK2 mRNA for protein kinase
Seq. No.
                   319
Contig ID
                   173 1.R1040
                   fC-gmf1700905635 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2246376
BLAST score
                   418
E value
                   1.0e-40
Match length
                   164
% identity
                   65
                   (Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   174 1.R1040
5'-most EST
                   fC-gmf1700905531 FL
Method
                   BLASTN
NCBI GI
                   g2739045
BLAST score
                   1015
E value
                   0.0e + 00
Match length
                   1015
% identity
                   100
                  Glycine max polyphosphoinositide binding protein Ssh2p
NCBI Description
                   (SSH2) mRNA, complete cds
Seq. No.
                   321
                   175 1.R1040
Contig ID
5'-most EST
                   zhf700957320.h1
Method
                   BLASTX
NCBI GI
                   g1352660
BLAST score
                   219
                   4.0e-17
E value
Match length
                   178
% identity
                   31
                   COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR
NCBI Description
                  >gi 924850 (U26264) CHOp24 [Cricetulus griseus]
Seq. No.
                   176 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800028f01a1
Method
                   BLASTX
NCBI GI
                   g3024013
BLAST score
                   761
E value
                   1.0e-80
Match length
                   304
% identity
                   51
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT
NCBI Description
                   (EIF-2-ALPHA) >gi_2706460_emb_CAA15918.1_ (AL021046)
                   translational initiation factor 2 alpha
```

[Schizosaccharomyces pombe]

- ...

% identity

```
323
Seq. No.
                   176 2.R1040
Contig ID
5'-most EST
                   jC-qmst02400020dc03d1
Method
                  BLASTN
                  q2264313
NCBI GI
BLAST score
                   39
                   2.0e-12
E value
                   47
Match length
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOP10, complete sequence [Arabidopsis thaliana]
                   324
Seq. No.
                   177 1.R1040
Contig ID
5'-most EST
                   kl1701213972.h1
Method
                  BLASTX
                   q3080435
NCBI GI
                   1657
BLAST score
                   0.0e+00
E value
Match length
                   412
                   78
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   178_1.R1040
Contig ID
5'-most EST
                   fC-qmf1700904235 FL
                  BLASTX
Method
NCBI GI
                   q584882
BLAST score
                   781
                   3.0e-83
E value
Match length
                   240
                   40
% identity
                  CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL
NCBI Description
                   CYCLASE) >gi 452446 (U02555) cycloartenol synthase;
                   (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
                   326
Seq. No.
                   179 1.R1040
Contig ID
5'-most EST
                   fC-qmf1700903662 FL
Method
                   BLASTX
NCBI GI
                   g2706515
BLAST score
                   1080
E value
                   1.0e-118
Match length
                   309
                   66
% identity
NCBI Description
                   (Y12689) isoflavone reductase-like protein [Citrus x
                  paradisi]
                   327
Seq. No.
                   180 1.R1040
Contig ID
                   fC-qmf1700902268 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1430846
BLAST score
                   665
E value
                   2.0e-69
                   220
Match length
```



```
NCBI Description
                  (X99210) myb-related transcription factor [Lycopersicon
                   esculentum
Seq. No.
                   328
                   180 2.R1040
Contig ID
5'-most EST
                   ncj700977108.hl
                   329
Seq. No.
Contig ID
                   180 3.R1040
                   leu701150112.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827545
BLAST score
                   379
                   1.0e-36
E value
Match length
                   69
                   94
% identity
                   (AL021635) myb-like protein [Arabidopsis thaliana]
NCBI Description
                   330
Seq. No.
Contig ID
                   181 1.R1040
                   fC-gmst700890686_FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3256068
BLAST score
                   325
E value
                   1.0e-29
Match length
                   135
                   50
% identity
                   (Y14068) Heat Shock Factor 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   182 1.R1040
5'-most EST
                   fC-gmro700844279 FL
                   BLASTX
Method
NCBI GI
                   g2687724
BLAST score
                   1622
E value
                   0.0e + 00
Match length
                   31.8
                   100
% identity
NCBI Description
                   (AJ003245) NADPH:isoflavone reductase [Glycine max]
                   332
Seq. No.
                   182 2.R1040
Contig ID
5'-most EST
                   fua701040175.hl
Method
                   BLASTN
NCBI GI
                   g2687723
BLAST score
                   544
E value
                   0.0e + 00
Match length
                   964
% identity
                   89
NCBI Description
                  Glycine max mRNA for putative NADPH:isoflavone reductase
Seq. No.
                   333
```

Contig ID 182\_3.R1040 5'-most EST g5057872 Method BLASTN NCBI GI g2687723 BLAST score 234

5'-most EST

```
1.0e-129
E value
                  371
Match length
                  93
% identity
                  Glycine max mRNA for putative NADPH:isoflavone reductase
NCBI Description
                  334
Seq. No.
                  183_1.R1040
Contig ID
                  fC-gmst700888747 FL
5'-most EST
Method
                  BLASTX
                  g544015
NCBI GI
BLAST score
                  566
E value
                  4.0e-58
Match length
                  122
% identity
                  80
                  ENDOCHITINASE PRECURSOR >gi_2118033_pir__S59947 chitinase
NCBI Description
                  (EC 3.2.1.14) Al precursor - garden pea
                  >gi 20687 emb CAA45359 (X63899) chitinase [Pisum sativum]
                  335
Seq. No.
                  183 2.R1040
Contig ID
5'-most EST
                  LIB3107-056-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q544015
BLAST score
                  1304
E value
                  1.0e-144
Match length
                  319
% identity
                  73
                  ENDOCHITINASE PRECURSOR >gi_2118033_pir__S59947 chitinase
NCBI Description
                  (EC 3.2.1.14) Al precursor - garden pea
                  >qi 20687 emb CAA45359 (X63899) chitinase [Pisum sativum]
Seq. No.
                  336
                  184_1.R1040
Contig ID
                  uC-gmrominsoy188g06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2924777
BLAST score
                  295
E value
                  3.0e-26
                  265
Match length
% identity
                  (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  337
Seq. No.
                  185 1.R1040
Contig ID
5'-most EST
                  fC-gmst700889963 FL
Method
                  BLASTX
NCBI GI
                  q1651197
BLAST score
                  416
                  1.0e-40
E value
Match length
                  135
% identity
NCBI Description
                  (D88156) tropinone reductase-I [Hyoscyamus niger]
Seq. No.
                  338
Contig ID
                  186 1.R1040
```

fC-qmse700675825 FL

```
339
Seq. No.
Contig ID
                    188 1.R1040
                    fC-gmst700889529 FL
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1518540
BLAST score
                    780
E value
                    3.0e-83
Match length
                    180
% identity
                    (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                    340
                    188 2.R1040
Contig ID
5'-most EST
                    zhf700964379.h1
Method
                    BLASTX
NCBI GI
                    g1518540
BLAST score
                    164
E value
                    1.0e-11
Match length
                    34
% identity
                    97
NCBI Description
                    (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
Contig ID
                    189 1.R1040
5'-most EST
                    fC-gmst700888192 FL
Method
                    BLASTX
NCBI GI
                    q1827893
BLAST score
                    314
E value
                    1.0e-28
                    93
Match length
% identity
                    61
NCBI Description
                   Maize Nonspecific Lipid Transfer Protein Complexed With
                    Palmitate >gi_1827894_pdb_1MZL_ Maize Nonspecific Lipid Transfer Protein >gi_2194092_pdb_1AFH_ Lipid Transfer
                    Protein From Maize Seedlings, Nmr, 15 Structures
                    342
Seq. No.
                    190 1.R1040
Contiq ID
                    fC-qmf1700902987 FL
5'-most EST
Method
                    BLASTN
NCBI GI
                    g2627180
BLAST score
                    276
                    1.0e-153
E value
                    468
Match length
% identity
                    90
NCBI Description
                   Pisum sativum mRNA for cycloartenol synthase, complete cds
                    343
Seq. No.
                    191 1.R1040
Contig ID
5'-most EST
                   LIB3139-030-P1-N1-A6
                    344
Seq. No.
                    192 1.R1040
Contig ID
5'-most EST
                    fC-gmro700845184 FL
Method
                   BLASTX
NCBI GI
                   g2465010
```

```
BLAST score
                   422
E value
                   3.0e-41
Match length
                   141 -
                   63
% identity
                   (AJ001446) acyl carrier protein [Fragaria vesca]
NCBI Description
Seq. No.
                   345
Contig ID
                   192 2.R1040
5'-most EST
                   fua701038142.hl
Method
                   BLASTX
NCBI GI
                   g2465010
BLAST score
                   382
E value
                   2.0e-36
Match length
                   139
% identity
                   58
                   (AJ001446) acyl carrier protein [Fragaria vesca]
NCBI Description
Seq. No.
Contig ID
                   193 1.R1040
5'-most EST
                   fC-gmst700790793 FL
Method
                   BLASTX
NCBI GI
                   g1708236
BLAST score
                   1861
E value
                   0.0e + 00
Match length
                   446
                   77
% identity
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
NCBI Description
                   (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi 2129617 pir JC4567 hydroxymethylglutaryl-CoA synthase
                   (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
Seq. No.
                   347
                   194 1.R1040
Contig ID
                   fC-zmf1700337153 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1155255
BLAST score
                   323
E value
                   1.0e-29
                   130
Match length
% identity
NCBI Description
                   (U39228) beta-glucosidase [Prunus avium]
Seq. No.
                   348
                   195 1.R1040
Contig ID
                   fC-zmf1700354918 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q548493
BLAST score
                   916
E value
                   7.0e-99
Match length
                   289
                   59
% identity
NCBI Description
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
```

(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

Match length

241

```
>gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                   mays]
Seq. No.
                   349
                   196 1.R1040
Contig ID
5'-most EST
                   fC-zmf1700354921 FL
                   BLASTN
Method
NCBI GI
                   q429006
BLAST score
                   39
E value
                   3.0e-12
Match length
                   95
                   85
% identity
NCBI Description
                   Rice mRNA for MCM3 (gene name SS300), partial cds
                   350
Seq. No.
                   197 1.R1040
Contig ID
5'-most EST
                   fC-zmf1700357449 FL
Method
                   BLASTX
NCBI GI
                   g3402722
BLAST score
                   1200
                   1.0e-132
E value
Match length
                   302
% identity
                   (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   351
                   198 1.R1040
Contig ID
5'-most EST
                   fC-zmf1700379641 FL
                   BLASTX
Method
NCBI GI
                   q3342242
BLAST score
                   1840
E value
                   0.0e + 00
Match length
                   463
% identity
                   72
NCBI Description
                   (AF030421) cell wall invertase; beta-fructofuranosidase;
                   fructosidase [Triticum aestivum]
                   352
Seq. No.
                   199 1.R1040
Contig ID
5'-most EST
                   fC-zmf1700379870 FL
Method
                   BLASTX
NCBI GI
                   g3057120
BLAST score
                   1314
E value
                   1.0e-145
Match length
                   292
% identity
                   82
                   (AF023159) starch synthase DULL1 [Zea mays]
NCBI Description
                   353
Seq. No.
                   200 1.R1040
Contig ID
5'-most EST
                   fC-zmro700829959 FL
Method
                   BLASTX
NCBI GI
                   g4154352
                   392
BLAST score
                   1.0e-37
E value
```

>gi\_629854\_pir\_\_S30067 polygalacturonase - maize

```
% identity
NCBI Description
                    (AF110333) PrMC3 [Pinus radiata]
Seq. No.
                    354
Contig ID
                    202 1.R1040
5'-most EST
                    fC-zmro700831955 FL
Method
                    BLASTX
NCBI GI
                    g3850630
BLAST score
                    700
                    1.0e-73
E value
Match length
                    199
                    62
% identity
                    (AJ012581) cytochrome P450 [Cicer arietinum]
NCBI Description
Seq. No.
                    355
                    202 2.R1040
Contig ID
                    fC-zmro700831544_FL
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3850630
BLAST score
                    234
E value
                    1.0e-36
Match length
                    119
% identity
NCBI Description
                    (AJ012581) cytochrome P450 [Cicer arietinum]
Seq. No.
                    356
Contig ID
                    202 3.R1040
5'-most EST
                    q43\overline{9}6629
Method
                    BLASTX .
NCBI GI
                    q4200044
BLAST score
                    1306
E value
                    1.0e-144
Match length
                    382
% identity
NCBI Description
                    (AB022732) cytochrome P450 [Glycyrrhiza echinata]
Seq. No.
                    357
                    203 1.R1040
Contig ID
5'-most EST
                    fC-zmro700832243 FL
Method
                    BLASTX
NCBI GI
                    g3335378
BLAST score
                    614
E value
                    2.0e-63
Match length
                    234
% identity
NCBI Description
                    (AC003028) Myb-related transcription activator [Arabidopsis
                    thaliana]
                    358
Seq. No.
                    204 1.R1040
Contiq ID
                    fC-qmle700870704h2
5'-most EST
Method
                   BLASTX
NCBI GI
                    q2129770
BLAST score
                   1151
E value
                    1.0e-126
Match length
                   291
% identity
                    71
```

xyloglucan endotransglycosylase-related protein XTR-2 -NCBI Description Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi 2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 359

204\_2.R1040 Contig ID

5'-most EST fC-gmse7000756651r1

BLASTX Method NCBI GI q2129770 BLAST score 517 E value 2.0e-52 145 Match length 66

NCBI Description

% identity

xyloglucan endotransglycosylase-related protein XTR-2 -

Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi 2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

360 Seq. No.

204 3.R1040 Contig ID

5'-most EST LIB3051-115-Q1-K1-D8

Method BLASTX q2129770 NCBI GI BLAST score 415 E value 1.0e-40 98 Match length % identity

xyloglucan endotransglycosylase-related protein XTR-2 -NCBI Description

Arabidopsis thaliana >gi\_1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 361

204 4.R1040 Contig ID

LIB3107-038-Q1-K1-C9 5'-most EST

Method BLASTX a2129770 NCBI GI BLAST score 109 E value 8.0e-13 52 Match length

% identity.

xyloglucan endotransglycosylase-related protein XTR-2 -NCBI Description

Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

.. :

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 362

204 5.R1040 Contig ID dpv701102314.hl 5'-most EST

Method BLASTX g2129770 NCBI GI BLAST score 177

E value

```
7.0e-13
E value
Match length
                  45
% identity
                  71
                  xyloglucan endotransglycosylase-related protein XTR-2 -
NCBI Description
                  Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan
                  transferase related protein [Arabidopsis thaliana]
Seq. No.
                  363
                  205_1.R1040
Contig ID
                  fC-zmro700833257 FL
5'-most EST
Method
                  BLASTX
                  g2494329
NCBI GI
BLAST score
                  378
E value
                  8.0e-36
Match length
                  310
% identity
NCBI Description
                  GLUCAN 1,3-BETA-GLUCOSIDASE PRECURSOR
                  (EXO-1,3-BETA-GLUCANASE) >gi_1150694_emb_CAA86952_ (Z46872)
                  exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase
                  [Yarrowia lipolytica]
                  364
Seq. No.
Contig ID
                  205 2.R1040
                  zsg701127354.h1
5'-most EST
Method
                  BLASTX
                  q1050956
NCBI GI
                  295
BLAST score
E value
                  4.0e-26
Match length
                  157
% identity
                  (U26160) 43 kDa secreted glycoprotein precursor
NCBI Description
                  [Paracoccidioides brasiliensis] >gi_1588394_prf__2208385A
                  glycoprotein gp43 [Paracoccidioides brasiliensis]
Seq. No.
                  365
                  206_1.R1040
Contig ID
5'-most EST
                  fC-zmro700833909 FL
                  BLASTX
Method
NCBI GI
                  q3128195
BLAST score
                  1524
E value
                  1.0e-170
Match length
                  361
% identity
NCBI Description
                  (AC004521) putative phosphoribosyl pyrophosphate synthetase
                  [Arabidopsis thaliana] >gi_3341673 (AC003672) putative
                  phosphoribosyl pyrophosphate synthetase [Arabidopsis
                  thaliana]
Seq. No.
                  366
Contig ID
                  207 1.R1040
5'-most EST
                  fC-zmro700833923 FL
Method
                  BLASTX
NCBI GI
                  g3540200
                  237
BLAST score
```

2.0e-19

Match length

```
Match length
                   186
% identity
                   35
NCBI Description
                   (AC004260) Similar to TINY [Arabidopsis thaliana]
                   367
Seq. No.
                   208 1.R1040
Contig ID
5'-most EST
                   fC-zmro700834004 FL
Method
                   BLASTX
NCBI GI
                   g2979553
BLAST score
                   511
                   1.0e-51
E value
Match length
                   166
% identity
                   59
                   (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   368
Seq. No.
                   210 1.R1040
Contig ID
5'-most EST
                   fC-gmro700845739 FL
                   369
Seq. No.
Contig ID
                   210 3.R1040
5'-most EST
                   LIB\overline{3}170-026-Q1-J1-F6
                   370
Seq. No.
Contig ID
                   210 4.R1040
5'-most EST
                   LIB3107-065-Q1-K1-B11
Seq. No.
                   371
Contig ID
                   211 1.R1040
5'-most EST
                   fC-gmro700849012 FL
Method
                   BLASTX
NCBI GI
                   g3643607
BLAST score
                   193
E value
                   1.0e-14
Match length
                   45
                   78
% identity
NCBI Description
                   (AC005395) unknown protein [Arabidopsis thaliana]
                   372
Seq. No.
                   212 1.R1040
Contig ID
                   fC-gmst700791347_FL
5'-most EST
Method
                   BLASTX
                   g3643601
NCBI GI
BLAST score
                   252
                   3.0e-21
E value
                   96
Match length
% identity
                   54
NCBI Description
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   373
                   213 3.R1040
Contig ID
5'-most EST
                   bth700845603.h1
Method
                   BLASTN
NCBI GI
                   q2804153
BLAST score
                   304
E value
                   1.0e-170
```

BLAST score

```
% identity
                   88
NCBI Description
                   Lupinus albus mRNA for aquaporin, partial
Seq. No.
                   213 4.R1040
Contig ID
5'-most EST
                   LIB\overline{3}073-005-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   g1175012
BLAST score
                   1285
E value
                   1.0e-142
Match length
                   283
% identity
                   86
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
                   B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                   protein TMP-B [Arabidopsis thaliana]
                   375
Seq. No.
                   213 5.R1040
Contig ID
                   leu701152670.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3037046
BLAST score
                   402
E value
                   0.0e+00
Match length
                   656
% identity
                   91
NCBI Description
                   Phaseolus vulgaris 1-aminocyclopropane-1-carboxylic acid
                   oxidase mRNA, complete cds
                   376
Seq. No.
Contig ID
                   213 6.R1040
5'-most EST
                   LIB3040-044-Q1-E1-D4
Method
                   BLASTN
NCBI GI
                   g2385377
BLAST score
                   162
E value
                   2.0e-85
Match length
                   517
% identity
                   85
NCBI Description
                   Nicotiana tabacum mRNA for aquaporin
                   377
Seq. No.
Contig ID
                   213 7.R1040
5'-most EST
                   g1575728 FL
Method
                   BLASTN
                   g1575728
NCBI GI
BLAST score
                   638
E value
                   0.0e + 00
Match length
                   790
% identity
                   95
NCBI Description
                   Glycine max 14-3-3 related protein SGF14C mRNA, complete
                   cds
                   378
Seq. No.
Contig ID
                   213 8.R1040
5'-most EST
                   uC-gmropic107f05b1
Method
                   BLASTN
                   g2149954
NCBI GI
```



```
E value
                   1.0e-120
Match length
                   801
                   88
% identity
NCBI Description
                   Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA,
                   complete cds
                   379
Seq. No.
                   214 1.R1040
Contig ID
5'-most EST
                   LIB3170-004-Q1-K1-H9
Method
                   BLASTX
NCBI GI
                   g1149595
BLAST score
                   1054
E value
                   1.0e-115
Match length
                   256
                   77
% identity
NCBI Description
                   (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase
                   [Brassica napus]
                   380
Seq. No.
                   214 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910070h01a1
Method
                   BLASTX
                   g1149595
NCBI GI
BLAST score
                   200
                   2.0e-15
E value
Match length
                   63
% identity
                   60
                   (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase
NCBI Description
                   [Brassica napus]
                   381
Seq. No.
Contig ID
                   215 1.R1040
                   g5605705
5'-most EST
                   BLASTX
Method
NCBI GI
                   g710626
BLAST score
                   155
E value
                   6.0e-10
Match length
                   42
                   57
% identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
                   382
Seq. No.
                   215 2.R1040
Contig ID
5'-most EST
                   g4291035
Method
                   BLASTX
NCBI GI
                   g710626
BLAST score
                   147
E value
                   5.0e-09
Match length
                   42
                   57
% identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
```

thaliana]

thaliana] >gi\_3894181 (AC005662) ERD15 protein [Arabidopsis

Contig ID

```
383
Seq. No.
                    215_3.R1040
Contig ID
5'-most EST
                    uC-gmrominsoy276h04b1
Method
                    BLASTX
NCBI GI
                    q710626
BLAST score
                    155
E value
                    4.0e-10
Match length
                    42
% identity
NCBI Description
                    (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
                    (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                    thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                    thaliana]
                    384
Seq. No.
                    215 4.R1040
Contig ID
5'-most EST
                    uC-qmrominsoy049c05b1
Method
                    BLASTX
NCBI GI
                    g710626
BLAST, score
                    155
                    3.0e-10
E value
                    42
Match length
                    57
% identity
                    (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                    (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                    thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                    thaliana]
                    385
Seq. No.
Contig ID
                    216 1.R1040
                    leu701148094.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3980406
BLAST score
                    346
E value
                    2.0e-32
Match length
                    103
% identity
                    (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                    thaliana]
                    386
Seq. No.
Contig ID
                    218 1.R1040
                    g5057891
5'-most EST
Method
                    BLASTX
                    g585973
NCBI GI
BLAST score
                    346
E value
                    2.0e-32
Match length
                    89
% identity
                    FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A
NCBI Description
                    fructokinase [Solanum tuberosum]
Seq. No.
```

219\_1.R1040

```
rca700997536.h1
5'-most EST
                    BLASTX
Method
                    g1653655
NCBI GI
BLAST score
                    364
                    5.0e-34
E value
Match length
                    163
                    44
 % identity
                    (D90915) ATP-dependent Clp protease proteolytic subunit
NCBI Description
                    [Synechocystis sp.]
                    388
Seq. No.
                    220_1.R1040
Contig ID
                    fC-gmro700844894_FL
5'-most EST
                    BLASTX
Method
                    g4512651
NCBI GI
BLAST score
                    616
E value
                    7.0e-64
                    222
Match length
                    50
 % identity
                    (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                    thaliana]
                    389
Seq. No.
                    221_1.R1040
Contig ID
                    jC-gmst02400054a06d1
·5'-most EST
                    BLASTX
Method
                    g349379
NCBI GI
BLAST score
                    337
E value
                    3.0e-31
Match length
                    127
                    63
 % identity
                    (L22847) HAHB-1 [Helianthus annuus]
NCBI Description
                    390
Seq. No.
                    221_2.R1040
Contig ID
 5'-most EST
                    gsv701054757.h1
Method
                    BLASTX
NCBI GI
                    g349379
                    295
BLAST score
                    2.0e-26
E value
                    129
Match length
 % identity
NCBI Description (L22847) HAHB-1 [Helianthus annuus]
                    391
Seq. No.
                    222_1.R1040
 Contig ID
 5'-most EST
                    fC-gmro700847730 FL
Method
                    BLASTX
NCBI GI
                    q4415914
 BLAST score
                    367
 E value
                    1.0e-34
                    198
Match length
 % identity
                    37
                    (AC006282) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
```

223\_1.R1040

Contig ID

Seq. No.

```
5'-most EST
                   fC-qmle7000741669a1
                   BLASTX
Method
                   a1169586
NCBI GI
BLAST score
                   1610
                   1.0e-180
E value
Match length
                   338
                   89
% identity
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)
                   fructose-1,6-bisphosphatase [Solanum tuberosum]
                   393
Seq. No.
                   223 2.R1040
Contig ID
                   fC-qmle7000741457a1
5'-most EST
Method
                   BLASTX
                   g3913640
NCBI GI
                   591
BLAST score
E value
                   4.0e-61
Match length
                   120
% identity
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 3041775 dbj_BAA25422_ (AB007193)
                   fructose-1,6-bisphosphatase [Oryza sativa]
                   394
Seq. No.
                   223 3.R1040
Contig ID
                   ncj700986460.hl
5'-most EST
Method
                   BLASTX
                   q3913640
NCBI GI
                   523
BLAST score
                   3.0e-53
E value
                   111
Match length
% identity
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 3041775_dbj_BAA25422 (AB007193)
                   fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                   223 4.R1040
Contig ID
5'-most EST
                   fC-qmle700873234a1
Method
                   BLASTX
NCBI GI
                   g2494416
BLAST score
                   434
E value
                   2.0e-61
Match length
                   127
% identity
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >qi 166956 (M80597) fructose-1,6-bisphosphatase [Beta
                   vulgaris] >gi 444324 prf 1906373A cytosolic fructose
                   bisphosphatase [Beta vulgaris]
```

NCBI Description

```
Contig ID
                   224_1.R1040
                   fC-gmro700849195 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4490335
BLAST score
                   267
E value
                   5.0e-23
Match length
                   153
                   44
% identity
NCBI Description
                   (AL035656) receptor kinase-like protein [Arabidopsis
                   thaliana]
                   397
Seq. No.
Contig ID
                   224 2.R1040
5'-most EST
                   fC-gmle700875134r1
                   398
Seq. No.
                   225 1.R1040
Contig ID
5'-most EST
                   LIB3092-012-Q1-K1-A12
                   399
Seq. No.
Contig ID
                   226_1.R1040
5'-most EST
                   fC-gmro700864101_FL
Method
                   BLASTX
NCBI GI
                   g2924777
BLAST score
                   187
                   8.0e-14
E value
Match length
                   107
                   43
% identity
                   (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   400
Seq. No.
Contig ID
                   226 2.R1040
                   LIB3139-100-P1-N1-A12
5'-most EST
                   401
Seq. No.
Contig ID
                   227 1.R1040
                   fC-gmro700865543 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455129
BLAST score
                   317
E value
                   1.0e-28
Match length
                   120
% identity
                   (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
NCBI Description
                   402
Seq. No.
Contig ID
                   227 2.R1040
5'-most EST
                   LIB3106-022-Q1-K1-E1
Method
                   BLASTX
                   q4455129
NCBI GI
                   201
BLAST score
E value
                   2.0e-16
Match length
                   80
% identity
                   61
```

(AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]

% identity

```
403
Seq. No.
                   228 1.R1040
Contig ID
5'-most EST
                   fC-gmro700868230 FL
Method
                   BLASTX
NCBI GI
                   q4544403
BLAST score
                   720
E value
                   5.0e-76
Match length
                   206
% identity
                   62
                   (AC007047) putative glucan endo-1,3-beta-D-glucosidase
NCBI Description
                  precursor [Arabidopsis thaliana]
Seq. No.
                   404
                   228_2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy169b02b1
                   BLASTX
Method
NCBI GI
                   q3641838
BLAST score
                   647
E value
                   1.0e-132
Match length
                   329
                   74
% identity
NCBI Description
                   (AL023094) putative protein (fragment) [Arabidopsis ...
                   thaliana]
Seq. No.
                   405
Contig ID
                   229 1.R1040
5'-most EST
                   fC-qmle700743613f1
                   BLASTN
Method
NCBI GI
                   q435678
BLAST score
                   132
E value
                   9.0e-68
Match length
                   323
                   86
% identity
NCBI Description
                  L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
                   406
Seq. No.
                   229 2.R1040
Contig ID
5'-most EST
                   qsv701055480.h1
Method
                  BLASTN
NCBI GI
                   g435678
BLAST score
                   120
E value
                   1.0e-60
Match length
                   323
% identity
                   85
NCBI Description
                  L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
                   407
Seq. No.
                   229 3.R1040
Contig ID
5'-most EST
                  V4L-01-Q1-B1-E8
Method
                  BLASTX
NCBI GI
                  q3249084
BLAST score
                  1818
E value
                  0.0e+00
Match length
                   567
```

NCBI GI

```
(AC004473) Similar to red-1 (related to thioredoxin) gene
NCBI Description
                   gb X92750 from Mus musculus. ESTs gb AA712687 and
                   gb Z37223 come from this gene [Arabidopsis thaliana]
Seq. No.
                   408
                   229 4.R1040
Contig ID
                   cf1700863563.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4567232
                                                    1.5
BLAST score
                   239
E value
                   1.0e-30
Match length
                   83
% identity
                   85
                   (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
NCBI Description
                   thaliana]
                   409
Seq. No.
                   230 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir037a08b1
Method
                   BLASTX
NCBI GI
                   g1922964
BLAST score
                   609
E value
                   8.0e-63
Match length
                   171
% identity
                   73
                   (AC000106) Similar to Schizosaccharomyces CCAAT-binding
NCBI Description
                   factor (gb U88525). EST gb_T04310 comes from this gene.
                   [Arabidopsis thaliana]
                   410
Seq. No.
Contig ID
                   231 1.R1040
5'-most EST
                   fC-gmro700566893r1
Method
                   BLASTX
                   g4538929
NCBI GI
BLAST score
                   672
E value
                   4.0e-70
Match length
                   362
% identity
                   42
                   (ALO49483) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   411
                   231_2.R1040
Contig ID
                   jC-\overline{gmle01810016c05d1}
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2342727
BLAST score
                   361
E value
                   3.0e-34
Match length
                   90
% identity
NCBI Description
                   (AC002341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   412
                   231 3.R1040
Contig ID
5'-most EST
                   fua701043550.h1
Method
                   BLASTX
```

q4538929

```
BLAST score
                   291
E value
                   1.0e-25
                   175
Match length
                   49
% identity
                   (AL049483) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   413
Seq. No.
                   231 4.R1040
Contig ID
5'-most EST
                   ASG32442DA-02-Q1-E1-F10
Method
                   BLASTX
NCBI GI
                   g4538929
BLAST score
                   163
E value
                   5.0e-11
Match length
                   58
% identity
                   55
                   (AL049483) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   414
Seq. No.
Contig ID
                   232_1.R1040
                   fC-zmro700830348 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3901012
BLAST score
                   1157
E value
                   1.0e-127
Match length
                   278
                   76
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
Seq. No.
                   415
Contig ID
                   232_2.R1040
5'-most EST
                   uC-gmropic018b01b1
Method
                   BLASTX
NCBI GI
                   q3901012
BLAST score
                   313
                   9.0e-29
E value
                   75
Match length
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   416
Seq. No.
                   232 3.R1040
Contig ID
5'-most EST
                   qsv701049278.h1
Method
                   BLASTX
NCBI GI
                   q2129771
BLAST score
                   334
                   5.0e-31
E value
Match length
                   164
% identity
NCBI Description
                   xyloglucan endotransglycosylase-related protein XTR-6 -
                   Arabidopsis thaliana >gi 1244758 (U43488) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
                   >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1,
4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]
```

```
417
Seq. No.
                   232 4.R1040
Contig ID
                   zzp700835657.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3901012
BLAST score
                   645
                   2.0e-67
E value
                   146
Match length
                   79
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   418
Seq. No.
                   232 6.R1040
Contig ID
                   LIB3139-037-P1-N1-B7
5'-most EST
                   BLASTX
Method
                   q3901012
NCBI GI
                   169
BLAST score
                   5.0e-12
E value
                   34
Match length
                   82
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   419
Seq. No.
Contig ID
                   233 1.R1040
                   fC-zmro700832181 FL
5'-most EST
Method
                   BLASTX
                                                                   ....
                   g266685
NCBI GI
BLAST score
                   969
                   1.0e-105
E value
                   439
Match length
                   38
% identity
                   DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE
NCBI Description
                   DEHYDROGENASE COMPLEX (E2) (PDC-E2) (70 KD MITOCHONDRIAL
                   AUTOANTIGEN OF PRIMARY BILIARY CIRRHOSIS) (PBC)
                   >gi_111580_pir__S21766 dihydrolipoamide S-acetyltransferase
                   (EC 2.3.1.12) - rat
                   420
Seq. No.
                   235 1.R1040
Contig ID
5'-most EST
                   fC-zmf1700381954 FL
Method
                   BLASTN
                   g22485
NCBI GI
BLAST score
                   798
E value ·
                   0.0e + 00
Match length
                   1075
                   98
% identity
                  Maize mRNA for sucrose synthase (EC 2.4.1.13)
NCBI Description
Seq. No.
                   421
                   236 1.R1040
Contig ID
5'-most EST
                   fC-zmf1700550326 FL
                   BLASTX
Method
                   g4426627
NCBI GI
```

300

BLAST score

NCBI GI

```
3.0e-27
E value
Match length
                   59
                   81
% identity
                   (AF099969) sterol-C5(6)-desaturase homolog [Nicotiana
NCBI Description
                   tabacum]
                   422
Seq. No.
                   238 1.R1040
Contig ID
5'-most EST
                   LIB3138-046-Q1-N1-E1
Method
                   BLASTX
                   g1834387
NCBI GI
BLAST score
                   1830
E value
                   0.0e + 00
                   389
Match length
                   88
% identity
                   (Y11022) chalcone synthase [Betula pendula]
NCBI Description
                   423
Seq. No.
                   239 1.R1040
Contig ID
5'-most EST
                   fC-gmle700557774 FL
Method
                   BLASTX.
NCBI GI
                   g3786006
BLAST score
                   589
E value
                   2.0e-60
Match length
                   177
                   67
% identity
NCBI Description
                   (AC005499) hypothetical protein [Arabidopsis thaliana]
                   424
Seq. No.
                   240 1.R1040
Contig ID
5'-most EST
                   fC-gmle700555604a1
Method
                   BLASTX
                   g3242708
NCBI GI
BLAST score
                   699
                   2.0e-73
E value
Match length
                   295
% identity
                   48
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   425
Seq. No.
Contig ID
                   240 2.R1040
5'-most EST
                   LIB3139-045-P1-N1-C3
Method
                   BLASTX
NCBI GI
                   g3242708
BLAST score
                   258
E value
                   4.0e-22
Match length
                   121
% identity
                   45
NCBI Description
                   (AC003040) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
                   426
Seq. No.
                   241 1.R1040
Contig ID
5'-most EST
                   fC-gmle700560462 FL
Method
                   BLASTN
```

g2463568

NCBI Description

```
BLAST score
                   115
E value
                   5.0e-58
Match length
                   203
% identity
                   89 .
                  Glycine max mRNA for squalene synthase, complete cds
NCBI Description
                   427
Seq. No.
                   241_2.R1040
Contig ID
                   jC-gmle01810087d08d1
5'-most EST
                  BLASTN
Method
NCBI GI
                   g2463568
BLAST score
                   48
E value
                   3.0e-18
                  124
Match length
                  84
% identity
NCBI Description
                  Glycine max mRNA for squalene synthase, complete cds
                   428
Seq. No.
                   242 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910002d12a1
Method
                  BLASTX
NCBI GI
                  g3805849
BLAST score
                   4092
                   0.0e+00
E value
Match length
                   897
% identity
NCBI Description
                   (AL031986) cytoplasmatic aconitate hydratase (citrate
                  hydro-lyase) (aconitase) (EC 4.2.1.3) [Arabidopsis thaliana]
                   429
Seq. No.
                   243 1.R1040
Contig ID
                   epx701108931.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2499488
BLAST score
                   2683
E value
                  0.0e + 00
Match length
                   610
% identity
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                  pyrophosphate-dependent phosphofructokinase alpha subunit
                   [Ricinus communis]
                   430
Seq. No.
Contig ID
                  243 2.R1040
5'-most EST
                  q5688064
Method
                  BLASTX
NCBI GI
                  g3790102 -
BLAST score
                   432
                  2.0e-42
E value
Match length
                  102
% identity
```

alpha subunit [Citrus X paradisi]

(AF095521) pyrophosphate-dependent phosphofructokinase

NCBI Description

```
431
Seq. No.
Contig ID
                   243 4.R1040
5'-most EST
                   jex700904315.hl
Method
                   BLASTN
NCBI GI
                   q3790101
BLAST score
                   44
                   1.0e-15
E value
                   80
Match length
% identity
                   89
                   Citrus X paradisi pyrophosphate-dependent
NCBI Description
                   phosphofructokinase alpha subunit (PPi-PFKa) mRNA, complete
                   432
Seq. No.
Contig ID
                   244 1.R1040
                   ssr700556101.hl
5'-most EST
Method
                   BLASTX
                   g3915599
NCBI GI
BLAST score
                   321
E value
                   3.0e-29
                   160
Match length
% identity
NCBI Description
                   FLORAL HOMEOTIC PROTEIN AGL3 >gi_1361993_pir__S57793
                   MADS-box protein AGL3 - Arabidopsis thaliana >gi 1737495
                   (U81369) MADS box protein [Arabidopsis thaliana]
                   >gi_4406762_gb_AAD20073_ (AC006836) MADS box protein AGL3
                   [Arabidopsis thaliana]
Seq. No.
                   433
                   244 2.R1040
Contig ID
5'-most EST
                   hyd700731174.h1
Seq. No.
                   434
                   245 1.R1040
Contig ID
                   fC-qmse700606016 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2129788
BLAST score
                   161
                   8.0e-11
E value
                   38
Match length
% identity
                   84
NCBI Description
                   biotin carboxyl carrier protein (clone BP7) - rape
                   (fragment) >gi_1070010_emb_CAA62266_ (X90732) Biotin
                   carboxyl carrier protein [\overline{B}rassica \overline{n}apus]
                   >gi_1589045_prf__2210244F Ac-CoA carboxylase:ISOTYPE=bp7
                   [Brassica napus]
Seq. No.
                   435
Contig ID
                   246 1.R1040
5'-most EST
                   LIB3051-115-Q1-K1-C12
Method
                   BLASTX
NCBI GI
                   q3335372
BLAST score
                   319
                   7.0e-29
E value
Match length
                   270
% identity
```

(AC003028) putative SRG1 protein [Arabidopsis thaliana]

BLAST score

E value

311 4.0e-28

. 5

```
436
Seq. No.
                   247_1.R1040
Contig ID
                                                    ...
5'-most EST
                   fC-gmle700553710 FL
                   BLASTX
Method
                   g4337187
NCBI GI
                   297
BLAST score
                   8.0e-27
E value
Match length
                   80
% identity
                   65
                   (AC006403) putative prolylcarboxypeptidase, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                   437
Seq. No.
                   247 2.R1040
Contig ID
                   LIB3170-041-Q1-K1-F1
5'-most EST
                   438
Seq. No.
                   248 1.R1040
Contig ID
5'-most EST
                   g5509667
Method
                   BLASTN
                   g403328
NCBI GI
BLAST score
                   59
                   3.0e-24
E value
Match length
                   95
                   91
% identity
                   T.repens TrMT1B mRNA for metallothionein-like protein
NCBI Description
                   439
Seq. No.
                   248 2.R1040
Contig ID
5'-most EST
                   g4300393
Method
                   BLASTN
NCBI GI
                   g403328
BLAST score
                   56
E value
                   1.0e-22
Match length
                   115
% identity
                   91
                   T.repens TrMT1B mRNA for metallothionein-like protein
NCBI Description
                   440
Seq. No.
                   248 3.R1040
Contig ID
5'-most EST
                   q42\overline{8}3686
Method
                   BLASTN
                   g403328
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
Match length
                   92
% identity
                   T.repens TrMT1B mRNA for metallothionein-like protein
NCBI Description
Seq. No.
                   441
                   249 1.R1040
Contig ID
5'-most EST
                   LIB3073-012-Q1-K1-H3
Method
                   BLASTX
                   g4574320
NCBI GI
```

BLAST score

```
107
Match length
% identity
                   61
NCBI Description
                   (AF117224) wound-induced protein WI12 [Mesembryanthemum
                   crystallinum]
Seq. No.
                   442
                   249 2.R1040
Contig ID
5'-most EST
                   zzp700831257.h1
Method
                   BLASTX
NCBI GI
                   q4574320
BLAST score
                   306
E value
                   2.0e-27
Match length
                   107
                   60
% identity
                   (AF117224) wound-induced protein WI12 [Mesembryanthemum
NCBI Description
                   crystallinum]
                   443
Seq. No.
                   249 3.R1040
Contig ID
5'-most EST
                   rca700999690.hl
Seq. No.
Contig ID
                   250 1.R1040
5'-most EST
                   jC-gmle01810014c12d1
Method
                   BLASTX
NCBI GI
                   q4468218
BLAST score
                   378
E value
                   6.0e-36
Match length
                   174
                   44
% identity
NCBI Description
                   (AJ010025) unr-interacting protein [Homo sapiens]
Seq. No.
                   445
Contig ID
                   251 1.R1040
5'-most EST
                   fC-gmse700840436 FL
Seq. No.
                   446
                   251 2.R1040
Contig ID
5'-most EST
                  LIB3050-012-Q1-E1-H5
Seq. No.
                   447
                   252 1.R1040
Contig ID
5'-most EST
                   fC-gmse700840647 FL
Method
                   BLASTX
NCBI GI
                   g3292817
BLAST score
                  838
E value
                   1.0e-89
Match length
                   209
% identity
                   77
                   (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   252 2.R1040
Contig ID
5'-most EST
                  g4260232
Method
                  BLASTX
NCBI GI
                  g3292817
```

E value

```
4.0e-45
E value
Match length
                   155
                   59
% identity
                   (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   449
Seq. No.
Contig ID
                   252 3.R1040
                   LIB3138-011-Q1-N1-B5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3292817
BLAST score
                   276
E value
                   2.0e-24
                   89
Match length
                   69
% identity
                   (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   450
Seq. No.
                   253 1.R1040
Contig ID
5'-most EST
                   fC-gmse700841225 FL
                   BLASTX
Method
NCBI GI
                   g2642430
BLAST score
                   432
E value
                   2.0e-42
Match length
                   157
% identity
                   62
                   (AC002391) putative AP2 domain containing protein
NCBI Description
                   [Arabidopsis thaliana]
                   451
Seq. No.
Contig ID
                   254 1.R1040
5'-most EST
                   LIB3049-015-Q1-E1-C2
Method
                   BLASTX
                   g2894605
NCBI GI
BLAST score
                   267
E value
                   5.0e-23
Match length
                   133
% identity
                   50
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   452
Seq. No.
                   254 2.R1040
Contig ID
5'-most EST
                   hrw701059629.hl
Method
                   BLASTX
                   g2894605
NCBI GI
BLAST score
                   301
                   3.0e-27
E value
Match length
                   131
% identity
                   55
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   453
Seq. No.
                   255 1.R1040
Contig ID
5'-most EST
                   dpv701100539.h1
Method
                   BLASTX
                   g3335372
NCBI GI
BLAST score
                   1134
```

1.0e-124

% identity

```
368
Match length
% identity
                   59
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
                   454
Seq. No.
                   255 2.R1040
Contig ID
                   fC-gmro700869137f3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3335372
BLAST score
                   682
E value
                   2.0e-71
Match length
                   305
% identity
                   59
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
                   455
Seq. No.
                   255 3.R1040
Contig ID
                   LIB3040-005-Q1-E1-G2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3335372
BLAST score
                   401
                   7:0e-39
E value
Match length
                   165
                   50
% identity
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
                   456
Seq. No.
                   255 4.R1040
Contig ID
                   LIB3049-047-Q1-E1-F9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3335372
BLAST score
                   150
                   7.0e-20
E value
                   141
Match length
                   41
% identity
NCBI Description
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
                   457
Seq. No.
                   255 5.R1040
Contig ID
5'-most EST
                   LIB3040-016-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   g3335372
BLAST score
                   113
E value
                   1.0e-12
Match length
                   84
% identity
NCBI Description
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
Seq. No.
                   458
                   256 1.R1040
Contig ID
5'-most EST
                   asn701139845.h1
Method
                   BLASTX
NCBI GI
                   q2702268
BLAST score
                   655
                   6.0e-77
E value
Match length
                   254
```

```
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]
                   459
Seq. No.
                   257 1.R1040
Contig ID
                   jC-qmro02910064g02a1
5'-most EST
                   BLASTX
Method
                   g1518540
NCBI GI
BLAST score
                   2252
                   0.0e + 00
E value
Match length
                   480
                   89
% identity
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   460
Seq. No.
                   257 2.R1040
Contig ID
                   fC-qmf1700899609f1
5'-most EST
                   BLASTX
Method
                   q3378650
NCBI GI
BLAST score
                   862
                   9.0e-93
E value
Match length
                   239
                   70
% identity
                   (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
                   461
Seq. No.
                   257 3.R1040
Contig ID
                   LIB3092-040-Q1-K1-H3
5'-most EST
                   462
Seq. No.
                   257 4.R1040
Contig ID
5'-most EST
                   ssr700556162.hl
                   463
Seq. No.
                   257 5.R1040
Contig ID
                   g4314063
5'-most EST
Seq. No.
                   464
                   257_6.R1040
Contig ID
                   jC-gmf102220146e08d1
5'-most EST
                   BLASTX
Method
                   q3378650
NCBI GI
BLAST score
                   215
                   3.0e-17
E value.
                   63
Match length
                   59
% identity
                   (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
Seq. No.
                   465
Contig ID
                   257 9.R1040
5'-most EST
                   jC-qmf102220114g07a1
Seq. No.
Contig ID
                   257 10.R1040
5'-most EST
                   uC-qmflminsoy047d09b1
Seq. No.
```

257\_11.R1040

Contig ID

```
jC-qmst02400056g02a1
5'-most EST
                   468
Seq. No.
Contig ID
                   258 1.R1040
                   jC-gmst02400062d08d1
5'-most EST
                  BLASTX
Method
                  q2146739
NCBI GI
                   1772
BLAST score
E value
                   0.0e + 00
                   469
Match length
% identity
                   72
                  hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi 881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
                   469
Seq. No.
                   258 2.R1040
Contig ID
                   jC-gmro02910073c05d1
5'-most EST
                   BLASTX
Method
                   g1899025
NCBI GI
BLAST score
                   692
                   1.0e-72
E value
Match length
                   185
                   71
% identity
                   (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232
NCBI Description
                   (AC005169) hexokinase [Arabidopsis thaliana]
                   470
Seq. No.
                   258_3.R1040
Contig ID
                   jC-qmf102220054c06a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2146739
                   267
BLAST score
                   3.0e-23
E value
                   68
Match length
                   78
% identity
                   hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
                   471
Seq. No.
                   259 1.R1040
Contig ID
                   jC-gmro02910035d12d1
5'-most EST
Method
                   BLASTX
                   q3702332
NCBI GI
                   342
BLAST score
                   1.0e-31
E value
                   193
Match length
% identity
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   472
                   260 1.R1040
Contig ID
                   fC-zmro700830504 FL
5'-most EST
Method
                   BLASTX
                   q4240116
NCBI GI
BLAST score
                   1159
                   1.0e-127
E value
```

247

Match length

```
% identity
                   87
                   (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                   thaliana] >gi_4240118_dbj_BAA74838_ (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                   473
                   260 2.R1040
Contig ID
5'-most EST
                  g4396819
                   474 ·
Seq. No.
Contig ID
                   261 1.R1040
5'-most EST
                   fC-zmro700830907 FL
Method
                  BLASTX
NCBI GI
                  g4191788
BLAST score
                  768
                   1.0e-81
E value
Match length
                   191
% identity
                   76
                   (AC005917) putative 1-aminocyclopropane-1-carboxylate
NCBI Description
                   oxidase [Arabidopsis thaliana]
                   475
Seq. No.
                  262 1.R1040
Contig ID
                  LIB3051-090-Q1-K1-G3
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1336096
BLAST score
                  581
                  0.0e+00
E value
                  1160
Match length
% identity
                  Pisum sativum pyruvate dehydrogenase Elbeta mRNA, nuclear
NCBI Description
                   gene encoding mitochondrial protein, complete cds
                   476
Seq. No.
                   262 2.R1040
Contig ID
5'-most EST
                  uC-gmropic021f10b1
Method
                  BLASTN
                  g1336096 ·
NCBI GI
BLAST score
                  153
E value
                   2.0e-80
Match length
                  347
% identity
                  86
NCBI Description
                  Pisum sativum pyruvate dehydrogenase Elbeta mRNA, nuclear
                  gene encoding mitochondrial protein, complete cds
                   477
Seq. No.
                  262 3.R1040
Contig ID
5'-most EST
                  LIB3051-081-Q1-K1-E5
Method
                  BLASTN
NCBI GI
                  q1336096
                  133
BLAST score
E value
                   2.0e-68
Match length
                  335
% identity
NCBI Description
                  Pisum sativum pyruvate dehydrogenase Elbeta mRNA, nuclear
```

gene encoding mitochondrial protein, complete cds

NCBI GI

```
478
Seq. No.
                  262 6.R1040
Contig ID
                  gsv701054233.hl
5'-most EST
Method
                  BLASTX
                  g1709454
NCBI GI
BLAST score
                  230
E value
                  2.0e-19
Match length
                  63
                  78
% identity
                  PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR
NCBI Description
                  (PDHE1-B) >gi_1336097 (U56697) pyruvate dehydrogenase
                  Elbeta [Pisum sativum]
                  479
Seq. No.
                  264 1.R1040
Contig ID
5'-most EST
                  fC-zmro700832582 FL
Method
                  BLASTX
                  g2959732
NCBI GI
BLAST score
                  353
                  3.0e-33
E value
Match length
                  71
% identity
                  (Y13649) homologous to GATA-binding transcription factors
NCBI Description
                  [Arabidopsis thaliana]
                  480
Seq. No.
Contig ID
                  265_1.R1040
                  fC-zmro700833374 FL
5'-most EST
                  BLASTX
Method
                  g1872521
NCBI GI
BLAST score
                  303
E value
                  4.0e-27
Match length
                  113
                  36
% identity
                  (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
NCBI Description
                  >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                  thaliana]
                  481
Seq. No.
Contig ID
                  267 1.R1040
                  LIB3052-002-Q1-B1-G3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1942405
BLAST score
                  4443
E value
                  0.0e + 00
Match length
                  857
                  98
% identity
NCBI Description
                  Lipoxygenase-3(Soybean) Non-Heme Fe(Ii) Metalloprotein
                  >gi_4388888_pdb_1BYT_ Lipoxygenase-3(Soybean) Complex With
                  4-Nitrocatechol >gi 1794172 (U50081) lipoxygenase-3
                  [Glycine max]
Seq. No.
                  482
                  268 2.R1040
Contig ID
                  fC-gmro700568375r1
5'-most EST
Method
                  BLASTX
```

g1931639

```
BLAST score
                   337
E value
                   3.0e-31
Match length
                   148
                   53
% identity
                   (U95973) lysophospholipase isolog [Arabidopsis thaliana]
NCBI Description
                   483
Seq. No.
                   268 3.R1040
Contig ID
5'-most EST
                   LIB3074-031-Q1-K2-E10
Method
                   BLASTX
NCBI GI
                   g2832681
BLAST score
                   199
                   7.0e-29
E value
                   71
Match length
% identity
                   82
NCBI Description
                   (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                   484
                   268 4.R1040
Contig ID
                   awf700841481.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1885372
BLAST score
                   601
                   0.0e + 00
E value
Match length
                   641
                   99
% identity
                   Glycine max small subunit ribosomal RNA gene, partial
NCBI Description
                   sequence, internal transcribed spacer 1, 5.8S ribosomal RNA
                   gene and internal transcribed spacer 2, complete sequence,
                   and large subunit ribosomal RNA gene, partial seq
                   485
Seq. No.
                   268 5.R1040
Contig ID
5'-most EST
                   asn701138178.h1
Method
                  BLASTX
                   g3157928
NCBI GI
BLAST score
                   911
E value
                   1.0e-155
Match length
                   404
% identity
                   (AC002131) Similar to fumarylacetoacetate hydrolase,
NCBI Description
                   gb L41670 from Emericella nidulans. [Arabidopsis thaliana]
                   486
Seq. No.
                  268 6.R1040
Contig ID
5'-most EST
                  LIB3107-080-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  g170019
BLAST score
                  599
                  0.0e+00
E value
                  1094
Match length
% identity
                  95
NCBI Description
                  Soybean maturation protein (MAT1) gene, complete cds
Seq. No.
                  487
```

268 7.R1040

uxk700672229.h1

Contig ID

5'-most EST

NCBI GI

```
Method
                    BLASTN
 NCBI GI
                    g497416
 BLAST score
                    628
                    0.0e + 00
 E value
 Match length
                    912
                    94
 % identity
                    Glycine max Essex dehydrin-like protein mRNA, complete cds
 NCBI Description
                    488
 Seq. No.
                    269 1.R1040
 Contig ID
                    leu701154837.hl
 5'-most EST
 Method
                    BLASTN
                    g20831
 NCBI GI
                    275
 BLAST score
                    1.0e-153
 E value
 Match length
                    791
                    84
 % identity
                    P.sativum petC mRNA for chloroplast Rieske FeS protein
 NCBI Description
                    489
 Seq. No.
                    270 1.R1040
Contig ID
 5'-most EST
                    fC-gmst7007923230 FL
 Method .
                    BLASTX
                    g4490737
 NCBI GI
                    765
BLAST score
                    4.0e-81
 E value
 Match length
                    284
 % identity
                    (AL035708) putative protein [Arabidopsis thaliana]
 NCBI Description
                    490
 Seq. No.
                    270 2.R1040
 Contig ID
                    LIB3039-004-Q1-E1-F9
 5'-most EST
                    BLASTX
 Method
                    g4490737
 NCBI GI
 BLAST score
                    266
                    3.0e-23
 E value
 Match length
                    87
 % identity
                    62
                    (AL035708) putative protein [Arabidopsis thaliana]
 NCBI Description
                    491
 Seq. No.
 Contig ID
                    270 3.R1040
                    dpv701097092.h1
 5'-most EST
                    BLASTX
 Method
                    g4490737
 NCBI GI
 BLAST score
                    155
 E value
                    2.0e-10
 Match length
                    55
 % identity
                    (AL035708) putative protein [Arabidopsis thaliana]
 NCBI Description
                    492
 Seq. No.
                    271 1.R1040
 Contig ID
                    fC-zmf1700381665_FL
 5'-most EST
 Method
                    BLASTX
```

g2129550

% identity

NCBI Description

74

```
1218
BLAST score
E value
                  1.0e-134
                  294
Match length
                  76
% identity
NCBI Description
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
                  Arabidopsis thaliana >gi_2129554_pir__S71901
                  calcium-dependent protein kinase 6 - Arabidopsis thaliana
                  >gi_836940 (U20623) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi_836944 (U20625)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
                  >gi 4454034 emb CAA23031.1_ (AL035394) calcium-dependent
                  protein kinase (CDPK6) [Arabidopsis thaliana]
Seq. No.
                  493
                  272 1.R1040
Contig ID
5'-most EST
                  fC-gmse700764850 FL
Method
                  BLASTX
                  g4417267
NCBI GI
BLAST score
                  315
                  1.0e-28
E value
Match length
                  152
% identity
                  46
                   (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  494
Seq. No.
                  273 3.R1040
Contig ID
5'-most EST
                  LIB3051-003-Q1-E1-D8
                  495
Seq. No.
                  273 4.R1040
Contig ID
5'-most EST
                  q5676977
                  496
Seq. No.
Contig ID
                  273_5.R1040
5'-most EST
                  jC-gmf102220132ag03d1
Seq. No.
                  497
Contig ID
                  273 6.R1040
                  LIB3051-067-Q1-K1-A9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2911280
BLAST score
                  482
E value
                  2.0e-48
Match length
                  107
                  87
% identity
                  (U73937) PK12 protein kinase [Nicotiana tabacum]
NCBI Description
                  498
Seq. No.
Contig ID
                  273 7.R1040
                  seb700650989.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g133438
BLAST score
                  677
E value
                  4.0e-71
Match length
                  180
```

DNA-DIRECTED RNA POLYMERASE BETA' CHAIN

Method

NCBI GI

**BLASTX** 

q2911280

```
499
Seq. No.
Contig ID
                   273 8.R1040
5'-most EST
                   LIB3040-060-Q1-E1-H9
Method
                   BLASTX
NCBI GI
                   q3548802
BLAST score
                   553
E value
                   2.0e-56
Match length
                   243
                   44
% identity
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4335769 gb AAD17446_ (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
Seq. No.
                   273 9.R1040
Contig ID
5'-most EST
                   LIB\overline{3}109-052-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2894568
BLAST score
                   173
E value
                   4.0e-12
                   93
Match length
% identity
                   46
                   (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
                   501
Seq. No.
                   273 10.R1040
Contig ID
5'-most EST
                   LIB3049-042-Q1-E1-E8
                   502
Seq. No.
                   273 11.R1040
Contig ID
5'-most EST
                   LIB3049-041-Q1-E1-H3
Seq. No.
                   503
                   273 12.R1040
Contig ID
5'-most EST
                   LIB3092-031-Q1-K1-H9
                   504
Seq. No.
Contig ID
                   273 13.R1040
5'-most EST
                   hrw701060522.hl
Method
                   BLASTX
NCBI GI
                   q294845
BLAST score
                   744
E value
                   1.0e-78
Match length
                   261
% identity
                   56
                   (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                   H65-70521
Seq. No.
                   505
                   273 14.R1040
Contig ID
5'-most EST
                   jC-gmle01810014h09d1
```

>gi\_81504\_pir\_\_B29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast >gi\_295120

(M55297) RNA polymerase [Spinacia oleracea]

```
BLAST score
                   594
E value
                   2.0e-67
Match length
                   197
% identity
                   69
NCBI Description
                   (U73937) PK12 protein kinase [Nicotiana tabacum]
Seq. No.
                   506
Contig ID
                   273 15.R1040
5'-most EST
                   jex700906210.h1
                   507
Seq. No.
Contig ID
                   273 16.R1040
5'-most EST
                   LIB3051-106-Q1-K1-E6
Method
                   BLASTN
NCBI GI
                   g2760164
BLAST score
                   52
E value
                   1.0e-19
                   182
Match length
                   86
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18P6, complete sequence [Arabidopsis thaliana]
                   508
Seq. No.
                   273 17.R1040
Contig ID
5'-most EST
                  LIB3170-049-Q1-K1-D12
Method
                  BLASTX
                   g3643249
NCBI GI
BLAST score
                   545
E value
                   1.0e-55
Match length
                  124
                   75
% identity
NCBI Description
                   (AF090143) thaumatin-like protein precursor Mdtl1 [Malus
                  domestica]
                  509
Seq. No.
Contig ID
                  273_18.R1040
5'-most EST
                  LIB3170-037-Q1-J1-A8
Method
                  BLASTN
NCBI GI
                  g22073
BLAST score
                  124
E value
                  1.0e-62
Match length
                  144
                  97
% identity
NCBI Description
                  Mung bean 25S rRNA - 18S rDNA spacer region
                  510
Seq. No.
Contig ID
                  273 19.R1040
5'-most EST
                  LIB3028-001-Q1-B1-G12
                  BLASTN
Method
NCBI GI
                  g1675195
BLAST score
                  99
E value
                  6.0e-48
Match length
                  316
% identity
NCBI Description
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
```

complete cds

```
Seq. No.
                   511
                   273 20.R1040
Contig ID
                   jsh701065521.h1
5'-most EST
Method
                   BLASTX
                   g1916809
NCBI GI
BLAST score
                   483
                   1.0e-48
E value
Match length
                   148
% identity
                   64
                   (U81163) auxin-binding protein [Prunus persica]
NCBI Description
                   512
Seq. No.
                   273_21.R1040
Contig ID
                   LIB3109-028-Q1-K1-C6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1703200
BLAST score
                   948
                   1.0e-102
E value
Match length
                   212
% identity
                   82
NCBI Description
                   PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase
                   [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)
                   protein kinase [Arabidopsis thaliana]
                   >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
Seq. No.
                   513
                   273 22.R1040
Contig ID
                   LIB3109-002-Q1-K3-G12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4337027
BLAST score
                   1473
                   1.0e-178
E value
                   687
Match length
                   72
% identity
NCBI Description
                   (AF123254) MFP2 [Arabidopsis thaliana]
Seq. No.
                   514
                   273 23.R1040
Contig ID
5'-most EST
                  LIB3138-064-Q1-N1-B5
Method
                   BLASTN
NCBI GI
                   q2656024
BLAST score
                   50
                   2.0e-18
E value
Match length
                   74
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15E6
Seq. No.
                   515
                   273 24.R1040
Contig ID
5'-most EST
                   leu701145525.hl
Method
                  BLASTX
NCBI GI
                   q4193388
BLAST score
                   182
E value
                   6.0e-20
Match length
```

```
% identity
                   (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                   brasiliensis]
Seq. No.
                   516
                   273 25.R1040
Contig ID
5'-most EST
                   q43\overline{1}3694
Method
                   BLASTX
NCBI GI
                   g4006890
BLAST score
                   472
E value
                   2.0e-46
Match length
                   112
% identity
                   78
NCBI Description
                   (Z99708) ubiquitin--protein ligase-like protein
                   [Arabidopsis thaliana]
                   517
Seq. No.
                   273 26.R1040
Contig ID
                   LIB3139-062-P1-N1-F8
5'-most EST
                   BLASTN
Method
                   g210811
NCBI GI
BLAST score
                   490
E value
                   0.0e + 00
Match length
                   1716
% identity
                   86
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
                   518
Seq. No.
                   274 1.R1040
Contig ID
5'-most EST
                   fC-qmse700606076 FL
Method
                   BLASTX
                   q1688233
NCBI GI
BLAST score
                   415
E value
                   2.0e-40
Match length
                   191
% identity
                   57
                   (U77655) DNA binding protein homolog [Solanum tuberosum]
NCBI Description
                   519
Seq. No.
                   275 1.R1040
Contig ID
5'-most EST
                   fC-gmst700648235 FL
Method
                   BLASTX
NCBI GI
                   q544134
BLAST score
                   722
E value
                   5.0e-76
Match length
                   353
% identity
                   47
NCBI Description
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
                   >gi 99720 pir S22863 hypothetical protein - Arabidopsis
                   thaliana >gi_421844_pir__A46260 RecA functional analog
                   DRT100 - Arabidopsis thaliana (fragment)
                   520
Seq. No.
                   276 1.R1040
Contig ID
5'-most EST
                   fC-gmst700658616 FL
Method
                   BLASTX
```

:162

```
g2497540
NCBÍ GI
BLAST score
                  646
E value
                  2.0e-67
Match length
                  183
                  69
% identity
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME G
NCBI Description
                  521
Seq. No.
                  277 1.R1040
Contig ID
                  LIB3167-027-P1-K1-F8
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2144584
BLAST score
                  522
                  7.0e-53
E value
                  198
Match length
                  56
% identity
                  trypsin inhibitor A (Kunitz) precursor - soybean
NCBI Description
                  >gi 18770_emb_CAA45777_ (X64447) trypsin inhibitor subtype
                  A [Glycine max]
                  522
Seq. No.
                  278_1.R1040
Contig ID
                  fC-gmst700650610i2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1362078
BLAST score
                  1082
                   1.0e-118
E value
                   286
Match length
                   67
% identity
                   endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
NCBI Description
                   - common nasturtium >gi 311835_emb_CAA48324_ (X68254)
                  cellulase [Tropaeolum majus]
                   523
Seq. No.
                   278 2.R1040
Contig ID
5'-most EST
                   LIB3106-099-Q1-K1-C4
Method
                   BLASTX
                   q1084391
NCBI GI
BLAST score
                   472
                   6.0e-47
E value
                   124
Match length
% identity
                   68.
                   endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG2)
NCBI Description
                   common nasturtium (fragment) >gi_311837_emb_CAA48325_
                   (X68255) cellulase [Tropaeolum majus]
Seq. No.
                   524
                   278 3.R1040
Contig ID
                   seb700650991.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1362078
BLAST score
                   197
E value
                   2.0e-15
Match length
                   49
                   69
% identity
                   endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
NCBI Description
                   - common nasturtium >gi_311835_emb_CAA48324_ (X68254)
```

5'-most EST



## cellulase [Tropaeolum majus]

525 Seq. No. Contig ID 279 1.R1040 5'-most EST fC-gmse700645511 FL Method BLASTX g3820648 NCBI GI BLAST score 1471 E value 0.0e + 00469 Match length % identity 67 (Y12636) allene oxide synthase [Arabidopsis thaliana] NCBI Description 526 Seq. No. Contig ID 279 2.R1040 jC-gmro02910032b07d1 5'-most EST Method BLASTX g1890152 NCBI GI BLAST score 520 E value 7.0e-53 122 Match length % identity 77 (X92510) allene oxide synthase [Arabidopsis thaliana] NCBI Description 527 Seq. No. Contig ID 279 3.R1040 5'-most EST jC-qmro02910032e06a1 BLASTX Method NCBI GI q1352186 BLAST score 406 E value 1.0e-39 Match length 141 61 % identity ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) NCBI Description (CYTOCHROME P450 74)  $>gi_404866$  (U00428) allene oxide synthase [Linum usitatissimum] 528 Seq. No. 279 4.R1040 Contig ID 5'-most EST LIB3139-066-P1-N1-A9 Method BLASTX NCBI GI g1352186 BLAST score 234 E value 2.0e-19 89 Match length % identity NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi 404866 (U00428) allene oxide synthase [Linum usitatissimum] 529 Seq. No. Contig ID 280 1.R1040 5'-most EST fC-gmse700657716 FL 530 Seq. No. 281 1.R1040 Contig ID

fC-gmse700657751 FL

Method

BLASTX

```
Method
                  BLASTX
NCBI GI
                   g4006895
BLAST score
                   423
                   2.0e-41
E value
Match length
                   139
                   55
% identity
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   531
Seq. No.
                   282_1.R1040
Contig ID
                   fC-gmse700657823_FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3157923
                  208
BLAST score
                   1.0e-16
E value
Match length
                  71
                   63
% identity
                   (AC002131) F12F1.7 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  532
Contig ID
                  283 1.R1040
5'-most EST
                   fC-gmse700657837_FL
                  533
Seq. No.
Contig ID
                  284 1.R1040
5'-most EST
                   fC-gmse700658078 FL
Seq. No.
                  534
                   285 1.R1040
Contig ID
5'-most EST
                   fC-gmse700658166 FL
                  535
Seq. No.
Contig ID
                  286 1.R1040
                  pst700645867.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4510402
                  806
BLAST score
E value
                   6.0e-86
Match length
                   311
% identity
                   (AC006587) putative AP2 domain [Arabidopsis thaliana]
NCBI Description
                  536
Seq. No.
                   287_1.R1040
Contig ID
                   fC-gmse700660136 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1531760
BLAST score
                  1055
E value
                   1.0e-115
Match length
                   329
                   62
% identity
NCBI Description
                   (X97075) proline oxidase [Arabidopsis thaliana]
                  537
Seq. No.
                  287 2.R1040
Contig ID
5'-most EST
                  LIB3170-037-Q1-J1-A5
```

```
NCBI GI
                   g1531760
BLAST score
                   295
E value
                   1.0e-26
Match length
                   86
                   69
% identity
NCBI Description
                   (X97075) proline oxidase [Arabidopsis thaliana]
                   538
Seq. No.
                   288 1.R1040
Contig ID
                   LIB3073-014-Q1-K1-F8
5'-most EST
Seq. No.
                   539
                   289 1.R1040
Contig ID
                   fC-gmse700661496 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2983642
                   732
BLAST score
                   4.0e-77
E value
                   409
Match length
                   39
% identity
                   (AE000728) diaminopimelate decarboxylase [Aquifex aeolicus]
NCBI Description
                   540
Seq. No.
                   290 1.R1040
Contig ID
                   uC-gmrominsoy258c06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4335756
BLAST score
                   833
                   3.0e-89
E value
                   229
Match length
                   72
% identity
                   (AC006284) putative ankyrin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   541
                   291_1.R1040
Contig ID
5'-most EST
                   fC-gmst700651107h1
Method
                   BLASTX
                   g2499611
NCBI GI
BLAST score
                   503
                   3.0e-98
E value
Match length
                   213
                   83
% identity
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
NCBI Description
                   (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein
                   kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis
                   thaliana]
                   542
Seq. No.
Contig ID
                   292_1.R1040
                   jC-gmro02800039g09d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q399046
                   557
BLAST score
                   6.0e-57
E value
                   141
Match length
                   82
% identity
```

```
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
                  >gi 99657_pir__S20867 adenine phosphoribosyltransferase (EC
                  2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
                   (X58640) adenine phosphoribosyltransferase [Arabidopsis
                   thaliana] >gi 433050 (L19637) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
                  >qi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
Seq. No.
                  543
                  292 2.R1040
Contig ID
5'-most EST
                  g4437087
Method
                  BLASTX
                  g399046
NCBI GI
BLAST score
                  714
                  2.0e-75
E value
                  160
Match length
% identity
                  86
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
NCBI Description
                  >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC
                  2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
                   (X58640) adenine phosphoribosyltransferase [Arabidopsis
                  thaliana] >gi_433050 (L19637) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
                  >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
Seq. No.
                  544
Contig ID
                  292 3.R1040
5'-most EST
                  g4313406
                  545
Seq. No.
                  293 1.R1040
Contig ID
5'-most EST
                  LIB3028-030-Q1-B1-A3
                  BLASTX
Method
NCBI GI
                  g2143629
BLAST score
                  227
E value
                  3.0e-18
Match length
                  172
% identity
                  Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV
NCBI Description
                   - rat >gi_986941 (L42810) 'Ca2+/calmodulin-dependent
                  protein kinase kinase' [Rattus norvegicus]
>gi_1583255_prf__2120334A Ca/calmodulin-dependent protein
                  kinase kinase [Rattus norvegicus]
                  546
Seq. No.
                  293 2.R1040
Contig ID
5'-most EST
                   zhf700964957.hl
Method
                  BLASTX
NCBI GI
                  q2143629
BLAST score
                  445
                  1.0e-43
E value
Match length
                  254
% identity
                  42
                  Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV
NCBI Description
                  - rat >gi_986941 (L42810) 'Ca2+/calmodulin-dependent
```

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protein kinase kinase' [Rattus norvegicus]

>gi 1583255 prf 2120334A Ca/calmodulin-dependent protein

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## kinase kinase [Rattus norvegicus]

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547
Seq. No.
                  293 3.R1040
Contig ID
5'-most EST
                  uC-gmronoir074f07b1
                  BLASTX
Method
                  g3024670
NCBI GI
BLAST score
                  206
                  7.0e-16
E value
                  126
Match length
                  35
% identity
                  SERINE/THREONINE-PROTEIN KINASE 11
NCBI Description
                   (SERINE/THREONINE-PROTEIN KINASE LKB1) >gi 1480861 (U63333)
                  serine/threonine protein kinase [Homo sapiens] >gi_2754827
                   (AF035625) serine threonine kinase 11 [Homo sapiens]
                  >gi 2791676 (AF032986) serine threonine kinase 11 [Homo
                  sapiens] >gi_3063585 (AF055327) Peutz-Jeghers syndrome
                  protein [Homo sapiens] >gi_4507271_ref NP 000446.1 pSTK11
                  serine/threonine kinase 11 (Peutz-Jeghers syndrome)
                  548
Seq. No.
                  294_1.R1040
Contig ID
                  uC-gmropic042b12b1
5'-most EST
Method
                  BLASTX
                  g3790188
NCBI GI
BLAST score
                  1521
                  1.0e-170
E value
Match length
                  360
% identity
                  82
                  (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana
NCBI Description
                  tabacum]
                  549
Seq. No.
                  294 3.R1040
Contig ID
                  epx701105402.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3790188
BLAST score
                  369
E value
                  2.0e-35
Match length
                  91
                  78
% identity
                  (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana
NCBI Description
                  tabacum]
                  550
Seq. No.
                  294 4.R1040
Contig ID
                  fC-\overline{g}mse700839576r1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3080424
BLAST score
                  142
                  7.0e-09
E value
Match length
                  41
                  76
% identity
                  (AL022604) NAD+ dependent isocitrate dehydrogenase subunit
NCBI Description
                  1 [Arabidopsis thaliana]
Seq. No.
                  551
```

```
Contig ID
                   295 1.R1040
5'-most EST
                   fC-gmst700661828 FL
Method
                   BLASTX
                   g119791
NCBI GI
BLAST score
                   1077
                   1.0e-117
E value
Match length
                   319
                   71
% identity
                   3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR
NCBI Description
                   (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)
                   >gi 1084385 pir _S22450 3-oxoacyl-[acyl-carrier-protein]
                   \overline{\text{reductase}} (\overline{\text{EC}} 1.1.1.100) precursor - Cuphea lanceolata
                   >gi_18046_emb_CAA45866_ (X64566) 3-oxoacyl-[acyl-carrier
                   protein] reductase [Cuphea lanceolata]
                   >gi 228929 prf 1814446A beta ketoacyl-ACP reductase
                   [Cuphea lanceolata]
Seq. No.
                   552
                   296 1.R1040
Contig ID
                   jsh701066535.hl
5'-most EST
Method
                   BLASTN
                   g2791947
NCBI GI
BLAST score
                   217
                   1.0e-118
E value
Match length
                   616
                   84
% identity
NCBI Description
                   Lupinus luteus mRNA for ribosomal protein L13a
                   553
Seq. No.
                   296 2.R1040
Contig ID
                   hrw701061971.h1
5'-most EST
                   BLASTX
Method
                   g3914535
NCBI GI
                   699
BLAST score
E value
                   8.0e-74
Match length
                   168
                   85
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L13A >gi 2791948_emb_CAA11283_
                   (AJ223363) ribosomal protein L13a [Lupinus luteus]
                   554
Seq. No.
                   296 3.R1040
Contig ID
5'-most EST
                   qsv701053623.h1
                   BLASTN
Method
NCBI GI
                   g2791947
BLAST score
                   186
                   1.0e-100
E value
Match length
                   584
                   83
% identity
                  Lupinus luteus mRNA for ribosomal protein L13a
NCBI Description
                   555
Seq. No.
Contig ID
                   296 4.R1040
                   LIB3051-088-Q1-K1-E9
5'-most EST
Method
                   BLASTX
```

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g3914535

560

NCBI GI

BLAST score

Match length

441

```
1.0e-57
E value
                   119
Match length
                   92
% identity
                   60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb CAA11283
NCBI Description
                   (AJ223363) ribosomal protein L13a [Lupinus luteus]
                   556
Seq. No.
                   297_1.R1040
Contig ID
                   fC-gmst700662785_FL
5'-most EST
                   BLASTX
Method
                   g2462749
NCBI GI
BLAST score
                   1006
                   1.0e-136
E value
Match length
                   374
                   70
% identity
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   557
Seq. No.
                   298_1.R1040
Contig ID
5'-most EST
                   fC-gmst700662976_FL
                   558
Seq. No.
                   298 2.R1040
Contig ID
5'-most EST
                   hyd700727184.hl
Seq. No.
                   559
                   299 1.R1040
Contig ID
                   fC-gmst700663110_FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2388581
BLAST score
                   1062
E value
                   1.0e-116
Match length
                   287
                   68
% identity
NCBI Description
                   (AC000098) Similar to Zea DWARF3 (gb U32579). [Arabidopsis
                   thaliana]
                   560
Seq. No.
                   300 1.R1040
Contig ID
                   fC-gmst700667704 FL
5'-most EST
                   BLASTX
Method
                   g169705
NCBI GI
                   1433
BLAST score
                   1.0e-159
E value
Match length
                   312
% identity
                   (M64737) ATP:pyruvate phosphotransferase [Ricinus communis]
NCBI Description
Seq. No.
                   561
                   301 1.R1040
Contig ID
                   LIB3106-093-Q1-K1-D3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q479386
BLAST score
                   2286
                   0.0e + 00
E value
```

Match length

721

. .

```
% identity
                  100
                  isocitrate dehydrogenase - soybean
NCBI Description
Seq. No.
                  302 1.R1040
Contig ID
                  fC-gmse700658185d3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2826842
BLAST score
                  1691
                  0.0e + 00
E value
Match length
                  491
% identity
                   (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
NCBI Description
                   563
Seq. No.
                   302 2.R1040
Contig ID
                   fC-qmf1700862926d1
5'-most EST
Method
                  BLASTX
                   q2826842
NCBI GI
BLAST score
                   366
                   6.0e-36
E value
                   109
Match length
% identity
                   (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
NCBI Description
                   564
Seq. No.
                   303 1.R1040
Contig ID
                   fC gmse700658351_FL
5'-most EST
                   BLASTX
Method
                   g730042
NCBI GI
BLAST score
                   154
                   7.0e-10
E value
                   144
Match length
% identity
                  MOSA PROTEIN >gi 1073154_pir__B53308 mosA protein -
NCBI Description
                Rhizobium meliloti (strain L5-30) >gi_310303 (L17071) mosA
                   [Rhizobium meliloti]
                   565
Seq. No.
                   304 1.R1040
Contig ID
                   fC gmf1700348376 FL
5'-most EST
Method
                   BLASTX
                   g2760839
NCBI GI
BLAST score
                   1044
                   1.0e-114
E value
Match length
                   475
% identity
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   305 1.R1040
Contig ID
5'-most EST
                   fC-qmse700658507 FL
Method
                   BLASTN
NCBI GI
                   g220729
BLAST score
                   709
                   0.0e+00
E value
```

BLAST score

129

```
% identity
                   100
                   Rat mRNA for cytochrome b5
NCBI Description
Seq. No.
                   567
                   306 1.R1040
Contig ID
                   fC-qmse700658880 FL
5'-most EST
Method
                   BLASTX
                   g3122333
NCBI GI
BLAST score
                   326
E value
                   6.0e-30
Match length
                   175
% identity
                   43
                   PUTATIVE 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT
NCBI Description
                   (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)
                   >qi 2648330 (AE000954) 3-isopropylmalate dehydratase, large
                   subunit (leuC) [Archaeoglobus fulgidus]
                   568
Seq. No.
                   307 1.R1040
Contig ID
5'-most EST
                   LIB3106-087-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   g3894183
BLAST score
                   432
                   3.0e-42
E value
Match length
                   212
                   50
% identity
                   (AC005662) calmodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   569
Seq. No.
                   308 1.R1040
Contig ID
5'-most EST
                   fC-qmse700659152 FL
Method
                   BLASTX
                   g2459435
NCBI GI
                   746
BLAST score
                   4.0e-79
E value
Match length
                   188
% identity
                   73
                  (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   570
Seq. No.
Contig ID
                   309 1.R1040
                   hrw701061722.h1
5'-most EST
Method
                   BLASTX
                   q1561774
NCBI GI
                   1806
BLAST score
E value
                   0.0e + 00
Match length
                   460
% identity
                   76
                   (U67426) malate dehydrogenase [Vitis vinifera]
NCBI Description
                   571
Seq. No.
Contig ID
                   309 2.R1040
5'-most EST
                   LIB3170-085-Q1-J1-B1
                   BLASTX
Method
                   q3687228
NCBI GI
```

```
4.0e-16
E value
Match length
                  86
                  59
% identity
                   (AC005169) putative malate dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  572
Seq. No.
                  310 1.R1040
Contig ID
                  fC-gmse700659382_FL
5'-most EST
                  BLASTX
Method
                  g1435021
NCBI GI
BLAST score
                  253
                  1.0e-21
E value
Match length
                  104
                  54
% identity
                   (D26575) DNA-binding protein [Daucus carota]
NCBI Description
Seq. No.
                  573
                  310 2.R1040
Contig ID
                  pmv700890809.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1435021
BLAST score
                  161
                  1.0e-13
E value
Match length
                  81
% identity
                  58
NCBI Description
                   (D26575) DNA-binding protein [Daucus carota]
                  574
Seq. No.
                  311 1.R1040
Contig ID
5'-most EST
                  fC-gmf1700906722f4
                  BLASTX
Method
                  g3877595
NCBI GI
                  379
BLAST score
E value
                  2.0e-36
                  158
Match length
                  50
% identity
                   (Z79696) predicted using Genefinder; Similarity to Human
NCBI Description
                  HEP27 protein (TR:G1079566); cDNA EST yk281b1.5 comes from
                  this gene; cDNA EST yk281b1.3 comes from this gene
                   [Caenorhabditis elegans] >gi_3879853_emb_CAB04734_
                  predicted using Genefinder; Similarity to Human HEP27
                  protein (TR:G1079566); cDNA EST yk281b1.5 comes from this
                  gene; cDNA EST yk281b1.3 comes from this gene
                   [Caenorhabditis elegans]
Seq. No.
                  575
Contig ID
                  311_2.R1040
5'-most EST
                  fC-gmse700659490 FL
Method
                  BLASTX
NCBI GI
                  g4105190
BLAST score
                  214
E value
                   3.0e-17
Match length
                  79
                  56
% identity
                   (AF044127) peroxisomal short-chain alcohol dehydrogenase
NCBI Description
                   [Homo sapiens]
```

BLAST score

1750

```
576
Seq. No.
                   311 3.R1040
Contig ID
                   zsg701117538.h2
5'-most EST
Method
                   BLASTX
                   g4105190
NCBI GI
BLAST score
                   165
                   1.0e-11
E value
                   94
Match length
                   48
% identity
                   (AF044127) peroxisomal short-chain alcohol dehydrogenase
NCBI Description
                   [Homo sapiens]
                   577
Seq. No.
                   312 1.R1040
Contig ID
                   LIB3106-052-Q1-K1-C2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3218410
BLAST score
                   1209
                   1.0e-133
E value
Match length:
                   412
% identity
                   (AL023859) putative prolyl-trna synthetase
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   578
Contig ID
                   312 2.R1040
                   ssr700553989.h1
5'-most EST
                   BLASTX
Method
                   g731640
NCBI GI
BLAST score
                   152
                   6.0e-10
E value
                   71
Match length
                   48
% identity
                   PUTATIVE PROLYL-TRNA SYNTHETASE YHRO20W (PROLINE--TRNA
NCBI Description
                   LIGASE) (PRORS) >gi_626755_pir__S46774 multifunctional
                   amino acid--tRNA ligase homolog - yeast (Saccharomyces
                   cerevisiae) >gi_500692 (U10399) Yhr020wp [Saccharomyces
                   cerevisiae]
                   579
Seq. No.
                   313 1.R1040
Contig ID
.5'-most EST
                   fC-gmse700659735 FL
Method
                   BLASTX
                   g1001478
NCBI GI
                   236
BLAST score
                   2.0e-19
E value
Match length
                   112
                   45
% identity
                   (D63999) hypothetical protein [Synechocystis sp.]
NCBI Description
                   580
Seq. No.
                   314 1.R1040
Contig ID
5'-most EST
                   g2934695 FL
Method
                   BLASTX
NCBI GI
                   q2934696
```

```
0.0e + 00
E value
Match length
                   333
                   96
% identity
                   (AB000097) class III acidic endochitinase [Glycine max]
NCBI Description
Seq. No.
                   581
                   314 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy253g01b1
Method
                   BLASTX
NCBI GI
                   g1345971
BLAST score
                   2308
                   0.0e + 00
E value
                   454
Match length
                   92
% identity
                  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_541947_pir__JQ2339 omega-3 fatty acid desaturase (EC
                   1.14.99.-) GMD - soybean >gi 408792 (L22965) omega-3 fatty
                   acid desaturase [Glycine soja]
                   582
Seq. No.
                   314 3.R1040
Contig ID
                   trc700562720.h1
5'-most EST
                   BLASTN
Method
                   g408791
NCBI GI
BLAST score
                   174
                   1.0e-92
E value
Match length
                   465
                   93
% identity
                  Glycine soja chloroplast omega-3 fatty acid desaturase
NCBI Description
                   (Fadd) mRNA, complete cds
                   583
Seq. No.
                   314 4.R1040
Contig ID
5'-most EST
                   g5688021
                   BLASTN
Method
NCBI GI
                   g408791
BLAST score
                   457
E value
                   0.0e+00
Match length
                   473
% identity
                   Glycine soja chloroplast omega-3 fatty acid desaturase
NCBI Description
                   (Fadd) mRNA, complete cds
                   584
Seq. No.
Contig ID
                   314 5.R1040
                   LIB3139-060-P1-N1-E3
5'-most EST
Method
                   BLASTN
NCBI GI
                   g408791
BLAST score
                   157
                   8.0e-83
E value
                   300
Match length
% identity
NCBI Description
                   Glycine soja chloroplast omega-3 fatty acid desaturase
                   (Fadd) mRNA, complete cds
Seq. No.
```

314\_9.R1040

Contig ID

```
zlv700807515.h1
5'-most EST
Method
                   BLASTN
                   q408791
NCBI GI
BLAST score
                   94
E value
                   2.0e-45
Match length
                   155
                   100
% identity
                   Glycine soja chloroplast omega-3 fatty acid desaturase
NCBI Description
                   (Fadd) mRNA, complete cds
                   586
Seq. No.
                   315_1.R1040
Contig ID
5'-most EST
                   uC-gmropic039f06b1
Method
                   BLASTN
                   g2055227
NCBI GI
BLAST score
                   258
                   1.0e-143
E value
                   494
Match length
                   100
% identity
                   Glycine max mRNA for SRC1, complete cds
NCBI Description
                   587
Seq. No.
                   315_2.R1040
Contig ID
                   uC-gmflminsoy077e06b1
5'-most EST
                   BLASTN
Method
                   g2055227
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
                   456
Match length
                   90
% identity
                   Glycine max mRNA for SRC1, complete cds
NCBI Description
                   588
Seq. No.
                   316 1.R1040
Contig ID
                   LIB3093-050-Q1-K1-E10
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2055229
BLAST score
                   941
                   0.0e + 00
E value
                   1100
Match length
                   100
% identity
                   Soybean mRNA for SRC2, complete cds
NCBI Description
                   589
Seq. No.
                   316_2.R1040
Contig ID
                   LIB\overline{3}138-048-Q1-N1-D6
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2055229
BLAST score
                   301
E value
                   1.0e-169
                   397
Match length
% identity
                   Soybean mRNA for SRC2, complete cds
NCBI Description
                   590
Seq. No.
```

316 3.R1040

uaw700661162.hl

Contig ID

5'-most EST

```
BLASTN
Method
                   g2055229
NCBI GI
                   205
BLAST score
                   1.0e-111
E value
                   718
Match length
                   93
% identity
                   Soybean mRNA for SRC2, complete cds
NCBI Description
                   591
Seq. No.
                   317 3.R1040
Contig ID
                   fC-gmse7000757201d1
5'-most EST
                   BLASTN
Method
                   g2605511
NCBI GI
BLAST score
                   161
                   2.0e-85
E value
                   283
Match length
                   89
% identity
                   Glycine max mRNA for beta subunit of beta conglycinin,
NCBI Description
                   complete cds
                   592
Seq. No.
                   317 4.R1040
Contig ID
                   LIB3170-033-Q1-K1-B12
5'-most EST
                   BLASTN
Method
                   g2605509
NCBI GI
BLAST score
                   250
                   1.0e-138
E value
                   309
Match length
                   95
% identity
                   Glycine max mRNA for alpha subunit of beta conglycinin,
NCBI Description
                   complete cds
                   593
Seq. No.
                   317_5.R1040
Contig ID
                   g50<del>5</del>7596
5'-most EST
                   BLASTN
Method
                   g2605511
NCBI GI
BLAST score
                   1041
                   0.0e + 00
E value
Match length
                   1510
                   95
% identity
                   Glycine max mRNA for beta subunit of beta conglycinin,
NCBI Description
                   complete cds
                   594
Seq. No.
                   317_6.R1040
Contig ID
                   vwf700678652.hl
5'-most EST
                   BLASTN
Method
                   g736001
NCBI GI
BLAST score
                   1339
                   0.0e + 00
E value
Match length
                   1782
                   96
% identity
                   G.soja (SH1) Gy5 mRNA for glycinin
NCBI Description
                   595
Seq. No.
```

317 7.R1040

Contig ID

```
5'-most EST
                   txt700732304.h1
Method
                   BLASTN
NCBI GI
                   q806555
BLAST score
                   619
                   0.0e + 00
E value
                   1898
Match length
% identity
                   95
                   G.soja mRNA for glycinin
NCBI Description
Seq. No.
                   596
                   317 8.R1040
Contig ID
5'-most EST
                   LIB3072-061-Q1-K1-F11
Method
                   BLASTN
NCBI GI
                   g4191813
BLAST score
                   1327
E value
                   0.0e+00
Match length
                   1706
% identity
                   96
                   Glycine max mRNA for alpha' subunit of beta-conglycinin,
NCBI Description
                   complete cds
                   597
Seq. No.
Contig ID
                   317 9.R1040
5'-most EST
                   g5688089
Method
                   BLASTN
NCBI GI
                   g18535
BLAST score
                   908
E value
                   0.0e + 00
Match length
                   1919
                   93
% identity
                   Soybean mRNA for the alpha subunit of beta-conglycinin
NCBI Description
                   598
Seq. No.
Contig ID
                   319 1.R1040
                   gsv701051475.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1944192
BLAST score
                   1302
E value
                   0.0e + 00
Match length
                   1339
                   99
% identity
                   Glycine max mRNA for nodulin 35, complete cds
NCBI Description
                   599
Seq. No.
                   321_1.R1040
Contig ID
                   leu701147347.hl
5'-most EST
Method
                   BLASTX
                   q902938
NCBI GI
                   2584
BLAST score
E value
                   0.0e + 00
Match length
                   496
% identity
NCBI Description
                   (D50866) beta-amylase [Glycine max]
```

max]

600

Seq. No.

>gi 2196550 dbj BAA20453 (AB004271) beta-amylase [Glycine

```
Contig ID
                   321 2.R1040
                   kl1701209436.hl
5'-most EST
Method
                   BLASTX
                   g1483177
NCBI GI
                   1690
BLAST score
                   0.0e+00
E value
Match length
                   730
% identity
                   49
                   (D86598) antifreeze-like protein (af70) [Picea abies]
NCBI Description
                   601
Seq. No.
Contig ID
                   321 3.R1040
5'-most EST
                   g5342495
Method
                   BLASTX
NCBI GI
                   g1483177
BLAST score
                   323
                   1.0e-29
E value
Match length
                   179
                   40
% identity
                   (D86598) antifreeze-like protein (af70) [Picea abies]
NCBI Description
                   602
Seq. No.
Contig ID
                   321 4.R1040
5'-most EST
                   g4395964
Method
                   BLASTX
NCBI GI
                   g1483177
BLAST score
                   829
E value
                   9.0e-89
Match length
                   318
% identity
                   (D86598) antifreeze-like protein (af70) [Picea abies]
NCBI Description
                   603
Seq. No.
                   321 6.R1040
Contig ID
                   LIB3139-056-P1-N1-E11
5'-most EST
                   BLASTX
Method
                   g3176874
NCBI GI
BLAST score
                   221
E value
                   4.0e-18
Match length
                   101
                   50
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   604
Seq. No.
                   321 7.R1040
Contig ID
                   jC-gmst02400066f01a2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1483177
                   208
BLAST score
                   3.0e-20
E value
Match length
                   122
                   51
% identity
                   (D86598) antifreeze-like protein (af70) [Picea abies]
NCBI Description
                   605
Seq. No.
                   322 1.R1040
Contig ID
```

```
5'-most EST
                   LIB3050-001-Q1-E1-A10
                   BLASTN
Method
                   q762878
NCBI GI
BLAST score
                   461
                   0.0e+00
E value
Match length
                   885
                   88
% identity
                   Psophocarpus tetragonolobus mRNA for chitinase, complete
NCBI Description
                   606
Seq. No.
                   322 2.R1040
Contig ID
                   fC-gmse700671501f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2370253
BLAST score
                   1290
                   1.0e-142
E value
Match length
                   575
                   49
% identity
                    (Y13273) putative protein kinase [Lycopersicon esculentum]
NCBI Description
                   607
Seq. No.
                   322 3.R1040
Contig ID
                   jC-\overline{g}mle01810025e02d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q762878
BLAST score
                   108
E value
                   1.0e-53
                   200
Match length
                   89
% identity
                   Psophocarpus tetragonolobus mRNA for chitinase, complete
NCBI Description
                   608
Seq. No.
                   322 5.R1040
Contig ID
                   fC-gmse700852775a1
.5'-most EST
Method
                   BLASTX
NCBI GI
                   g2370253
                   418
BLAST score
                   4.0e-41
E value
                   140
Match length
% identity
                    (Y13273) putative protein kinase [Lycopersicon esculentum]
NCBI Description
                   609
Seq. No.
                   322 7.R1040
Contig ID
5'-most EST
                   LIB\overline{3}051-022-Q1-K1-G7
                   610
Seq. No.
Contig ID
                   323 1.R1040
                    zsg701120865.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2463569
BLAST score
                   2103
                   0.0e+00
E value
Match length
                   413
```

97

% identity

```
(AB007503) squalene synthase [Glycine max]
NCBI Description
Seq. No.
                   611
                   323 2.R1040
Contig ID
                   gsv701053241.hl
5'-most EST
Method
                   BLASTN
                   g2463568
NCBI GI
                   287
BLAST score
                   1.0e-160
E value
                   377
Match length
                   97
% identity
                   Glycine max mRNA for squalene synthase, complete cds
NCBI Description
                   612
Seq. No.
                   324 1.R1040
Contig ID
                   epx701105763.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2529229
                   2535
BLAST score
                   0.0e + 00
E value
                   511
Match length
                   96
% identity
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                   613
Seq. No.
                   324 3.R1040
Contig ID
                   crh700851941.h1
5'-most EST
Method
                   BLASTN
                   g2529228
NCBI GI
                   71
BLAST score
                   1.0e-31
E value
                   79
Match length
                   97
% identity
                   Glycine max mRNA for 6-phosphogluconate dehydrogenase,
NCBI Description
                   complete cds
                   614
Seq. No.
                   324 4.R1040
Contig ID
                   jC-gmf102220061h02d1
5'-most EST
                   BLASTN
Method
                   g2529228
NCBI GI
                   90
BLAST score
                   6.0e-43
E value
                   90
Match length
                   100
% identity
                   Glycine max mRNA for 6-phosphogluconate dehydrogenase,
NCBI Description
                   complete cds
                   615
Seq. No.
                   324 5.R1040
Contig ID
                   trc700561367.hl
5'-most EST
Method
                   BLASTN
                   g2529228
NCBI GI
BLAST score
                   129
E value
                   3.0e-66
                   280
Match length
```

86

% identity

Contig ID

```
NCBI Description
                   Glycine max mRNA for 6-phosphogluconate dehydrogenase,
                   complete cds
                   616
Seq. No.
                   324 6.R1040
Contig ID
                   epx701109643.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2529228
BLAST score
                   83
                   5.0e-39
E value
                   139
Match length
                   90
% identity
                   Glycine max mRNA for 6-phosphogluconate dehydrogenase,
NCBI Description
                   complete cds
                   617
Seq. No.
                   324 7.R1040
Contig ID
5'-most EST
                   kl1701214664.h1
Method
                   BLASTN
                   q2529228
NCBI GI
                   102
BLAST score
                   3.0e-50
E value
                   166
Match length
                   90
% identity
                   Glycine max mRNA for 6-phosphogluconate dehydrogenase,
NCBI Description
                   complete cds
Seq. No.
                   618
                   325 1.R1040
Contig ID
                   fua701043454.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1705587
BLAST score
                   4790
                   0.0e + 00
E value
                   967
Match length
                   95
% identity
NCBI Description
                   PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE)
                   >gi 474020 dbj BAA03100 (D13998) phosphoenolpyruvate
                   carboxylase [Glycine max]
                   619
Seq. No.
                   325 2.R1040
Contig ID
5'-most EST
                   g218266_FL
Method
                   BLASTX
                   g399182
NCBI GI
BLAST score
                   4874
E value
                   0.0e + 00
Match length
                   967
                   97
% identity
                   PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME
NCBI Description
                   (PEPCASE) >gi_320128_pir__S28428 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - soybean
                   >gi_218267_dbj_BAA01560_ (D10717) phosphoenolpyruvate
                   carboxylase [Glycine max]
                   620
Seq. No.
```

325 3.R1040

Match length

506

```
uC-gmropic021f08b1
5'-most EST
                  BLASTX
Method
                   g1705587
NCBI GI
                   4817
BLAST score
                   0.0e+00
E value
                   967
Match length
                   96
% identity
                  PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE)
NCBI Description
                  >gi_474020_dbj_BAA03100_ (D13998) phosphoenolpyruvate
                  carboxylase [Glycine max]
Seq. No.
                   621
                   325 7.R1040
Contig ID
                   sat701006212.h2
5'-most EST
                   BLASTN
Method
                   g467551
NCBI GI
BLAST score
                   212
                   1.0e-116
E value
                   227
Match length
                   99
% identity
NCBI Description
                   Soybean mRNA for phosphoenolpyruvate carboxylase
                   622
Seq. No.
                   325 9.R1040
Contig ID
                   uaw700663617.h1
5'-most EST
Method
                   BLASTN
                   g218266
NCBI GI
                   82
BLAST score
                   2.0e-38
E value
                   188
Match length
                   97
% identity
                  Glycine max mRNA for phosphoenolpyruvate carboxylase,
NCBI Description
                   complete cds >gi_2175011_dbj_E06829_E06829 cDNA encoding
                   phosphoenolpyruvate carboxylase
                   >gi_2176575_dbj_E08459_E08459 cDNA encoding phosphoenol
                   pyruvate carboxylase
Seq. No.
                   623
                   328 1.R1040
Contig ID
                   rca701002203.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2626748
BLAST score
                   180
                   7.0e-97
E value
                   180
Match length
                   100
% identity
                   Glycine max mRNA for phosphoenolpyruvate carboxylase,
NCBI Description
                   partial cds, clone:GmPEPC4
                   624
Seq. No.
                   329 1.R1040
Contig ID
                   fde700873777.h1
5'-most EST
Method
                   BLASTN
                   q20906
NCBI GI
BLAST score
                   146
E value
                   4.0e-76
```

E value

```
% identity
NCBI Description
                  P.sativum mRNA for thioredoxin F isoform
Seq. No.
                  625
Contig ID
                  329 2.R1040
5'-most EST
                  LIB3138-071-P1-N1-B5
Method
                  BLASTX
                  g2266947
NCBI GI
BLAST score
                  977
E value
                  1.0e-106
Match length
                  201
% identity
                  89
NCBI Description
                  (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium
                  hirsutum]
                  626
Seq. No.
                  329 3.R1040
Contig ID
5'-most EST
                  LIB3106-005-Q1-K2-A3
                  BLASTN
Method
NCBI GI
                  g20906
BLAST score
                  78
                  9.0e-36
E value
                  242
Match length
                  83
% identity
NCBI Description
                  P.sativum mRNA for thioredoxin F isoform
Seq. No.
                  627
Contig ID
                  329 5.R1040
5'-most EST
                  ncj700987503.h1
Method
                  BLASTN
NCBI GI
                  q2626749
BLAST score
                  245
E value
                  1.0e-135
Match length
                  319
% identity
                  94
NCBI Description
                  Glycine max mRNA for phosphoenolpyruvate carboxylase,
                  partial cds, clone:GmPEPC4
                  628
Seq. No.
                  329_6.R1040
Contig ID
                  jC-gmle01810059a04d1
5'-most EST
Method
                  BLASTN
                  g2266946
NCBI GI.
                  92
BLAST score
E value
                  4.0e-44
Match length
                  132
% identity
                  92
NCBI Description
                  Gossypium hirsutum phosphoenolpyruvate carboxylase 1
                  (PEPC1) mRNA, complete cds
                  629
Seq. No.
Contig ID
                  331 1.R1040
5'-most EST
                  LIB3049-042-Q1-E1-A11
Method
                  BLASTX
NCBI GI
                  q3914403
BLAST score
                  1640
```

0.0e + 00

```
498
Match length
                   65
% identity
                   PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II)
NCBI Description
                   (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II)
                   >gi 2370335_emb_CAA73866_ (Y13466) protoporphyrinogen
                   oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_
                   (AB020500) mitochondrial protoporphyrinogen oxidase
                   [Nicotiana tabacum] >gi_4105188 (AF044129)
                   protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]
                   630
Seq. No.
                   332 3.R1040
Contig ID
                   uaw700661729.h1
5'-most EST
                   631
Seq. No.
                   332 4.R1040
Contig ID
                   jC-qmro02800042b12a1
5'-most EST
Method
                   BLASTN
                   q170048
NCBI GI
                   156
BLAST score
                   2.0e-82
E value
                   220
Match length
                   100
% identity
                   Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                   complete cds ·
                   632
Seq. No.
                   332 5.R1040
Contig ID
                   LIB\overline{3}170-028-Q1-K1-F2
5'-most EST
                   633
Seq. No.
                   332 6.R1040
Contig ID
                   LIB3170-059-Q1-J1-H2
5'-most EST
                   634
Seq. No.
                   332 7.R1040
Contig ID
                   LIB3049-008-Q1-E1-E3
5'-most EST
                   BLASTX
Method
                   q4490728
NCBI GI
                   197
BLAST score
                   1.0e-14
E value
                   110
Match length
                   42
% identity
                   (AL035709) putative protein [Arabidopsis thaliana]
NCBI Description
                   635
Seq. No.
                   333 1.R1040
Contig ID
5'-most EST
                   LIB3092-005-Q1-K1-G11
                   BLASTN
Method
NCBI GI
                   g1944318
BLAST score
                   875
E value
                   0.0e + 00
                   1051
Match length
% identity
                   Glycine max mRNA for cysteine proteinase inhibitor,
NCBI Description
```

complete cds

NCBI Description

```
636
Seq. No.
Contig ID
                   333 2.R1040
                   jC-gmf102220077a10d1
5'-most EST
Method
                  BLASTN
                  g1944318
NCBI GI
BLAST score
                  251
                  1.0e-139
E value
                   473
Match length
                  92
% identity
                  Glycine max mRNA for cysteine proteinase inhibitor,
NCBI Description
                  complete cds
                   637
Seq. No.
                   333 3.R1040
Contig ID
                   leu701150049.hl
5'-most EST
Method
                  BLASTN
                  g1944341
NCBI GI
                  245
BLAST score
                   1.0e-135
E value
                  456
Match length
                  91
% identity
                  Glycine max DNA for cysteine proteinase inhibitor, complete
NCBI Description
                   638
Seq. No.
                   333 5.R1040
Contig ID
5'-most EST
                  LIB3106-051-Q1-K1-E6
Method
                  BLASTN
                  g1944318
NCBI GI
                   151
BLAST score
                   2.0e-79
E value
Match length
                   339
                   90
% identity
                  Glycine max mRNA for cysteine proteinase inhibitor,
NCBI Description
                   complete cds
                  639
Seq. No.
Contig ID
                   334 1.R1040
                   jC-gmro02910051h08a1
5'-most EST
Method
                   BLASTX
                   g1752734
NCBI GI
BLAST score
                   3069
E value
                   0.0e+00
                   668
Match length
                   88
% identity
NCBI Description
                   (D78510) beta-glucan-elicitor receptor [Glycine max]
                   640
Seq. No.
                   335_1.R1040
Contig ID
                   sat701005149.hl
5'-most EST
                   BLASTX
Method
                   g1408322
NCBI GI
BLAST score
                   2318
                   0.0e+00
E value
                   501
Match length
% identity
```

(D86351) cytochrome P-450 (CYP93A2) [Glycine max]

```
641
Seq. No.
                   335 2.R1040
Contig ID
                   LIB3170-060-Q1-K1-G8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3913192
BLAST score
                   2659
                   0.0e+00
E value
                   509
Match length .
                   100
% identity
                   CYTOCHROME P450 93A1 >gi_2129824_pir__S62899 cytochrome
NCBI Description
                   P450 (CYP93 A1) - soybean >gi_1232111_dbj_BAA12159_
                   (D83968) Cytochrome P-450 (CYP93A1) [Glycine max]
                   >gi 1588679_prf 2209281A cytochrome P450 [Glycine max]
Seq. No.
                   642
                   335 3.R1040
Contig ID
                   LIB3051-072-Q1-K1-A6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3334665
BLAST score
                   2452、
                   0.0e+00
E value
                   503
Match length
                   95
% identity
                   (Y10492) putative cytochrome P450 [Glycine max]
NCBI Description
Seq. No.
                   643
Contig ID
                   335 4.R1040
                   jC-gmst02400015c10d1
5'-most EST
                   644
Seq. No.
                   335 5.R1040
Contig ID
                   LIB3051-054-Q1-K2-E2
5'-most EST
                   645
Seq. No.
                   335 7.R1040
Contig ID
5'-most EST
                   g5126796
Method
                   BLASTN
NCBI GI
                   g3334664
BLAST score
                   221
E value
                   1.0e-121
Match length
                   221
% identity
                   100
                  G.max mRNA for putative cytochrome P450, clone CP5
NCBI Description
                   646
Seq. No.
Contig ID
                   336 1.R1040
5'-most EST
                   LIB3139-056-P1-N1-H4
Method
                   BLASTX
NCBI GI
                   g1663724
BLAST score
                   2054
                   0.0e + 00
E value
Match length
                   542
% identity
NCBI Description
                   (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
```

647

Seq. No.

```
Contig ID
                   336 3.R1040
                   gsv701045038.hl
5'-most EST
Method
                   BLASTN
                   g18517
NCBI GI
BLAST score
                   177
                   9.0e-95
E value
                   315
Match length
                   94
% identity
                  Glycine max L. Merr mRNA for 4-coumarate:CoA ligase (clone
NCBI Description
                  4CL14)
                   648
Seq. No.
                   337 1.R1040
Contig ID
                   uC-gmrominsoy236d07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3258637
                   2115
BLAST score
E value
                   0.0e + 00
                   537
Match length
                   77
% identity
                   (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
NCBI Description
                   649
Seq. No.
                   338 1.R1040
Contig ID
                   jC-gmst02400078b03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3355486
BLAST score
                   1358
                   1.0e-150
E value
Match length
                   419
                   63
% identity
                   (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                   650
Seq. No.
                   338 2.R1040
Contig ID
5'-most EST
                   g4218186 FL
Method
                   BLASTX
NCBI GI
                   g4218187
BLAST score
                   4397
                   0.0e + 00
E value
                   854
Match length
% identity
                   (AJ010165) leghemoglobin activating factor [Glycine max]
NCBI Description
                   651
Seq. No.
                   339_1.R1040
Contig ID
                   jC-gmro02910013b11a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4468193
BLAST score
                   2258
                   0.0e+00
E value
                   502
Match length
                   90
% identity
                   (AJ010201) inosine monophosphate dehydrogenase [Glycine
NCBI Description
                   max]
```

652

Seq. No.

```
Contig ID
                   339 2.R1040
5'-most EST
                   ncj700980815.hl
                   BLASTN
Method
                   g4468192
NCBI GI
BLAST score
                   208
E value
                   1.0e-113
Match length
                   314
% identity
                   94
                  Glycine max mRNA for inosine monophosphate dehydrogenase
NCBI Description
                   653
Seq. No.
Contig ID
                   340 1.R1040
                   g4127861 FL
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4127861
BLAST score
                   802
E value
                   0.0e+00
Match length
                   832
% identity
                   99
NCBI Description
                  Glycine max mRNA for glyoxalase I
Seq. No.
Contig ID
                   340 2.R1040
                  rlr700898056.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                   g4127861
BLAST score
                   192
E value
                   1.0e-104
Match length
                   248
                   94
% identity
NCBI Description
                  Glycine max mRNA for glyoxalase I
                   655
Seq. No.
Contig ID
                   341 1.R1040
5'-most EST
                   jC-gmf102220132ae12a1
Method
                   BLASTX
NCBI GI
                   q4127878
BLAST score
                   3244
E value
                   0.0e + 00
Match length
                   626
% identity
NCBI Description
                   (AJ011831) NDX1 homeobox protein [Glycine max]
Seq. No.
Contig ID
                   342 1.R1040
5'-most EST
                   leu701153789.h1
Method
                   BLASTN
NCBI GI
                   q3341442
BLAST score
                   1010
E value
                   0.0e + 00
                  1023
Match length
                  100
% identity
                  Glycine max mRNA for root nodule acid phosphatase
NCBI Description
Seq. No.
                   657
```

342 2.R1040

leu701149822.h1

Contig ID

5'-most EST

Method

NCBI GI

BLASTN

g296444

```
Method
                    BLASTN
 NCBI GI
                    g3341442
BLAST score
                    219
 E value
                    1.0e-120
 Match length
                    386
 % identity
                    92
 NCBI Description Glycine max mRNA for root nodule acid phosphatase
 Seq. No.
                    658
 Contig ID
                   342 3.R1040
 5'-most EST
                   jC-gmf102220114h03a1
Method
                   BLASTN
NCBI GI
                   g3341442
 BLAST score
                   187
E value
                   1.0e-101
Match length
                   301
% identity
                   92
NCBI Description Glycine max mRNA for root nodule acid phosphatase
Seq. No.
                   659
Contig ID
                   343 1.R1040
5'-most EST
                   LIB3072-047-Q1-K1-D6
Method
                   BLASTN
NCBI GI
                   g296442
BLAST score
                   621
E value
                   0.0e+00
Match length
                   703
% identity
                   97
NCBI Description
                  G.max ADR11 mRNA
Seq. No.
                   660
Contig ID
                   343_2.R1040
5'-most EST
                   LIB3028-010-Q1-B1-C1
Method
                   BLASTN
NCBI GI
                   g296442
BLAST score
                   376
E value
                   0.0e + 00
Match length
                   721
% identity
                   94
NCBI Description
                  G.max ADR11 mRNA
Seq. No.
                   661
Contig ID
                   343 3.R1040
5'-most EST
                  LIB3170-024-Q1-K1-B4
Method
                  BLASTN
NCBI GI
                  g296442
BLAST score
                  101
E value
                  3.0e-49
Match length
                  288
% identity
                  93
NCBI Description G.max ADR11 mRNA
Seq. No.
                  662
Contig ID
                  344 3.R1040
5'-most EST
                  g5678078
```

BLAST score

E value

64.9

0.0e + 00

```
BLAST score
                   238
E value
                   1.0e-131
Match length
                   242
% identity
                   100
                   G.max ADR6 mRNA
NCBI Description
Seq. No.
                   663
                   344 4.R1040
Contig ID
5'-most EST
                   jC-gmro02910013g10a1
Method
                   BLASTN
NCBI GI
                   g296444
BLAST score
                   170
E value
                   1.0e-90
Match length
                   182
                   99
% identity
NCBI Description
                   G.max ADR6 mRNA
Seq. No.
                   664
                   344 5.R1040
Contig ID
                   LIB3106-102-Q1-K1-C11
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2317899
BLAST score
                   172
E value
                   1.0e-91
Match length
                   184
                   98
% identity
NCBI Description
                   Glycine max Sali3-2 mRNA, complete cds
Seq. No.
                   665
                   344 6.R1040
Contig ID
                   uC-gmropic061g09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2317900
BLAST score
                   930
E value
                   1.0e-100
Match length
                   279
                   62
% identity
                   (U89693) Sali3-2 [Glycine max]
NCBI Description
                   666
Seq. No.
                   344 7.R1040
Contig ID
5'-most EST
                   g4290365
Method -
                   BLASTN
NCBI GI
                   g2317899
BLAST score
                   523
                   0.0e + 00
E value
Match length
                   1054
                   91
% identity
NCBI Description
                  Glycine max Sali3-2 mRNA, complete cds
Seq. No.
                   667
Contig ID
                   344 8.R1040
5'-most EST
                   jsh701069031.h1
Method
                   BLASTN
NCBI GI
                   g296444
```

5'-most EST

Method

```
1123
Match length
                   94
% identity
                  G.max ADR6 mRNA
NCBI Description
                   668
Seq. No.
                   346 1.R1040
Contig ID
5'-most EST
                   bth700848391.h1
Method
                   BLASTN
NCBI GI
                   g2687725
BLAST score
                   12-32
                   0.0e+00
E value.
Match length
                   1357
                   98
% identity
NCBI Description
                   Glycine max mRNA for putative 2-hydroxydihydrodaidzein
                   reductase
                   669
Seq. No.
                   346 3.R1040
Contig ID
5'-most EST
                   jC-gmro02800032e12d1
Method
                   BLASTN
                   g2687725
NCBI GI
BLAST score
                   172
                   7.0e-92
E value
Match length
                   354
% identity
                   88
                  Glycine max mRNA for putative 2-hydroxydihydrodaidzein
NCBI Description
                  reductase
                   670
Seq. No.
Contig ID
                   348 1.R1040
5'-most EST
                  LIB3093-001-Q1-K1-B4
Method
                  BLASTX
                   g3334449
NCBI GI
BLAST score
                   1703
E value
                   0.0e+00
Match length
                  321
                   100
% identity
                  ALTERNATIVE OXIDASE 1 PRECURSOR >gi 395216 emb CAA48653
NCBI Description
                   (X68702) alternative oxidase [Glycine max]
                   >gi 740229 prf 2004454A respiratory chain terminal oxidase
                   [Glycine max]
                   671
Seq. No.
                  350 1.R1040
Contig ID
5'-most EST
                   vwf700677744.hl
Method
                  BLASTN
NCBI GI
                   q479144
BLAST score
                   553
E value
                   0.0e + 00
Match length
                   611
                   97
% identity
NCBI Description
                  G.max mRNA for ATP synthase subunit
                   672
Seq. No.
                  351 1.R1040
Contig ID
```

LIB3072-052-Q1-E1-E12

BLASTN

Method

NCBI GI

BLAST score

BLASTX

2330

q3334659

```
g18540
NCBI GI
BLAST score
                   432
                   0.0e+00
E value
Match length
                   481 🧓
% identity
                   98
NCBI Description
                   G.max BBI mRNA for proteinase inhibitor
Seq. No.
                   351 2.R1040
Contig ID
5'-most EST
                   LIB3029-009-Q1-B1-A6
Method
                   BLASTN
NCBI GI
                   g18540
BLAST score
                   200
                   1.0e-108
E value
Match length
                   431
% identity
                   95
NCBI Description
                   G.max BBI mRNA for proteinase inhibitor
                   674
Seq. No.
Contig ID
                   352 1.R1040
5'-most EST
                   euj700697942.hl
Method
                   BLASTX
NCBI GI
                   q434061
BLAST score
                   2023
                   0.0e + 00
E value
Match length
                   421
% identity
                   (D16107) basic 7S globulin [Glycine max]
NCBI Description
Seq. No.
Contig ID
                   352 2.R1040
5'-most EST
                   zpv700757208.h1
Method
                   BLASTN
NCBI GI
                   q434060
BLAST score
                   347
E value
                   0.0e+00
Match length
                   483
% identity
                   95
                   Soybean DNA for basic 7S globulin, complete cds
NCBI Description
                   676
Seq. No.
Contig ID
                   352 6.R1040
5'-most EST
                   txt700732264.h1
Method
                   BLASTN
NCBI GI
                   q18542
BLAST score
                   220
E value
                   1.0e-120
Match length
                   343
% identity
NCBI Description
                  Soybean Bg gene for basic 7S globulin
Seq. No.
Contig ID
                   353 1.R1040
5'-most EST
                   g3334658 FL
```

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Match length

504

```
0.0e + 00
E value
Match length
                   480
% identity
NCBI Description
                   (Y10489) putative cytochrome P450 [Glycine max]
                   678
Seq. No.
                   354 1.R1040
Contig ID
5'-most EST
                   g3334660_FL
Method
                   BLASTX
                   g3334661
NCBI GI
BLAST score
                   2337
E value
                   0.0e+00
Match length
                   496
                   92
% identity
NCBI Description
                   (Y10490) putative cytochrome P450 [Glycine max]
                   679
Seq. No.
Contig ID
                   354 3.R1040
                   leu701150560.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3334661
BLAST score
                   526
E value
                   1.0e-53
Match length
                   154
% identity
                   69
NCBI Description
                   (Y10490) putative cytochrome P450 [Glycine max]
                   680
Seq. No.
Contig ID
                   355 1.R1040
5'-most EST
                   g3334662_FL
Method
                   BLASTX
NCBI GI
                   g3334663
BLAST score
                   2601
                   0.0e+00
E value
Match length
                   522
% identity
NCBI Description
                   (Y10491) putative cytochrome P450 [Glycine max]
                   681
Seq. No.
                   355 2.R1040
Contig ID
                   LIB3170-032-Q1-J1-E8
5'-most EST
Method
                   BLASTX
                   g2765093
NCBI GI
BLAST score
                   229
                   2.0e-20
E value
                   74
Match length
% identity
                   68
NCBI Description
                   (Y10983) putative cytochrome P450 [Glycine max]
                   682
Seq. No.
                   357_1.R1040
Contig ID
5'-most EST
                   g3334666_FL
Method
                   BLASTX
NCBI GI
                   g3334667
BLAST score
                   2548
                   0.0e+00
E value
```

Method

BLASTN

```
% identity
NCBI Description
                    (Y10493) putative cytochrome P450 [Glycine max]
                   683
Seq. No.
                   358 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910006h12a1
                   BLASTX
Method
NCBI GI
                   q398957
                   2529
BLAST score
E value
                   0.0e + 00
Match length
                   484
                   99
% identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (ACC SYNTHASE)
NCBI Description
                    (S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE)
                   >gi_99885_pir__S25002 1-aminocyclopropane-1-carboxylate
synthase (EC 4.4.1.14) - soybean >gi_18558_emb_CAA47474_
                   (X67100) 1-aminocyclopropane 1-carboxylate synthase
                    [Glycine max] >gi 1090777_prf__2019442A aminocyclopropane
                   carboxylate synthase [Glycine max]
                   684
Seq. No.
Contig ID
                   359 1.R1040
                   LIB3055-002-Q1-B1-F10
5'-most EST
Method
                   BLASTX
                   q3059095
NCBI GI
BLAST score
                   6994
E value
                   0.0e + 00
Match length
                   1383
                   98
% identity
                   (AJ001091) magnesium chelatase subunit [Glycine max]
NCBI Description
Seq. No.
                   359 2.R1040
Contig ID
5'-most EST
                   fC-qmle7000743672r1
Method
                   BLASTN
NCBI GI
                   g3059094
BLAST score
                   204
                   1.0e-111
E value
Match length
                   324
% identity
                   91
                   Glycine max mRNA for magnesium chelatase subunit
NCBI Description
                   686
Seq. No.
                   359 3.R1040
Contig ID
5'-most EST
                   fC-gmle700557852f2
                   BLASTN
Method
NCBI GI
                   g3059094
BLAST score
                   164
                   3.0e-87
E value
Match length
                   212
                   94
% identity
NCBI Description
                   Glycine max mRNA for magnesium chelatase subunit
Seq. No.
Contig ID
                   360 1.R1040
5'-most EST
                   LIB3072-010-Q1-E1-B3
```

```
q169944
NCBI GI
BLAST score
                   425
                   0.0e+00
E value
Match length
                   476
                   98
% identity
                  Soybean protease inhibitor C-II mRNA, complete cds
NCBI Description
Seq. No.
                   361 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910036a01a1
                  BLASTX
Method
NCBI GI
                  g3915111
                   2471
BLAST score
                   0.0e + 00
E value
Match length
                   506
                   95
% identity
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                   4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_1044868_emb_CAA63172_ (X92437) cinnamic acid
                   4-hydroxylase [Glycine max]
Seq. No.
                   689
                   361 2.R1040
Contig ID
                                                                          377
5'-most EST
                   q42\overline{9}8689
Method
                  BLASTN
NCBI GI
                  g1044867
BLAST score
                  287
                   1.0e-160
E value
Match length
                   454
                   94
% identity
                  Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73)
NCBI Description
Seq. No.
                   690
                   361 3.R1040
Contig ID
                   taw700660393.h1
5'-most EST
                  BLASTN
Method
                  g1044867
NCBI GI
BLAST score
                   248
E value
                   1.0e-137
Match length
                   443
                   90
% identity
                  Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73)
NCBI Description
Seq. No.
                   691
Contig ID
                   362 1.R1040
5'-most EST
                   jsh701065321.h1
Method
                  BLASTX
NCBI GI
                  g1362047
BLAST score
                  1962
                  0.0e+00
E value
                   380
Match length
                   97
% identity
                  cysteine proteinase (EC 3.4.22.-) precursor - soybean
NCBI Description
                  >gi_479060_emb_CAA83673_ (Z32795) cysteine proteinase
                   [Glycine max] >gi_1096153_prf__2111244A Cys protease
```

[Glycine max]

```
692
Seq. No.
                   362 8.R1040
Contig ID
                   awf700839974.h1
5'-most EST
                   BLASTN
Method
                   g479059
NCBI GI
BLAST score
                   126
E value
                   1.0e-64
Match length
                   138
% identity
                   98
                   G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
                   693
Seq. No.
                   363 1.R1040
Contig ID
                   LIB3072-023-Q1-E1-B2
5'-most EST
                   BLASTN
Method
NCBI GI
                   g18571
BLAST score
                   416
E value
                   0.0e + 00
                   444
Match length
                   99
% identity
NCBI Description
                  G.max D-II mRNA for proteinase isoinhibitor D-II
                   694
Seq. No.
Contig ID
                   365 1.R1040
5'-most EST
                  LIB3073-008-Q1-K1-E7
Method
                  BLASTN
NCBI GI
                   g886869
BLAST score
                   659
E value
                   0.0e + 00
Match length
                   789
                   96
% identity
NCBI Description
                  G.max ENOD40-2 gene
                   695
Seq. No.
                   367 1.R1040
Contig ID
5'-most EST
                   g218253 FL
Method
                  BLASTN
NCBI GI
                   g218253
BLAST score
                   643
E value
                   0.0e+00
                   735 -
Match length
                   100 .
% identity
NCBI Description
                  Soybean mRNA for early nodulin
Seq. No.
                   696
Contig ID
                   367 2.R1040
5'-most EST
                  LIB3170-042-Q1-J1-A10
Method
                  BLASTX
NCBI GI
                  g134892
BLAST score
                   357
                   1.0e-33
E value
Match length
                   146
% identity
                   46
                  SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
NCBI Description
                   (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                  >gi 88607 pir A29440 signal recognition particle receptor
                   - human >gi 30866 emb CAA29608 (X06272) docking protein
```

Match length

NCBI Description

% identity

909

98

[Homo sapiens] >gi\_4507223\_ref\_NP\_003130.1\_pSRPR\_ signal recognition particle receptor ('docking protein')

Seq. No. 367 3.R1040 Contig ID LIB3139-078-P1-N1-A12 5'-most EST Method BLASTX NCBI GI g134892 BLAST score 184 E value 4.0e-13 Match length 125 % identity 42 SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT NCBI Description (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi\_88607\_pir\_\_A29440 signal recognition particle receptor - human >gi 30866 emb CAA29608 (X06272) docking protein [Homo sapiens] >gi 4507223 ref\_NP\_003130.1\_pSRPR\_ signal recognition particle receptor ('docking protein') Seq. No. Contig ID 367 4.R1040 5'-most EST rlr700898123.hl Method BLASTX NCBI GI q134891 BLAST score 392 E value 8.0e-38 Match length 113 % identity 66 SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT NCBI Description (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi\_89066\_pir\_\_A24570 signal recognition particle receptor precursor - dog >gi\_997\_emb\_CAA26945\_ (X03184) signal recognition particle receptor [Canis sp.] >gi 224778 prf 1112224A signal recognition particle receptor [Canis familiaris] 699 Seq. No. 367 5.R1040 Contig ID LIB3092-036-Q1-K1-F9 5'-most EST Method BLASTN NCBI GI g18584 BLAST score 316 E value 1.0e-177 562 Match length 98 % identity NCBI Description G.max ENOD55-1 mRNA Seq. No. 370 1.R1040 Contig ID 5'-most EST LIB3051-027-Q1-K1-D6 Method BLASTN NCBI GI g2052028 824 BLAST score 0.0e+00E value

G.max mRNA for glutathione transferase

% identity

98

```
701
Seq. No.
Contig ID
                   370 2.R1040
                   jC-gmle01810024d08a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2920665
BLAST score
                   779
E value
                   0.0e+00
Match length
                   858
                   97
% identity
                   Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
Seq. No.
Contig ID
                   370 3.R1040
5'-most EST
                   LIB3051-051-Q1-K1-A5
Method
                   BLASTN
NCBI GI
                   q2920665
BLAST score
                   329
E value
                   0.0e + 00
Match length
                   341
% identity
                   99
                   Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
Seq. No.
                   370 5.R1040
Contig ID
                   LIB3051-097-Q1-K1-E8
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2920665
                   252
BLAST score
                   1.0e-139
E value
Match length
                   284
% identity
                   97
NCBI Description
                   Glycine max 2,4-D inducible glutathione S-transferase
                   (GSTa) mRNA, complete cds
                   704
Seq. No.
                   374 1.R1040
Contig ID
5'-most EST
                   pxt700943646.h1
Method
                   BLASTN
                   g505584
NCBI GI
                   915
BLAST score
                   0.0e+00
E value
Match length
                   931
% identity
                   100
                  G.max mRNA for Glyoxalase I
NCBI Description
                   705
Seq. No.
                   376 1.R1040
Contig ID
                   fC-gmst700653759a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g121336
BLAST score
                   1799
E value
                   0.0e+00
Match length
                   342
```

Method

NCBI GI

BLASTN

g256142

```
GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME (GLUTAMATE--AMMONIA
 NCBI Description
                    LIGASE) >gi_81774_pir__JQ0937 glutamate--ammonia ligase (EC 6.3.1.2), cytosolic - soybean >gi_256143_bbs_113802
                    (S46513) cytosolic glutamine synthetase, GS (EC 6.3.1.2)
                    [Glycine max=soybeans, var Prize, Peptide, 355 aa] [Glycine
                    max]
 Seq. No.
                    706
                    376 2.R1040
 Contig ID
 5'-most EST
                    asj700967306.hl
                    BLASTX
Method
                    g3128203
 NCBI GI
 BLAST score
                    465
E value
                    3.0e-61
                    171
Match length
                    73
 % identity
                    (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    707
                    376 3.R1040
Contig ID
                    LIB3109-056-Q1-K1-D5
 5'-most EST
Method
                    BLASTN
NCBI GI
                    g547507
                    1332
BLAST score
E value
                    0.0e + 00
                    1431
Match length
                    99
 % identity
                    G.max mRNA for glutamine synthetase
NCBI Description
Seq. No.
                    376 4.R1040
Contig ID
 5'-most EST
                    g587119 FL
Method
                    BLASTX
NCBI GI
                    g587120
BLAST score
                    1756
E value
                    0.0e + 00
Match length
                    340
                    96
 % identity
                    (X81460) glutamate--ammonia ligase [Glycine max]
NCBI Description
                    709
Seq. No.
                    376 5.R1040
Contig ID
                    jC-gmst02400005f10d1
 5'-most EST
                    BLASTN
Method
NCBI GI
                    g256142
                    397
BLAST score
                    0.0e+00
E value
                    458
Match length
                    95
 % identity
                    cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                    Prize, mRNA, 1450 nt]
Seq. No.
                    710
                    376 6.R1040
Contig ID
 5'-most EST
                    fC-gmst700653759h1
```

Match length

% identity

93

- 132's

```
BLAST score
                   453
                   0.0e+00
E value
Match length
                   707
% identity
                   cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
Seq. No.
                   711
Contig ID
                   376 7.R1040
5'-most EST
                   pcp700994236.hl
Seq. No.
                   712
                   376 10.R1040
Contig ID
5'-most EST
                   zhf700959375.h1
Seq. No.
                   713
                   376 11.R1040
Contig ID
5'-most EST
                   fde700875135.hl
                   BLASTN
Method
                   g312300
NCBI GI
BLAST score
                   77
                   3.0e-35
E value
Match length
                   242
% identity
                   94
NCBI Description
                   G.max cDNA for glutamine synthetase (3' region)
                   714
Seq. No.
Contig ID
                   379 1.R1040
5'-most EST
                   LIB3051-029-Q1-K1-E5
Method
                   BLASTN
NCBI GI
                   g18642
BLAST score
                   720
E value
                   0.0e + 00
Match length
                   737
% identity
                   99
                   G.max mRNA from stress-induced gene (H4)
NCBI Description
Seq. No.
                   379 2.R1040
Contig ID
                   LIB3051-111-Q1-K1-C1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g18743
BLAST score
                   743
                   0.0e + 00
E value
                   771
Match length
% identity
                   99
                   G.max mRNA from stress-induced gene (SAM22)
NCBI Description
                   716
Seq. No.
                   379 4.R1040
Contig ID
5'-most EST
                   LIB3051-111-Q1-K1-G5
Method
                   BLASTN
NCBI GI
                   g18642
BLAST score
                   409
E value
                   0.0e+00
                   662
```

```
NCBI Description G.max mRNA from stress-induced gene (H4)
                   717
Seq. No.
                   379 5.R1040
Contig ID
5'-most EST
                   g4396357
Method
                   BLASTN
NCBI GI
                   g18743
BLAST score
                   266
                   1.0e-148
E value
Match length
                   478
                   93
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
Seq. No.
                   379_6.R1040
Contig ID
5'-most EST
                   zsg701125214.h1
Method
                   BLASTN
NCBI GI
                   g18743
BLAST score
                   425
                   0.0e+00
E value
Match length
                   547
                   96
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                   719
Seq. No.
Contig ID
                   379 10.R1040
5'-most EST
                   LIB3051-048-Q1-K1-C11
Method
                   BLASTN
NCBI GI
                   g18743
BLAST score
                   337
E value
                   0.0e+00
Match length
                   431
                   98
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
                   720
Seq. No.
                   379 15.R1040 ·
Contig ID
5'-most EST
                  LIB3051-022-Q1-K1-F2
Method
                  BLASTN
                   g18743
NCBI GI
BLAST score
                   140
E value
                   9.0e-73
Match length
                   309
% identity
                   93
NCBI Description G.max mRNA from stress-induced gene (SAM22)
Seq. No.
                   721
Contig ID
                   380 1.R1040
5'-most EST
                   kll701212864.hl
                  BLASTN
Method
NCBI GI
                   g18644
BLAST score
                   761
                   0.0e + 00
E value
Match length
                   761
% identity
                   100
```

NCBI Description Soybean mRNA for HMG-1 like protein

Contig ID

```
Seq. No.
                    722
                    380 2.R1040
 Contig ID
 5'-most EST
                    LIB3167-078-P1-K2-H1
 Method
                    BLASTN
                    g18644
 NCBI GI
 BLAST score
                    148
 E value
                    2.0e-77
                    172
 Match length
                    97
 % identity
                    Soybean mRNA for HMG-1 like protein
 NCBI Description
 Seq. No.
                    380 3.R1040
 Contig ID
                    jC-\overline{gmst02400001g11a1}
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    g18644
 BLAST score
                    287
 E value
                    1.0e-160
 Match length
                    339
 % identity
                    96
NCBI Description
                    Soybean mRNA for HMG-1 like protein
 Seq. No.
                    724
                    380 4.R1040
 Contig ID
 5'-most EST
                    uC-gmflminsoy069c08b1 .
 Method
                    BLASTN
 NCBI GI
                    g18644
 BLAST score
                    148
                    2.0e-77
 E value
 Match length
                    311
                    95
 % identity
 NCBI Description
                    Soybean mRNA for HMG-1 like protein
                    725
 Seq. No.
                    381 1.R1040
 Contig ID
 5'-most EST
                    k11701213229.h1
                    BLASTN
 Method
 NCBI GI
                    g18646
 BLAST score
                    791
                    0.0e+00
 E value
                    832
 Match length
                    99
 % identity
                    Soybean mRNA for HMG-Y related protein, variant A
 NCBI Description
 Seq. No.
                    726
 Contig ID
                    381 2.R1040
 5'-most EST
                    LIB3039-026-Q1-E1-H1
 Method
                    BLASTN
 NCBI GI
                    g18648
 BLAST score
                    577
                    0.0e+00
 E value
                    585
 Match length
                    100
 % identity
                    Soybean mRNA for HMG-Y related protein, variant B
 NCBI Description
 Seq. No.
```

383 1.R1040

```
5'-most EST
                   g662923 FL
Method
                  BLASTN
NCBI GI
                   g662923
BLAST score
                   504
E value
                   0.0e + 00
Match length
                   654
% identity
                   100
NCBI Description
                  G.max mRNA for heat shock transcription factor
Seq. No.
Contig ID
                   384 1.R1040
5'-most EST
                   jC-gmro02910010e01a1
Method
                  BLASTN
NCBI GI
                  g662925
BLAST score
                  1373
                  0.0e+00
E value
Match length
                  1373
                  100
% identity
NCBI Description
                  G.max mRNA for heat shock transcription factor
                  729
Seq. No.
Contig ID
                   384 2.R1040
5'-most EST
                   jC-gmro02910074f07a1
                  BLASTN
Method
                  g662927
NCBI GI
BLAST score
                  1188
E value
                  0.0e+00
Match length
                  1188
                  100
% identity
NCBI Description
                  G.max mRNA for heat shock transcription factor
Seq. No.
Contig ID
                  384 3.R1040
                  ncj700982933.h1
5'-most EST
                  731
Seq. No.
Contig ID
                  385 1.R1040
5'-most EST
                  g662931 FL
                  BLASTX
Method
NCBI GI
                  g2129832
BLAST score
                  1659
E value
                  0.0e+00
Match length
                  370
% identity
                  87
NCBI Description
                  heat shock transcription factor 5 - soybean
                  >gi_671868_emb_CAA87080_ (Z46956) heat shock transcription
                  factor 5 [Glycine max]
Seq. No.
                  732
Contig ID
                  385 2.R1040
5'-most EST
                  g662926 FL
Method
                  BLASTN
NCBI GI
                  g662926
BLAST score
                  988
E value
                  0.0e + 00
```

1014

100

Match length

% identity

```
NCBI Description G.max mRNA for heat shock transcription factor
                   733
Seq. No.
Contig ID
                   385 3.R1040
5'-most EST
                   fC-gmse700725253a1
Method
                   BLASTN
NCBI GI
                   g662931
BLAST score
                   212
E value
                   1.0e-115
Match length
                   489
% identity
                   89
NCBI Description
                   G.max mRNA for heat shock transcription factor
Seq. No.
                   387 1.R1040
Contig ID
5'-most EST
                   bth700845329.h1
Method
                   BLASTN
NCBI GI
                   g662929
BLAST score
                   1376
E value
                   0.0e + 00
Match length
                   1380
                   100
% identity
                   G.max mRNA for heat shock transcription factor
NCBI Description
Seq. No.
                  735
                   387 2.R1040
Contig ID
5'-most EST
                   g56<u>0</u>6125
                   BLASTN
Method
NCBI GI
                   g662929
BLAST score
                   465
E value
                   0.0e+00
Match length
                   541
                   97
% identity
NCBI Description
                   G.max mRNA for heat shock transcription factor
                   736
Seq. No.
                   387 3.R1040
Contig ID
5'-most EST
                   dpv701100361.h1
Method
                   BLASTN
NCBI GI
                   g662929
BLAST score
                   161
                   3.0e-85
E value
Match length
                   427
% identity
                   90
NCBI Description
                  G.max mRNA for heat shock transcription factor
Seq. No.
                   737
Contig ID
                   387 4.R1040
5'-most EST
                   uC-gmrominsoy044a01b1
Method
                   BLASTN
NCBI GI
                   g662929
BLAST score
                   281
E value
                   1.0e-157
Match length
                   472
% identity
                   94
```

NCBI Description G.max mRNA for heat shock transcription factor

BLAST score

```
738
 Seq. No.
                    389 1.R1040
 Contig ID
                    epx701104693.h1
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    q18658
 BLAST score
                    547
                    0.0e+00
 E value
 Match length
                    668
                    99
 % identity
 NCBI Description
                    Soybean hsp22 mRNA
 Seq. No.
                    390 1.R1040
 Contig ID
                    hrw701060990.h1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g418854
 BLAST score
                    1149
. E value
                    1.0e-126
 Match length
                    230
                    25
 % identity
                    ubiquitin precursor - parsley >gi_288112_emb_CAA45621
 NCBI Description
                    (X64344) polyubiquitin [Petroselinum crispum]
                    >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                    [Petroselinum crispum]
                    740
 Seq. No.
 Contig ID
                    390 2.R1040 ·
 5'-most EST
                    LIB3028-001-Q1-B1-C10
 Method
                    BLASTX
 NCBI GI
                    g418854
 BLAST score
                    1528
                    1.0e-170
 E value
 Match length
                    306
 % identity
                    ubiquitin precursor - parsley >gi_288112_emb_CAA45621_
 NCBI Description
                    (X64344) polyubiquitin [Petroselinum crispum]
                    >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                    [Petroselinum crispum]
 Seq. No.
                    741
 Contig ID
                    391 1.R1040
 5'-most EST
                    epx701105962.h1
 Method
                    BLASTN
 NCBI GI
                    q1575724
 BLAST score
                    712
                    0.0e+00
 E value
 Match length
                    988
 % identity
 NCBI Description
                    Glycine max 14-3-3 related protein SGF14A mRNA, complete
 Seq. No.
                    742
                    391 2.R1040
 Contig ID
 5'-most EST
                    LIB3051-029-Q1-K1-G4
 Method
                    BLASTN
                    q1575724
 NCBI GI
```

NCBI GI

```
E value
                   1.0e-109
Match length
                   426
% identity
                   91
NCBI Description
                   Glycine max 14-3-3 related protein SGF14A mRNA, complete
                   cds
Seq. No.
                   743
                   392 1.R1040
Contig ID
5'-most EST.
                   uC-gmropic050e09b1
Method
                   BLASTN
NCBI GI
                   q3452090
BLAST score
                   390
E value
                   0.0e + 00
Match length
                   398
                   99
% identity
                   Glycine max mRNA for rudimentary enhancer, partial
NCBI Description
Seq. No.
                   392 2.R1040
Contig ID
                   kl1701213706.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3452090
BLAST score
                   202
E value
                   1.0e-110
Match length
                   243
                   96
% identity
NCBI Description Glycine max mRNA for rudimentary enhancer, partial
Seq. No.
                   745
                   393 1.R1040
Contig ID
5'-most EST
                   LIB3051-007-Q1-E1-D10
                   BLASTN
Method
                   g3452136
NCBI GI
BLAST score
                   235
E value
                   1.0e-129
Match length
                   243
% identity
                   100
                   Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
                   746
Seq. No.
                   393 2.R1040
Contig ID
5'-most EST
                   hrw701063583.h1
                                                  ·..
Method
                   BLASTN
NCBI GI
                   g603218
BLAST score
                   392
E value
                   0.0e + 00
Match length
                   752
                   88
% identity
                  Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
NCBI Description
                   complete cds
Seq. No.
                   747
Contig ID
                   395_1.R1040
5'-most EST
                   rlr700896427.h1
Method
                   BLASTN
```

g3452143

Method

```
529
BLAST score
                   0.0e+00
E value
                   643
Match length
                   96
% identity
NCBI Description
                  Glycine max mRNA for chalcone isomerase, partial
Seq. No.
                   748
                   396 1.R1040
Contig ID
                   LIB3051-107-Q1-K1-D2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g510514
BLAST score
                   683
E value
                   0.0e + 00
                   747
Match length
                   98
% identity
NCBI Description
                  G.max KTi-S mRNA
                   749
Seq. No.
Contig ID
                   397 1.R1040
5'-most EST
                   LIB3065-009-Q1-N1-C8
                   BLASTX
Method
NCBI GI
                   g2129827 *
BLAST score
                   2163
E value
                   0.0e + 00
Match length
                   473
                   91
% identity
                   embryonic abundant protein group 3 precursor (clone PM10) -
NCBI Description
                   soybean >gi_414977 (U02966) 51 kDa seed maturation protein
                   [Glycine max]
                   750
Seq. No.
                   397 2.R1040
Contig ID
5'-most EST
                   g311697 FL
Method
                   BLASTX
NCBI GI
                   g421875
BLAST score
                   1921
E value
                   0.0e + 00
Match length
                   458
% identity
                   83
                  Lea protein - soybean >gi_311698_emb_CAA80491 (Z22872) Lea
NCBI Description
                  protein [Glycine max]
                   751
Seq. No.
Contig ID
                   398 1.R1040
5'-most EST
                   zpv700762262.h1
Method
                   BLASTX
                   q505138
NCBI GI
BLAST score
                   4431
E value
                   0.0e + 00
Match length
                   866
% identity
NCBI Description
                   (D13949) lipoxygenase-2 [Glycine max]
Seq. No.
                   752
Contig ID
                   398 2.R1040
5'-most EST
                   g18674 FL
```

BLASTX

```
NCBI GI
                   q126398
BLAST score
                   4277
                   0.0e+00
E value
Match length
                   839
                   98
% identity
NCBI Description
                   SEED LIPOXYGENASE-1 (L-1) >gi_2144382_pir__DASYL2
                   lipoxygenase (EC 1.13.11.12) 1 - soybean
                   >gi 1000060 pdb 2SBL B Lipoxygenase-1 (Soybean)
                   (E.C.1.13.11.12) >gi 2392632 pdb 1YGE_
                                                             Lipoxygenase-1
                   (Soybean) At 100k >gi_18675_emb_CAA47717_ (X67304)
                   lipoxygenase [Glycine max] >gi 295118 (J02795)
                   lipoxygenase-1 [Glycine max]
Seq. No.
                   400_1.R1040
Contig ID
                   uC-gmrominsoy125f04b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1262439
BLAST score
                   229
E value
                   1.0e-125
Match length
                   585
% identity
                   85
                   Glycine max lipoxygenase (vlxC) mRNA, complete cds
NCBI Description
Seq. No.
                   754
                   400 2.R1040
Contig ID
5'-most EST
                   dpv701096996.hl
Method
                   BLASTX
NCBI GI
                   g436169
BLAST score
                   752
E value
                   6.0e-80
                   219
Match length
% identity
NCBI Description
                   (U04526) lipoxygenase [Glycine max]
Seq. No.
                   400 3.R1040
Contig ID
                   dpv701102162.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3319774
BLAST score
                   174
                   3.0e-12
E value
Match length
                   43
                   72
% identity
                   (Y16228) TOM7 protein [Solanum tuberosum]
NCBI Description
                   756
Seq. No.
                   400 4.R1040
Contig ID
5'-most EST
                   fC-qmse7000756638a1
Method
                   BLASTX
NCBI GI
                   g126409
BLAST score
                   1062
E value
                   0.0e+00
Match length
                   739
% identity
                   78
NCBI Description
                   LIPOXYGENASE 1 >gi 100005 pir S22153 lipoxygenase (EC
```

1.13.11.12) - kidney bean >gi\_21017\_emb\_CAA45088\_ (X63525)

. ....

5'-most EST

Method

## lipoxygenase [Phaseolus vulgaris]

```
757
Seq. No.
                   400 5.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy016g08b1
Method
                   BLASTX
NCBI GI
                   g1262440
BLAST score
                   1354
                   0.0e + 00
E value
Match length
                   861
% identity
NCBI Description
                   (U26457) lipoxygenase [Glycine max]
Seq. No.
                   400 6.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy011c10b1
Method
                  BLASTX
NCBI GI
                   g126411
BLAST score
                   1189
E value
                   0.0e + 00
Match length
                  874
% identity
                   61
NCBI Description
                  SEED LIPOXYGENASE >gi 99932 pir S13381 lipoxygenase (EC
                  1.13.11.12) - soybean >gi 18746 emb CAA39604 (X56139)
                  lipoxygenase [Glycine max]
                  759
Seq. No.
Contig ID
                   400 7.R1040
5'-most EST
                  uC-gmrominsoy256a03b1
Method
                  BLASTX
NCBI GI
                  g126404
BLAST score
                  1058
E value
                  0.0e + 00
Match length
                  873
                   49
% identity
NCBI Description
                  SEED LIPOXYGENASE-2 (L-2) >gi 66331 pir DASYL1
                  lipoxygenase (EC 1.13.11.12) 2 - soybean >gi 170014
                   (J03211) lipoxygenase (EC 1.13.11.12) [Glycine max]
Seq. No.
                  760
                  401 1.R1040
Contig ID
5'-most EST
                  ncj700981157.h1
                  BLASTX
Method
NCBI GI
                  g116157
BLAST score
                  1901
                  0.0e + 00
E value
Match length
                  455
% identity
NCBI Description
                  G2/MITOTIC-SPECIFIC CYCLIN S13-6 (B-LIKE CYCLIN)
                  >gi 99895 pir S16522 cyclin, mitotic - soybean
                  >gi 18682 emb CAA44632 (X62820) mitotic cyclin [Glycine
                  max]
                  761
Seq. No.
Contig ID
                  403 1.R1040
```

uC-gmropic091h10b1

BLASTN

BLAST score

```
NCBI GI
                   g18688
BLAST score
                   497
E value
                   0.0e+00
Match length
                   813
                   96
% identity
NCBI Description
                   Soybean nodulin-20 gene
Seq. No.
                   404 1.R1040
Contig ID
5'-most EST
                   g18693 FL
                   BLASTN
Method
                   g18693
NCBI GI
BLAST score
                   810
E value
                   0.0e+00
Match length
                   810
                   100
% identity
                   Soybean mRNA for Nodulin-21
NCBI Description
Seq. No.
                   763
                   406 1.R1040
Contig ID
                   k11701203084.h1
5'-most EST
Method
                   BLASTN
                   g18709
NCBI GI
BLAST score
                   1060
E value
                   0.0e + 00
                   1107
Match length
                   99
% identity
                   Soybean mRNA for nodulin-26
NCBI Description
                   764
Seq. No.
                   409 1.R1040
Contig ID
5'-most EST
                   g18711_FL
Method
                   BLASTN
NCBI GI
                   g18711
BLAST score
                   892
                   0.0e+00
E value
                   892
Match length
                   100
% identity
NCBI Description
                   Soybean mRNA for nodulin-27
                   765
Seq. No.
                   410 1.R1040
Contig ID
5'-most EST
                   g18717_FL
Method
                   BLASTN
NCBI GI
                   g18717
BLAST score
                   1299
E value
                   0.0e+00
Match length
                   1303
                   100
% identity
                   Soy bean mRNA for nodulin (E27)
NCBI Description
                   766
Seq. No.
                   410 2.R1040
Contig ID
5'-most EST
                   g18715_FL
Method
                   BLASTN
NCBI GI
                   q18715
```

```
0.0e+00
E value
Match length
                   954
                   100
% identity
                   Soy bean mRNA for nodulin (C51)
NCBI Description
Seq. No.
                   767
Contig ID
                   415 1.R1040
5'-most EST
                   g2765090_FL
Method
                   BLASTX
NCBI GI
                   g2765091
BLAST score
                   2601
                   0.0e+00
E value
                   527
Match length
                   95
% identity
                   (Y10982) putative cytochrome P450 [Glycine max]
NCBI Description
                   768
Seq. No.
                   416 1.R1040
Contig ID
5'-most EST
                   uC-gmropic050h11b1
Method
                   BLASTX
NCBI GI
                   g2765093
                   1441
BLAST score
                   0.0e + 00
E value
Match length
                   527
                   91
% identity
                   (Y10983) putative cytochrome P450 [Glycine max]
NCBI Description
Seq. No.
Contig ID
                   416 2.R1040
5'-most EST
                   uC-gmflminsoy040f06b1
Method
                   BLASTX
NCBI GI
                   g2765093
BLAST score
                   541
E value
                   1.0e-105
Match length
                   293
% identity
                   (Y10983) putative cytochrome P450 [Glycine max]
NCBI Description
Seq. No.
                   770
Contig ID
                   416_3.R1040
5'-most EST
                   fC-gmst700663360d4
                   BLASTN
Method
NCBI GI
                   g2765092
BLAST score
                   86
E value
                   2.0e-40
Match length
                   198
% identity
                  Glycine max mRNA for cytochrome P450-like protein, clone
NCBI Description
                   CP9
                   771
Seq. No.
Contig ID
                   417 1.R1040
                   leu701144651.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g18723
BLAST score
                   1082
```

0.0e+00

E value •

E value

```
1109
 Match length
                    99
 % identity
 NCBI Description
                    Glycine max mRNA for pyrroline-5-carboxylate reductase
                    772
 Seq. No.
                    418 1.R1040
 Contig ID
 5'-most EST
                    LIB3040-022-Q1-E1-A7
 Method
                    BLASTN
 NCBI GI
                    g18725
 BLAST score
                    783
 E value
                    0.0e + 00
 Match length
                    874
                    97
 % identity
 NCBI Description
                    Soybean (G. max) mRNA for proliferating cell nuclear
                    antigen (PCNA), partial
 Seq. No. ___
Contig ID
                    773
                    418 2.R1040
 5'-most EST
                    LIB3040-005-Q1-E1-E6
 Method
                    BLASTN

    NCBI GI

                    g18725
 BLAST score
                    311
 E value
                    1.0e-175
 Match length
                    315
 % identity
                    100
                    Soybean (G. max) mRNA for proliferating cell nuclear
 NCBI Description
                    antigen (PCNA), partial
                    774
 Seq. No.
                    419 1.R1040
 Contig ID
 5'-most EST
                    LIB3049-020-Q1-E1-E6
 Method
                    BLASTN
 NCBI GI
                    g3021374
 BLAST score
                    361
 E value
                    0.0e + 00
 Match length
                    389
                    98
 % identity
 NCBI Description
                    Glycine max mRNA for profilin, PRO1
 Seq. No.
                    419 2.R1040
 Contig ID
 5'-most EST
                    leu701145541.h1
Method
                    BLASTN
 NCBI GI
                    g556835
BLAST score
                    309
E value
                    1.0e-173
Match length
                    617
                    89
 % identity
                    P. vulgaris mRNA for profilin
NCBI Description
                    776
 Seq. No.
Contig ID
                    419 3.R1040
 5'-most EST
                    LIB3040-004-Q1-E1-E1
                    BLASTX
Method
NCBI GI
                    g2213610
BLAST score
                    245
```

1.0e-20

% identity

```
Match length
                   142
% identity
                   26
                   (AC000103) F21J9.4 [Arabidopsis thaliana]
NCBI Description
                   777 -
Seq. No.
                   419 4.R1040
Contig ID
5'-most EST
                   LIB3109-006-Q1-K1-B7
Method
                   BLASTN
NCBI GI
                   g3021372
BLAST score
                   182
                   2.0e-97
E value
Match length
                   381
% identity
                   91
                  Glycine max mRNA for profilin, PRO2
NCBI Description
Seq. No.
                   419 5.R1040
Contig ID
5'-most EST
                   trc700567705.hl
Method
                   BLASTN
NCBI GI
                   g3021372
BLAST score
                   70
E value
                   8.0e-31
                   98
Match length
% identity
                   93
NCBI Description Glycine max mRNA for profilin, PRO2
                   779
Seq. No.
                   419 6.R1040
Contig ID
5'-most EST
                   LIB3107-052-Q1-K1-D1
Method
                   BLASTN
NCBI GI
                   g3021372
BLAST score
                  217
E value
                   1.0e-118
Match length
                  269
                  96
% identity
                  Glycine max mRNA for profilin, PRO2
NCBI Description
Seq. No.
Contig ID
                   419 7.R1040
5'-most EST
                  hrw701059647.hl
                  BLASTN
Method
NCBI GI
                   g3021374
BLAST score
                  229
E value
                   1.0e-126
Match length
                   349
                   91
% identity
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                   781
Contig ID
                   419 9.R1040
                  sat701006165.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3021374
BLAST score
                  142
E value
                   7.0e-74
                  229
Match length
```

NCBI Description

```
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                   782
Contig ID
                   419 10.R1040
5'-most EST
                   jsh701070477.hl
Method
                   BLASTN
NCBI GI
                   g3021372
BLAST score
                   34
                   2.0e-09
E value
Match length
                   58
% identity
NCBI Description
                  Glycine max mRNA for profilin, PRO2
Seq. No.
                   419 11.R1040
Contig ID
5'-most EST
                   fua701042750.h1
Method
                   BLASTN
NCBI GI
                   g3021374
BLAST score
                  129
E value
                   2.0e-66
Match length
                  137
                   99
% identity
                  Glycine max mRNA for profilin, PRO1
NCBI Description
                   784
Seq. No.
                   419 14.R1040
Contig ID
5'-most EST
                  LIB3072-021-Q1-E1-B8
Method
                  BLASTN
NCBI GI
                  g3021374
BLAST score
                   83
E value
                   9.0e-39
Match length
                  123
% identity
                   92
                  Glycine max mRNA for profilin, PRO1
NCBI Description
Seq. No.
Contig ID
                   419 21.R1040
5'-most EST
                  LIB3050-021-Q1-K1-C3
Method
                  BLASTN
NCBI GI
                  g3021374
BLAST score
                  116
E value
                   1.0e-58
Match length
                  140
% identity
                  96
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                   786
                   421 1.R1040
Contig ID
5'-most EST
                  g1321819 FL
Method
                  BLASTX
NCBI GI
                  g1321820
BLAST score
                  1854
E value
                  0.0e + 00
Match length
                  392
% identity
                   92
```

(X96864) phosphoribosylamine--glycine ligase [Glycine max]

% identity

67

```
787
Seq. No.
                   422 1.R1040
Contig ID
5'-most EST
                   g1321821 FL
Method
                   BLASTN
NCBI GI
                   g1321821
BLAST score
                   720
E value
                   0.0e+00
Match length
                   1302
                   99
% identity
NCBI Description
                   G.max mRNA for glycinamide ribonucleotide transformylase
Seq. No.
Contig ID
                   422 2.R1040
5'-most EST
                   epx701103931.h1
Method
                   BLASTN
NCBI GI
                   g1321821
BLAST score
                   169
E value
                   4.0e-90
Match length
                   306
                   98
% identity
                   G.max mRNA for glycinamide ribonucleotide transformylase
NCBI Description
                   789
Seq. No.
                   423 1.R1040
Contig ID
5'-most EST
                   sat701005463.h1
Method
                   BLASTX
NCBI GI
                   g112837
BLAST score
                   1630
E value
                   0.0e+00
Match length
                   315
                   100
% identity
                   NAD(P) H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE
NCBI Description
                   >gi 99953 pir S14222 reductase - soybean
                   >gi_18728_emb_CAA39261_ (X55730) reductase [Glycine max]
Seq. No.
                   423 2.R1040
Contig ID
5'-most EST
                   bth700849472.h1
Method
                   BLASTX
NCBI GI
                   g112837
BLAST score
                   1139
E value
                   1.0e-125
Match length
                   315
% identity
                   66
NCBI Description
                  NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE
                   >gi 99953 pir S14222 reductase - soybean
                   >gi_18728_emb_CAA39261_ (X55730) reductase [Glycine max]
                   791
Seq. No.
Contig ID
                   423 3.R1040
5'-most EST
                   uC-gmrominsoy046b12b1
Method
                   BLASTX
NCBI GI
                   g112837
BLAST score
                   447
E value
                   1.0e-50
Match length
                   147
```

. .

BLAST score

```
NAD (P) H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE
NCBI Description
                   >gi 99953_pir__S14222 reductase - soybean
                   >gi 18728_emb_CAA39261 (X55730) reductase [Glycine max]
                   792
Seq. No.
                   423 5.R1040
Contig ID
5'-most EST
                   zsg701128036.hl
Method
                   BLASTN
NCBI GI
                   g18727
BLAST score
                   213
                   1.0e-116
E value
Match length
                   320
% identity
                   94
                   Soybean mRNA for reductase involved in deoxychalcone
NCBI Description
                   synthesis (NAD(P)H dependent 6'-deoxychalcone synthase)
                   793
Seq. No.
                   424 1.R1040
Contig ID
5'-most EST
                   g2764803_FL
Method
                   BLASTX
NCBI GI
                   g1304227
BLAST score
                   1849
E value
                   0.0e+00
Match length
                   341
% identity
                   100
                   (D63781) Epoxide hydrolase [Glycine max]
NCBI Description
                   >gi 2764804 emb CAA55293 (X78547) epoxide hydrolase
                   [Glycine max]
                   794
Seq. No.
                   424 2.R1040
Contig ID
5'-most EST
                   ssr700559402.h1
Method
                   BLASTN
NCBI GI
                   g1304226
                   385
BLAST score
                   0.0e + 00
E value
                   473
Match length
                   95
% identity
NCBI Description
                   Soybean mRNA for epoxide hydrolase, complete cds
Seq. No.
                   795
                   424 3.R1040
Contig ID
5'-most EST
                   crh700850094.h1
                   BLASTN
Method
NCBI GI
                   g2764803
BLAST score
                   209
                   1.0e-113
E value
Match length
                   805
                   90
% identity
NCBI Description
                  G.max mRNA for epoxide hydrolase
Seq. No.
                   426 1.R1040
Contig ID
5'-most EST
                   LIB3072-018-Q1-E1-A9
Method
                   BLASTN
                   g18747
NCBI GI
```

```
0.0e+00
E value
                   427
Match length
                  98
% identity
                  G.max mRNA for a protein similar to potato tuber protein
NCBI Description
                  p322 homolgous to Bowman-Birk Proteinase Inhibitor
                  797
Seq. No.
                   427 1.R1040
Contig ID
                  LIB3093-005-Q1-K1-E2
5'-most EST
Method
                  BLASTX
                  g3913724
NCBI GI
BLAST score
                  1851
                  0.0e+00
E value
                  373
Match length
                   96
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-2 SUBUNIT
NCBI Description
                   (GP-ALPHA-2) >gi_1834453_emb_CAA64834_ (X95582) G protein
                   [Glycine max]
                  798
Seq. No.
                   428 1.R1040
Contig ID
                  LIB3170-044-Q1-J1-A5
5'-most EST
                  BLASTN
Method
NCBI GI
                  q18749
BLAST score
                  714
                  0.0e+00
E value
                  714
Match length
                  100
% identity
NCBI Description G.max mRNA for seed maturation polypeptide
                  799
Seq. No.
                   428 2.R1040
Contig ID
5'-most EST
                  LIB3051-102-Q1-K1-G3
                  BLASTN
Method
NCBI GI
                  g170007
                  836
BLAST score
                  0.0e + 00
E value
                  836
Match length
                  100
% identity
                  Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                  mRNA, complete cds
                  800
Seq. No.
Contig ID
                   429 1.R1040
5'-most EST
                  LIB3039-021-Q1-E1-A3
Method
                  BLASTN
                  g1055367
NCBI GI
BLAST score
                   639
                  0.0e + 00
E value
Match length
                  706
                  100
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  801
Contig ID
                   429 2.R1040
5'-most EST
                  LIB3055-005-Q1-N1-G4
```

```
Method
                   BLASTN
                   g1055367
NCBI GI
BLAST score
                   199
E value
                   1.0e-108
Match length
                   371
% identity
                   94
NCBI Description
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
Seq. No.
                   802
                   429 4.R1040
Contig ID
5'-most EST
                   wrg700786845.h2
                   BLASTN
Method
NCBI GI
                   g1055367
BLAST score
                   155
E value
                   1.0e-81
Match length
                   175
                   98
% identity
NCBI Description
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
                   803
Seq. No.
Contig ID
                   429 9.R1040
5'-most EST
                  LIB3074-039-Q1-K1-F4
Method
                  BLASTN
NCBI GI
                   g1055367
BLAST score
                   222
E value
                   1.0e-121
Match length
                   521
                   95
% identity
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
Seq. No.
Contig ID
                   429 10.R1040
5'-most EST
                  LIB3106-110-Q1-K1-A9
Method
                  BLASTN
NCBI GI
                   g1055367
BLAST score
                   224
E value
                   1.0e-123
Match length
                   396
% identity
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
                   805
Seq. No.
                   431 1.R1040
Contig ID
5'-most EST
                  LIB3107-037-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  g18761
BLAST score
                  988
                   0.0e+00
E value
                  988
Match length
% identity
NCBI Description
                  Soybean stem mRNA for 31 kD glycoprotein
```

806

Seq. No.

```
Contig ID
                   431 2.R1040
5'-most EST
                   g169897_FL
Method
                  BLASTN
NCBI GI
                  g169897
BLAST score
                  1074
E value
                  0.0e + 00
                  1074
Match length
                   100
% identity
NCBI Description G.max 28 kDa protein, complete cds
                  807
Seq. No.
Contig ID
                   431 4.R1040
                  taw700658005.h1
5'-most EST
                  BLASTN
Method
                  g1079735
NCBI GI
BLAST score
                  111
E value
                  1.0e-55
Match length
                  115
                   99
% identity
                  Glycine soja ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit precursor (rbcS) gene, nuclear gene encoding
                  chloroplast protein, complete cds
                  808
Seq. No.
                  431 5.R1040
Contig ID
5'-most EST
                  LIB3106-051-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  g18761
BLAST score
                  175
                  2.0e-93
E value
Match length
                  425
                  85
% identity
                  Soybean stem mRNA for 31 kD glycoprotein
NCBI Description
                  809
Seq. No.
Contig ID
                  431 6.R1040
5'-most EST
                  LIB3039-029-Q1-E1-H3
Method
                  BLASTN
NCBI GI
                  g169974
BLAST score
                  170
E value
                  1.0e-90
Match length
                  323
                  98
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                  810
Seq. No.
                  431 7.R1040
Contig ID
5'-most EST
                  LIB3106-091-Q1-K1-D9
Method
                  BLASTN
                  g170089
NCBI GI
BLAST score
                  394
E value
                  0.0e + 00
Match length
                  518
% identity
                  98
NCBI Description
                  G.max vegetative storage protien mRNA (VSP27), complete cds
```

811

Seq. No.

% identity

NCBI Description

```
431 8.R1040
Contig ID
5'-most EST
                   g5058414
                   BLASTN
Method
NCBI GI
                   g169897
BLAST score
                   218
                   1.0e-119
E value
Match length
                   683
                   95
% identity
                   G.max 28 kDa protein, complete cds
NCBI Description
                   812
Seq. No.
                   431 9.R1040
Contig ID
                   LIB3106-064-Q1-K1-D8
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   283
                   1.0e-158
E value
Match length
                   299
                   99
% identity
NCBI Description
                   Glycine max vegetative storage protein (vspB) gene,
                   complete cds
Seq. No.
                   813
                   431 11.R1040
Contig ID
5'-most EST
                   LIB3039-035-Q1-E1-F7
                   BLASTN
Method
NCBI GI
                   g169897
BLAST score
                   266
E value
                   1.0e-148
Match length
                   568
                   96
% identity
                   G.max 28 kDa protein, complete cds
NCBI Description
Seq. No.
                   814
                   432 1.R1040
Contig ID
5'-most EST
                   g256428 FL
Method
                   BLASTN
NCBI GI
                   g256428
BLAST score
                   1212
                   0.0e+00
E value
Match length
                   1264
                   99
% identity
                   KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
NCBI Description
                   Forrest, mRNA, 1259 nt]
Seq. No.
                   815
                   432 5.R1040
Contig ID
5'-most EST
                   LIB3072-020-Q1-E1-G8
Method
                   BLASTN
NCBI GI
                   g256428
BLAST score
                   324
                   0.0e+00
E value
Match length
                   406
                   96
```

Forrest, mRNA, 1259 nt]

KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Match length

```
816
Seq. No.
                   434 1.R1040
Contig ID
5'-most EST
                   LIB3051-050-Q1-K1-D12
                   817
Seq. No.
                   434 2.R1040
Contig ID
5'-most EST
                  LIB3051-049-Q1-K1-F6
Method
                   BLASTN
NCBI GI
                   g312988
BLAST score
                  226
E value
                   1.0e-124
Match length
                   414
% identity
                   89
NCBI Description
                  G.max mRNA for beta-tubulin, partial cds
Seq. No.
                   818
                   434 3.R1040
Contig ID
5'-most EST
                  LIB3039-007-Q1-E1-C3
Method
                  BLASTN
NCBI GI
                   g1399449
BLAST score
                   147
                   7.0e-77
E value
Match length
                   367
% identity
                   86
                  Lupinus albus beta-tubulin 2 (TubB2) gene, complete cds
NCBI Description
Seq. No.
                   819
Contig ID
                   434 4.R1040
5'-most EST
                  ncj700983044.hl
                  BLASTN
Method
                  g1403142
NCBI GI
BLAST score
                   454
E value
                   0.0e + 00
Match length
                  1207
                  86
% identity
NCBI Description
                  C.arietinum mRNA for beta-tubulin
Seq. No.
                  820
Contig ID
                   434 5.R1040
5'-most EST
                  LIB3087-010-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3915083
BLAST score
                  1635
                  0.0e+00
E value
                   423
Match length
% identity
                  71
                  TUBULIN BETA CHAIN >gi 1403143 emb CAA67056 (X98406)
NCBI Description
                  beta-tubulin [Cicer arietinum]
Seq. No.
                   434 6.R1040
Contig ID
5'-most EST
                  LIB3049-011-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  g1351202
BLAST score
                  749
E value
                  2.0e-79
```

Match length

```
% identity
                   TUBULIN BETA CHAIN >gi 312989 emb CAA42777 (X60216)
NCBI Description
                   beta-tubulin [Glycine max]
                   822
Seq. No.
Contig ID
                   434 7.R1040
5'-most EST
                   g4289599
Method
                   BLASTN
NCBI GI
                   g312988
                                             A 20
BLAST score
                   1134
                   0.0e+00
E value
Match length
                   1234
% identity
                   98
                  G.max mRNA for beta-tubulin, partial cds
NCBI Description
Seq. No.
                   434 8.R1040
Contig ID
                   uC-gmflminsoy118b09b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170061
BLAST score
                   327
E value
                   0.0e + 00
Match length
                   495
% identity
                   96
                   Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete
NCBI Description
                   cds
                   824
Seq. No.
                   434 9.R1040
Contig ID
5'-most EST
                   jC-gmf102220136d01d1
Method
                   BLASTN
                   g4098318
NCBI GI
BLAST score
                   123
                   1.0e-62
E value
                   375
Match length
                   84
% identity
                  Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds
NCBI Description
Seq. No.
                   825
                   435 1.R1040
Contig ID
5'-most EST
                   g392820_FL
                   BLASTN
Method
NCBI GI
                   g392820
BLAST score
                   1045
                   0.0e + 00
E value
Match length
                   1045
                   100
% identity
NCBI Description Glycine max Williams cellulase mRNA, partial cds
Seq. No.
                   437 1.R1040
Contig ID
5'-most EST
                   LIB3109-001-Q1-K1-C11
                   BLASTN
Method
NCBI GI
                   q555615
BLAST score
                   1040
                   0.0e + 00
E value
```

Method

BLASTX

```
% identity
NCBI Description
                  Glycine max Mandarin cytokinin induced message (cim1) mRNA,
                  complete cds
                  827
Seq. No.
                  438 1.R1040
Contig ID
                  jsh701065288.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1170214
BLAST score .
                  1876
                  0.0e+00
E value
Match length
                  412
                  90
% identity
                  DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR
NCBI Description
                   (PORPHOBILINOGEN SYNTHASE) (ALADH) >qi 468000 (U04525)
                  delta-aminolevulinic acid dehydratase [Glycine max]
                  828
Seq. No.
Contig ID
                  441 1.R1040
5'-most EST
                  LIB3139-110-P1-N1-F10
Method
                  BLASTN
NCBI GI
                  g472849
BLAST score
                  479
                  0.0e+00
E value
Match length
                  551
                  97
% identity
                  Glycine max Essex desiccation protectant protein Leal4
NCBI Description
                  homolog mRNA, complete cds
Seq. No.
                  829
                  441 2.R1040
Contig ID
5'-most EST
                  dpv701101866.hl
Method
                  BLASTN
NCBI GI
                  g472849
BLAST score
                  150
                  1.0e-78
E value
Match length
                  198
% identity
                  Glycine max Essex desiccation protectant protein Leal4
NCBI Description
                  homolog mRNA, complete cds
                  830
Seq. No.
                  442 1.R1040
Contig ID
5'-most EST
                  gsv701049208.h1
Method
                  BLASTX
NCBI GI
                  g2642238
BLAST score
                  2675
                  0.0e+00
E value
Match length
                  668
% identity
                  91
                  (AF031241) endoplasmic reticulum HSC70-cognate binding
NCBI Description
                  protein precursor [Glycine max]
Seq. No.
Contig ID
                  442 2.R1040
                  g475601_FL
5'-most EST
```

Contig ID

```
q475602
NCBI GI
BLAST score
                   3011
E value
                   0.0e + 00
Match length
                   642
                   93
% identity
NCBI Description
                   (U08384) BiP isoform A [Glycine max]
Seq. No.
                   832
Contig ID
                   442 3.R1040
5'-most EST
                   kl1701206325.hl
Method
                   BLASTX
NCBI GI
                   g2924518
BLAST score
                   316
                   2.0e-28
E value
Match length
                   189
                   37
% identity
                   (AL022023) putative protein [Arabidopsis thaliana]
NCBI Description
                   833
Seq. No.
Contig ID
                   442 4.R1040
5'-most EST
                   LIB3030-012-Q1-B1-E11
Seq. No.
                   834
Contig ID
                   442 7.R1040
5'-most EST
                   ssr700558430.hl
Method
                   BLASTN
NCBI GI
                   q475597
BLAST score
                   161
E value
                   2.0e-85
Match length
                   254
                   97
% identity
                   Glycine max Century 84 BiP isoform C mRNA, partial cds
NCBI Description
Seq. No.
                                                1
Contig ID
                   444 1.R1040
5'-most EST
                   LIB3051-020-Q1-E1-G10
Method
                   BLASTN
NCBI GI
                   g475603
BLAST score
                   769
                   0.0e+00
E value
Match length
                   919
                   99
% identity
                  Glycine max Century 84 beta-1,3-glucanase mRNA, partial cds
NCBI Description
Seq. No.
                   836
                   444 2.R1040
Contig ID
5'-most EST
                   LIB3051-027-Q1-K1-G3
Method
                   BLASTN
NCBI GI
                   g475603
BLAST score
                   346
E value
                   0.0e + 00
Match length
                   615
                   95
% identity
NCBI Description
                  Glycine max Century 84 beta-1,3-glucanase mRNA, partial cds
Seq. No.
                   837
```

445 1.R1040

```
fua701037217.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q550452
BLAST score
                    3467
E value
                    0.0e + 00
Match length
                    674
% identity
                    100
NCBI Description
                    (U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier
                    domain [Glycine max]
Seq. No.
                    838
                    448 1.R1040
Contig ID
5'-most EST
                    LIB3052-013-Q1-N1-A10
Method
                    BLASTX
NCBI GI
                    q267076
BLAST score
                    1628
E value
                    0.0e + 00
Match length
                    334.
% identity
                    93
                    TUBULIN BETA-3 CHAIN >gi_81953_pir__ S20870 tubulin beta-3 chain - garden pea (fragment) >gi_388255_emb_CAA38615_
NCBI Description
                    (X54846) beta-tubulin 3 [Pisum sativum]
Seq. No.
                    839
                    448 2.R1040
Contig ID
                    ncj700978473.hl
5'-most EST
Method
                    BLASTN
NCBI GI
                    g1399449
BLAST score
                    370
E value
                    0.0e + 00
                    789
Match length
                    90
% identity
                   Lupinus albus beta-tubulin 2 (TubB2) gene, complete cds
NCBI Description
Seq. No.
                    840
                    448 3.R1040
Contig ID
5'-most EST
                    LIB3049-023-Q1-E1-F11
Method
                    BLASTX
NCBI GI
                    q2983997
BLAST score
                    348
                    1.0e-34
E value
Match length
                    159
                    45
% identity
                    (AE000749) hypothetical protein [Aquifex aeolicus]
NCBI Description
Seq. No.
                    841
                    448 4.R1040
Contig ID
5'-most EST
                    pmv700892602.hl
Method
                    BLASTN
NCBI GI
                    g170061
BLAST score
                    545
                    0.0e+00
E value
                    932
Match length
% identity
                    94
NCBI Description
                   Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete
```

Seq. No.

```
842
Seq. No.
                   448 5.R1040
Contig ID
5'-most EST
                  LIB3040-037-Q1-E1-B9
                   BLASTX
Method
NCBI GI
                   g2983997
BLAST score
                   153
E value
                   5.0e-10
Match length
                   53
% identity
                   51
                   (AE000749) hypothetical protein [Aquifex aeolicus]
NCBI Description
Seq. No.
                   448 6.R1040
Contig ID
                  LIB3170-026-Q1-K1-H6
5'-most EST
Method
                  BLASTN
NCBI GI
                   g515691
BLAST score
                   46
E value
                   9.0e-17
Match length
                   70
                   91
% identity
                  Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds
NCBI Description
                   844
Seq. No.
                   448 7.R1040
Contig ID
5'-most EST
                  LIB3170-065-Q1-J1-E6
                  BLASTN
Method
                   g1399449
NCBI GI
BLAST score
                   78
E value
                   2.0e-35
Match length
                  141
                   89
% identity
NCBI Description
                  Lupinus albus beta-tubulin 2 (TubB2) gene, complete cds
                  845
Seq. No.
                   448 9.R1040
Contig ID
5'-most EST
                  ncj700979970.h1
Method
                  BLASTN
NCBI GI
                   g515691
BLAST score
                  218
E value
                   1.0e-119
                   302
Match length
                   93
% identity
                  Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds
NCBI Description
Seq. No.
                  846
                   448 10.R1040
Contig ID
5'-most EST
                  sat701013054.hl
                  BLASTN
Method
NCBI GI
                  g170061
BLAST score
                  235
E value
                   1.0e-129
Match length
                   416
                   97
% identity
                  Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete
NCBI Description
```

% identity

```
448 11.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy019d02b1
Seq. No.
                   448 13.R1040
Contig ID
5'-most EST
                   zhf700953739.h1
Method
                   BLASTN
NCBI GI
                   g515691
BLAST score
                   294
E value
                   1.0e-164
                   464
Match length
                   95
% identity
                   Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds
NCBI Description
                   849
Seq. No.
                   449 1.R1040
Contig ID
5'-most EST
                   pcp700990393.hl
Method
                   BLASTX
NCBI GI
                   g530088
BLAST score
                   2101
                   0.0e + 00
E value
Match length
                   389
                   100
% identity
NCBI Description
                   (U12735) aminoalcoholphosphotransferase [Glycine max]
                   850
Seq. No.
                                          25
                   449 2.R1040
Contig ID
5'-most EST
                   LIB3093-040-Q1-K1-C9
Method
                   BLASTN
NCBI GI
                   g530086
BLAST score
                   231
                   1.0e-127
E value
Match length
                   283
% identity
                   95
                   Glycine max aminoalcoholphosphotransferase (AAPT1) mRNA,
NCBI Description
                   complete cds
                   851
Seq. No.
                   450 1.R1040
Contig ID
5'-most EST
                   g927574_FL
Method
                   BLASTX
NCBI GI
                   g927575
BLAST score
                   2221
E value
                   0.0e+00
Match length
                   422
% identity
                   (U12926) alpha galactosidase [Glycine max]
NCBI Description
Seq. No.
                   852
Contig ID
                   451 1.R1040
5'-most EST
                   LIB3139-012-P1-N1-F8
Method
                   BLASTX
NCBI GI
                   g2370312
BLAST score
                   1779
E value
                   0.0e + 00
                   420
Match length
```

```
(AJ000995) DnaJ-like protein [Medicago sativa] >gi 3202020
NCBI Description
                   (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]
Seq. No.
                   451 2.R1040
Contig ID
                   jC-gmle01810083a09d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g532700
BLAST score
                   209
E value
                   1.0e-114
                   261
Match length
                   95
% identity
                  Glycine max clone GMFP1 isoprenylated protein mRNA, partial
NCBI Description
                   854
Seq. No.
                   451 3.R1040
Contig ID
5'-most EST
                   uC-gmropic071d07b1
Method
                   BLASTN
NCBI GI
                   g2370311
BLAST score
                   33
E value
                   8.0e-09
                  104
Match length
                  - 89
% identity
NCBI Description Medicago sativa mRNA for DnaJ-like protein
Seq. No.
                   855
                   451 5.R1040
Contig ID
5'-most EST
                   jC-gmro02910030f08d1
                   BLASTN
Method
                   g2370311
NCBI GI
BLAST score
                   131
E value
                   2.0e-67
                   263
Match length
% identity
                   87
                  Medicago sativa mRNA for DnaJ-like protein
NCBI Description
                   856
Seq. No.
                   452 1.R1040
Contig ID
5'-most EST
                  LIB3106-100-Q1-K1-A11
Method
                   BLASTN
NCBI GI
                   g532702
BLAST score
                   372
E value
                   0.0e+00
Match length
                   428
% identity
                  Glycine max clone GMFP2 isoprenylated protein mRNA, partial
NCBI Description
                  cds
Seq. No.
                   857
                   452 2.R1040
Contig ID
                  LIB3092-062-Q1-K1-H7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q123620
BLAST score
                  2996
```

0.0e + 00

618

E value

Match length

% identity

```
% identity
NCBI Description
                   HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950
                   heat shock cognate protein 70 - tomato
                   >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
                   70 [Lycopersicon esculentum]
                   858
Seq. No.
Contig ID
                   452 3.R1040
5'-most EST
                   bth700848091.h1
Method
                   BLASTN
NCBI GI
                   g532704
BLAST score
                   465
E value
                   0.0e + 00
Match length
                   473
% identity
                   78
                  Glycine max clone GMFP3 isoprenylated protein mRNA, partial
NCBI Description
                   859
Seq. No.
                   452 4.R1040
Contig ID
                   sat701012856.hl
5'-most EST
                   860
Seq. No.
                   452 5.R1040
Contig ID
5'-most EST
                   jex700907339.h1
                   861
Seq. No.
                   452 8.R1040
Contig ID
5'-most EST
                  LIB3039-040-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   g1565257
BLAST score
                   194
E value
                   2.0e-14
                   170
Match length
% identity
                   30
                   (X57108) cerebroside sulfate activator [Homo sapiens]
NCBI Description
Seq. No.
                   452 10.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy064b08b1
Method
                  BLASTX
NCBI GI
                   g3043415
BLAST score
                  230
E value
                   3.0e-31
Match length
                   92
% identity
                   (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  863
Contig ID
                   452 14.R1040
5'-most EST
                  g5510286
Method
                  BLASTN
NCBI GI
                  g1430886
BLAST score
                  150
E value
                  2.0e-78
Match length
                  378
```

```
NCBI Description M.sativa mRNA for 70 kD heat shock protein
                   864
Seq. No.
Contig ID
                   454 1.R1040
5'-most EST
                   pcp700989850.h1
Method
                   BLASTN
NCBI GI
                   g532706
BLAST score
                   200
E value
                   1.0e-108
Match length
                   249
% identity
                   99
                   Glycine max clone GMFP6 isoprenylated protein mRNA, partial
NCBI Description
                   865
Seq. No.
                   455 1.R1040
Contig ID
                   uC-gmrominsoy298d08b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4389417
BLAST score
                   4507
E value
                   0.0e+00
Match length
                   890
% identity
                   94
                   (AF055369) nitrate reductase [Glycine max]
NCBI Description
Seq. No.
                   455 2.R1040
Contig ID
                   kmv700739087.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4337177
BLAST score
                   1687
E value
                   0.0e+00
Match length
                   376
% identity
                   (AC006416) Identical to gb_Y10557 g5bf gene from
NCBI Description
                   Arabidopsis thaliana. ESTs gb R30578, gb R90475,
                   gb T22384, gb T22425, gb N6493\overline{4} and gb T4\overline{6}767 come from
                   this gene. [Arabidopsis thaliana]
Seq. No.
                   867
                   455 3.R1040
Contig ID
5'-most EST
                   fua701042206.h1
Method
                   BLASTX
NCBI GI
                   g1709267
BLAST score
                   4552
                   0.0e + 00
E value
Match length
                   886
                   95
% identity
                   INDUCIBLE NITRATE REDUCTASE 1 (NR) >qi 1262166 (L23854)
NCBI Description
                   nitrate reductase [Glycine max]
                   868
Seq. No.
Contig ID
                   455 4.R1040
5'-most EST
                   jC-gmro02910013d05d1
Method
                   BLASTX
```

g1906830

1531

NCBI GI BLAST score

5'-most EST

```
E value
                   1.0e-171
Match length
                   324
% identity
                   90
                   (Y11829) heat shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   455 5.R1040
5'-most EST
                   jC-gmle01810080a04a1
Method
                   BLASTX
NCBI GI
                  q1076758
BLAST score
                   1114
                   1.0e-122
E value
Match length
                   272
                   77
% identity
                  heat-shock protein precursor - rye >gi 2130093 pir S65776
NCBI Description
                  heat-shock protein, 82K, precursor - rye
                  >gi 556673_emb_CAA82945_ (Z30243) heat-shock protein
                   [Secale cereale]
Seq. No.
                   870
                   455 7.R1040
Contig ID .
                   jC-gmle01810082h03d1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g1262165
BLAST score
                  130
                  5.0e-67
E value
                  146
Match length
% identity
                   97
NCBI Description
                  Soybean nitrate reductase (INR1) mRNA, complete cds
Seq. No.
                  871
Contig ID
                  457 1.R1040
5'-most EST
                  LIB3051-081-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1705678
BLAST score
                  4065
E value
                  0.0e + 00
Match length
                  807
% identity
                  98
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                  PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                  valosin-containing protein [Glycine max]
Seq. No.
                   457 2.R1040
Contig ID
                  fC-gmro700745012a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4432856
BLAST score
                  539
E value
                  6.0e-55
Match length
                  214
% identity
                  (AC006300) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  873
Contig ID
                  457 3.R1040
```

epx701107517.h1

NCBI Description

```
BLASTN
Method
NCBI GI
                   g862479
BLAST score -
                   145
                   2.0e-75
E value
                                                                - - . . .
Match length
                   221
% identity
                   91
NCBI Description Glycine max valosin-containing protein mRNA, complete cds
                   874
Seq. No.
                   457 4.R1040
Contig ID
5'-most EST
                   crh700851542.hl
                   875
Seq. No.
                   457 5.R1040
Contig ID
                   LIB3170-060-Q1-J1-F8
5'-most EST
Method
                   BLASTN
NCBI GI
                   g862479
BLAST score
                   252
E value
                   1.0e-139
Match length
                   415
                   90
% identity
NCBI Description
                   Glycine max valosin-containing protein mRNA, complete cds
Seq. No.
                   457 6.R1040
Contig ID
5'-most EST
                   LIB3170-060-Q1-K1-F8
Method
                   BLASTN
NCBI GI
                   g862479
BLAST score
                   85
E value
                   5.0e-40
                   133
Match length
% identity
                   91
NCBI Description Glycine max valosin-containing protein mRNA, complete cds
Seq. No.
                   457 9.R1040
Contig ID
5'-most EST
                   g4302765
Method
                   BLASTN
NCBI GI
                   g862479
BLAST score
                   415
                   0.0e + 00
E value
Match length
                   597
% identity
                   Glycine max valosin-containing protein mRNA, complete cds
NCBI Description
Seq. No.
                   458 1.R1040
Contig ID
5'-most EST
                   ncj700986139.hl
Method
                   BLASTX
NCBI GI
                   g3334138
BLAST score
                   2332
                   0.0e + 00
E value
Match length
                   510
% identity
                   87
```

[Glycine max]

CALNEXIN HOMOLOG PRECURSOR >qi 669003 (U20502) calnexin

Seq. No.

```
879
Seq. No.
                   458 2.R1040
Contig ID
5'-most EST
                  LIB3170-056-Q1-K1-G8
Method
                  BLASTN
                  g669002
NCBI GI
BLAST score
                  183
                   3.0e-98
E value
Match length
                   412
% identity
                  86
                  Glycine max calnexin mRNA, complete cds
NCBI Description
Seq. No.
                   458 3.R1040
Contig ID
                  leu701147326.h1
5'-most EST
                  BLASTX
Method
                  q3334138
NCBI GI
BLAST score
                   600
                   6.0e-88
E value
Match length
                  243
                   69
% identity
                  CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
NCBI Description
                   [Glycine max]
Seq. No.
                  881
                   458 4.R1040
Contig ID
5'-most EST
                  g4301841
Method
                  BLASTN
NCBI GI
                  g669002
BLAST score
                  290
                   1.0e-162
E value
                   642
Match length
                   92
% identity
NCBI Description Glycine max calnexin mRNA, complete cds
Seq. No.
                  882
                   458 7.R1040
Contig ID
                  ncj700975503.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g669002
BLAST score
                  161
E value
                   3.0e-85
Match length
                  303
                   100
% identity
NCBI Description
                  Glycine max calnexin mRNA, complete cds
Seq. No.
                   458 9.R1040
Contig ID
5'-most EST
                  LIB3051-082-Q1-K1-F9
Method
                  BLASTN
NCBI GI
                  g669002
BLAST score
                   69
                  2.0e-30
E value
Match length
                  169
                  85
% identity
NCBI Description
                  Glycine max calnexin mRNA, complete cds
```

NCBI Description

```
459 1.R1040
Contig ID
                   LIB3138-014-Q1-N2-C2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g710431
BLAST score
                   918
                   0.0e+00
E value
Match length
                   948
% identity
                   99
                  Glycine max low molecular weight heat shock protein Hsp23.9
NCBI Description
                   (Gmhsp23.9) mRNA, complete cds
Seq. No.
                   459 2.R1040
Contig ID
                   LIB3051-016-Q1-E1-C10
5'-most EST
Method
                   BLASTN
NCBI GI
                   g710431
BLAST score
                   248
                   1.0e-137
E value
                   252
Match length
                   100
% identity
                  Glycine max low molecular weight heat shock protein Hsp23.9
NCBI Description
                   (Gmhsp23.9) mRNA, complete cds
Seq. No.
                   460 1.R1040
Contig ID
5'-most EST
                  LIB3107-065-Q1-K1-D5
Method
                   BLASTN
NCBI GI
                   g710433
                   361
BLAST score
                   0.0e+00
E value
Match length
                   707
                   99
% identity
                  Glycine max low molecular weight heat shock protein Hsp22.3
NCBI Description
                   (Gmhsp22.3) mRNA, complete cds
                   887
Seq. No.
                   461 1.R1040
Contig ID
5'-most EST
                  hrw701058941.h1
Method
                   BLASTN
NCBI GI
                   g710435
BLAST score
                   723
E value
                   0.0e + 00
                   727
Match length
% identity
                  Glycine max low molecular weight heat shock protein Hsp22.5
NCBI Description
                   (Gmhsp22.5) mRNA, complete cds
                   888
Seq. No.
                   462 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy194b09b1
Method
                  BLASTX
NCBI GI
                  g2129826
                   3024
BLAST score
E value
                   0.0e + 00
Match length
                   610
% identity
                  dynamin-like protein phragmoplastin 5 - soybean >gi 1218004
```

E value

Match length

## (U36430) SDL5A [Glycine max]

```
Seq. No.
                   889
                   462 2.R1040
Contig ID
5'-most EST
                   g1217993 FL
Method
                   BLASTX
NCBI GI
                   g2129825
BLAST score
                   3029
E value
                   0.0e + 00
Match length
                   610
                   98
% identity
                   dynamin-like protein phragmoplastin 12 - soybean
NCBI Description
                   >gi 1217994 (U25547) SDL [Glycine max]
                   890
Seq. No.
                   462 3.R1040
Contig ID
                   jC-gmro02910024d01d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1217993
BLAST score
                   118
E value
                   1.0e-59
Match length
                   258
                   86
% identity
                  Glycine max dynamin-like protein SDL12A mRNA, complete cds
NCBI Description
Seq. No.
                   463 1.R1040
Contig ID
                   sat701012537.hl
5'-most EST
Method
                   BLASTN
                   g886099
NCBI GI
BLAST score
                   983
                   0.0e + 00
E value
Match length
                   1196
                   96
% identity
                   Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                   complete cds
                   892
Seq. No.
                   463 2.R1040
Contig ID
                   leu701151271.h1
5'-most EST
                   BLASTN
Method
                   g886099
NCBI GI
BLAST score
                   220
E value
                   1.0e-120
Match length
                   582
% identity
                  Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                   complete cds
                 . 893
Seq. No.
                   463 3.R1040
Contig ID
5'-most EST
                   LIB3039-019-Q1-E1-A2
Method
                   BLASTN
NCBI GI
                   g886099
BLAST score
                   204
```

1.0e-111

BLAST score

```
% identity
                   Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   894
Contig ID
                   463 4.R1040
5'-most EST
                   LIB3028-013-Q1-B1-E3
Method
                   BLASTX
NCBI GI
                   q3158476
BLAST score
                   829
E value
                   5.0e-89
Match length
                   176
% identity
                   91
NCBI Description
                   (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                   463 5.R1040
Contig ID
                   LIB3109-035-Q1-K1-C7
5'-most EST
Method
                   BLASTN
NCBI GI
                   g886099
BLAST score
                   339
                   0.0e+00
E value
Match length
                   426
% identity
                   96
NCBI Description
                   Glycine max putative water channel protein (Pipl) mRNA,
                   complete cds
                   896
Seq. No.
                   463 6.R1040
Contig ID
5'-most EST
                   hyd700730567.h1
Method
                   BLASTN
NCBI GI
                   g886099
BLAST score
                   157
E value
                   1.0e-82
                                                      Match length
                   369
% identity
                   92
                  Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   897
                   463 7.R1040
Contig ID
5'-most EST
                   LIB3049-044-Q1-E1-B10
Method
                   BLASTN
NCBI GI
                   g886099
BLAST score
                   278
E value
                   1.0e-155
                   477
Match length
% identity
                  Glycine max putative water channel protein (Pipl) mRNA,
NCBI Description
                   complete cds
                   898
Seq. No.
                   463 8.R1040
Contig ID
5'-most EST
                   sat701004493.h1
Method
                   BLASTN
                   q886099
NCBI GI
```

```
3.0e-75
E value
Match length
                   230
                   93
% identity
                   Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   899
                   463 9.R1040
Contig ID
                   LIB3109-001-Q1-K1-G12
5'-most EST
Method
                   BLASTN
                   q886099
NCBI GI
BLAST score
                   77
E value
                   3.0e-35
Match length
                   104
                   94
% identity
                   Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                   complete cds
                   900
Seq. No.
Contig ID
                   464 1.R1040
5'-most EST
                   fC-gmst700605267f5
Method
                   BLASTN
NCBI GI
                   g1234899
BLAST score
                   605
                   0.0e + 00
E value
                   1049
Match length
                   91
% identity
                   G.max mRNA for homeobox-leucine zipper protein
NCBI Description
Seq. No.
                   464 2.R1040
Contig ID
5'-most EST
                   g5666790
Method
                   BLASTN
NCBI GI
                   g1234899
BLAST score
                   313
                   1.0e-175
E value
                   753
Match length
                   94
% identity
NCBI Description
                  G.max mRNA for homeobox-leucine zipper protein
                   902
Seq. No.
                   464_3.R1040
Contig ID
5'-most EST
                   jex700909715.hl
Method
                   BLASTN
NCBI GI
                   g1234899
BLAST score
                   549
E value
                   0.0e + 00
Match length
                   553
                   100
% identity
NCBI Description G.max mRNA for homeobox-leucine zipper protein
                   903 -
Seq. No.
                   465 1.R1040
Contig ID
5'-most EST
                   LIB3051-069-Q1-K1-A2
Method
                   BLASTN
```

g945086

944

NCBI GI

BLAST score

NCBI GI

```
E value
                   0.0e+00
Match length
                   1054
                   97
% identity
NCBI Description
                   Glycine max transcription factor TFIIB mRNA, complete cds
Seq. No.
                   465 2.R1040
Contig ID
5'-most EST
                   LIB3170-030-01-K1-D2 -
                   BLASTN
Method
NCBI GI
                   g945086
BLAST score
                   246
                   1.0e-136
E value
                   272
Match length
                   98
% identity
                   Glycine max transcription factor TFIIB mRNA, complete cds
NCBI Description
Seq. No.
                   905
Contig ID
                   466 1.R1040
5'-most EST
                   uC-gmflminsoy069d12b1
Method
                   BLASTN
                   q1208536
NCBI GI
BLAST score
                   941
                   0.0e + 00
E value
                   949
Match length
% identity
                   Glycine max guanine nucleotide regulatory protein (rab2)
NCBI Description
                   mRNA, complete cds
                   906
Seq. No.
Contig ID
                   466 2.R1040
5'-most EST
                   zzp700836092.h1
                   BLASTN
Method
NCBI GI
                   q1208536
BLAST score
                   283
E value
                   1.0e-158
Match length
                   319
% identity
NCBI Description
                   Glycine max guanine nucleotide regulatory protein (rab2)
                   mRNA, complete cds
                   907
Seq. No.
Contig ID
                   467 1.R1040
5'-most EST
                   g1161925 FL
Method
                   BLASTX
NCBI GI
                   q1161926
BLAST score
                   3255
E value
                   0.0e + 00
Match length
                   689
% identity
NCBI Description
                   (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
                   max]
Seq. No.
                   908
Contig ID
                   467 2.R1040
5'-most EST
                   q1143321 FL
Method
                   BLASTX
```

q1143322

5'-most EST

```
BLAST score
                   3213
E value
                   0.0e + 00
Match length
                   670
                   95
% identity
                   (U40979) alfa-carboxyltransferase precursor [Glycine max]
NCBI Description
Seq. No.
                   909
                   468 1.R1040
Contig ID
5'-most EST
                   epx701106015.h1
Method
                   BLASTN
NCBI GI
                   g506628
BLAST score
                   650
E value
                   0.0e+00
                   901
Match length
                   96
% identity
NCBI Description
                   Glycine max cv. Dare photosystem II type I chlorophyll
                   a/b-binding protein (lhcb1*7) gene, complete cds
                   910
Seq. No.
                   468 2.R1040
Contig ID
5'-most EST
                   LIB3039-038-Q1-E1-A12
Method
                   BLASTN
NCBI GI
                   g1053215
BLAST score
                   579
                  0.0e + 00
E value
Match length
                   990
                   92
% identity
NCBI Description
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
                   nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                   911
                   468 3.R1040
Contig ID
5'-most EST
                   LIB3039-027-Q1-E1-C12
Method
                   BLASTN
NCBI GI
                   g18551
BLAST score
                   522
E value
                   0.0e+00
Match length
                   844
% identity
                   95
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
Seq. No.
                   912
Contig ID
                   471 1.R1040
5'-most EST
                   g1399302 FL
Method
                   BLASTX
NCBI GI
                   q1399303
BLAST score
                   2911
E value
                   0.0e + 00
Match length
                   549
% identity
                   (U41473) phosphoinositide-specific phospholipase C P12
NCBI Description
                   [Glycine max]
Seq. No.
                   913
Contig ID
                   472 1.R1040
```

leu701146691.hl

```
Method
                   BLASTX
NCBI GI
                   g1399305
BLAST score
                   3091
                   0.0e+00
E value
Match length
                   600
                   97
% identity
                   (U41474) phosphoinositide-specific phospholipase C P13
NCBI Description
                   [Glycine max]
Seq. No.
                   914
                   472 2.R1040
Contig ID
                   k11701212082.h1
5'-most EST
Method
                   BLASTX
                   q1399307
NCBI GI
BLAST score
                   2378
                   0.0e+00
E value
                   627
Match length
                   80
% identity
                   (U41475) phosphoinositide-specific phospholipase C P25
NCBI Description
                   [Glycine max]
Seq. No.
                   472 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy197g12b1
Method
                   BLASTX
NCBI GI
                   q945039
BLAST score
                   3122
                   0.0e+00
E value
Match length
                   600
                   98
% identity
                   (U25027) phosphatidylinositol-specific phospholipase C
NCBI Description
                   [Glycine max]
                   916
Seq. No.
                   474 1.R1040
Contig ID
                  g5753651
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1125103
BLAST score
                   996
                  0.0e+00
E value
                  1015
Match length
                  100
% identity
                  Glycine max seed coat peroxidase isozyme (SPOD4.1) mRNA,
NCBI Description
                  partial cds
                   917
Seq. No.
Contig ID
                   475 1.R1040
5'-most EST
                  g3258669
Method
                  BLASTX
NCBI GI
                  g1399380
                  1933
BLAST score
                  0.0e + 00
E value
                   367
Match length
% identity
NCBI Description
                   (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
```

methyltransferase [Glycine max]

E value

```
918
Seq. No.
                   475 2.R1040
Contig ID
5'-most EST.
                   LIB3049-011-Q1-E1-D2
Method
                   BLASTX
NCBI GI
                   q4185509
BLAST score
                   614
                   1.0e-63
E value
Match length
                   13.9
% identity
                   (AF102821) actin depolymerizing factor 3 [Arabidopsis
NCBI Description
                   thaliana]
                   919
Seq. No.
Contig ID
                   475 3.R1040
5'-most EST
                   LIB3051-062-Q1-K1-H3
                  BLASTX
Method
NCBI GI
                   g1408471
BLAST score
                   620
E value
                   2.0e-64
Match length
                   139
                   83
% identity
NCBI Description
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
Seq. No.
Contig ID
                   475 4.R1040
5'-most EST
                   jC-qmst02400038f11a1
Method
                   BLASTX
NCBI GI
                   g1408471
BLAST score
                   630
E value
                   1.0e-65
                  139
Match length
% identity
NCBI Description
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   921
Seq. No.
                   475 5.R1040
Contig ID
                  LIB3087-010-Q1-K1-H12
5'-most EST
Method
                  BLASTX
                  g4185511
NCBI GI
BLAST score
                   410
E value
                   4.0e-40
Match length
                   90
% identity
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   922
                   475 6.R1040
Contig ID
5'-most EST
                  uC-gmropic057g10b1
                  BLASTN
Method
NCBI GI
                  g1399379
BLAST score
                  325
```

0.0e + 00

Method

BLASTN

```
459
Match length
                   95
% identity
                   Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                   methyltransferase mRNA, complete cds
                   923
Seq. No.
                   475 9.R1040
Contig ID
                   crh700854308.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1399379
BLAST score
                   184
                   5.0e-99
E value
                   200
Match length
% identity
NCBI Description
                   Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
                  methyltransferase mRNA, complete cds
                   924
Seq. No.
                   476 1.R1040
Contig ID
5'-most EST
                   LIB\overline{3}051-085-Q1-K1-H9
Method
                   BLASTN
                   g1236950
NCBI GI
BLAST score
                   620
E value
                   0.0e+00
Match length
                   717
% identity
                   97
                  Glycine max nucleoside diphosphate kinase mRNA, complete
NCBI Description
Seq. No.
                   925
Contig ID
                   476 2.R1040
5'-most EST
                  LIB3049-042-Q1-E1-A12
Method
                  BLASTN
NCBI GI
                   g1236950
BLAST score
                   372
E value
                   0.0e + 00
Match length
                   609
% identity
                   92
                  Glycine max nucleoside diphosphate kinase mRNA, complete
NCBI Description
                  cds
                   926
Seq. No.
                   476 3.R1040
Contig ID
                  ncj700981096.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1236950
BLAST score
                  184
                   3.0e-99
E value
                  271
Match length
% identity
NCBI Description
                  Glycine max nucleoside diphosphate kinase mRNA, complete
                  cds
                  927
Seq. No.
                   476 4.R1040
Contig ID
5'-most EST
                  jsh701070081.h2
```

Method

NCBI GI

BLASTN

g1277165

```
NCBI GI
                   q1236950
BLAST score
                   326
E value
                   0.0e + 00
Match length
                   342
% identity
                   99
                   Glycine max nucleoside diphosphate kinase mRNA, complete
NCBI Description
Seq. No.
                   928
Contig ID
                   477 1.R1040
5'-most EST
                   LIB3109-035-Q1-K4-B1
Method
                   BLASTN
NCBI GI
                   g1277163
BLAST score
                   449
E value
                   0.0e + 00
Match length
                   467
                   99
% identity
                   Glycine max cysteine proteinase inhibitor mRNA, partial cds
NCBI Description
Seq. No.
                  · 478 1.R1040
Contig ID
5'-most EST
                   leu701154606.hl
Method
                   BLASTN
NCBI GI
                   g1277165
BLAST score
                   221
E value
                   1.0e-121
Match length
                   488
                   90
% identity
                   Glycine max cysteine proteinase inhibitor mRNA, partial cds
NCBI Description
                   930
Seq. No.
                   478 2.R1040
Contig ID
                   leu701147147.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1277165
                                  .
BLAST score
                   198
E value
                   1.0e-107
Match length
                   332
                   95
% identity
NCBI Description
                   Glycine max cysteine proteinase inhibitor mRNA, partial cds
                   931
Seq. No.
                   478 3.R1040
Contig ID
5'-most EST
                   LIB3106-070-P1-K1-A4
Method
                   BLASTN
NCBI GI
                   g1277165
BLAST score
                   315
E value
                   1.0e-177
                   554
Match length
                   92
% identity
                  Glycine max cysteine proteinase inhibitor mRNA, partial cds
NCBI Description
                   932
Seq. No.
                   478 4.R1040
Contig ID
5'-most EST
                   LIB3028-036-Q1-B1-A12
```

BLAST score

E value

78

2.0e-35

```
206
BLAST score
E value
                   1.0e-112
Match length
                   365
                   96
% identity
                  Glycine max cysteine proteinase inhibitor mRNA, partial cds
NCBI Description
                   933
Seq. No.
                   478 6.R1040
Contig ID
5'-most EST
                   LIB3073-003-Q1-K1-E2
Method
                   BLASTN
                   g1277165
NCBI GI
BLAST score
                   103
                   2.0e-50
E value
Match length
                   227
                   92
% identity
                   Glycine max cysteine proteinase inhibitor mRNA, partial cds
NCBI Description
Seq. No.
Contig ID
                   479 1.R1040
5'-most EST
                   ncj700988504.hl
Method
                   BLASTN
NCBI GI
                   g1277167
BLAST score
                   425
                   0.0e + 00
E value
Match length
                   455
                   98
% identity
                  Glycine max cysteine proteinase inhibitor mRNA, partial cds
NCBI Description
                   935
Seq. No.
                   480 2.R1040
Contig ID
                   LIB3051-019-Q1-E1-H7
5'-most EST
                   BLASTN
Method
NCBI GI
                   g310560
BLAST score
                   63
E value
                   8.0e-27
Match length
                   127
                   98
% identity
                   Soybean ascorbate peroxidase mRNA, complete cds
NCBI Description
Seq. No.
                   480 3.R1040
Contig ID
5'-most EST
                   jC-\overline{g}mst02400069e04a1
Method
                   BLASTX
NCBI GI
                   g1679794
BLAST score
                   415
E value
                   3.0e-53
                   372
Match length
                   37
% identity
                  (U77627) Allele: hi2 [Danio rerio]
NCBI Description
Seq. No.
                   937
                   480 4.R1040
Contig ID
5'-most EST
                   LIB3170-046-Q1-J1-G3
Method
                   BLASTN
NCBI GI
                   g1336081
```

E value

```
Match length
                   102
% identity
                   94
NCBI Description
                   Glycine max var. Century ascorbate peroxidase 2 (APx2)
                   mRNA, complete cds
Seq. No.
Contig ID
                   480 5.R1040
5'-most EST
                   LIB3093-046-Q1-K1-H1
Method
                   BLASTN
NCBI GI
                   g2055227
BLAST score
                   44
E value
                   3.0e-15
Match length
                   111
% identity
                   95
NCBI Description
                  Glycine max mRNA for SRC1, complete cds
Seq. No.
                   939
Contig ID
                   480 6.R1040
5'-most EST
                   LIB3052-013-Q1-N1-H3
Method
                   BLASTN
NCBI GI
                   q310560
BLAST score
                   893
E value
                   0.0e + 00
Match length
                   1043
% identity
                   98
NCBI Description Soybean ascorbate peroxidase mRNA, complete cds
Seq. No.
                   480 7.R1040
Contig ID
5'-most EST
                   LIB3028-001-Q1-B1-F10
Method
                   BLASTN
NCBI GI
                   g1336081
BLAST score
                   640
E value
                   0.0e + 00
Match length
                   1075
% identity
                   93
                  Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                  mRNA, complete cds
                   941
Seq. No.
                   482 1.R1040
Contig ID
                   g1679655 FL
5'-most EST
Method .
                   BLASTN
NCBI GI
                   g1679655
BLAST score
                   1156
E value
                   0.0e+00
                  1180
Match length
                   99
% identity
                  Glycine max metalloproteinase mRNA, complete cds
NCBI Description
                   942
Seq. No.
                   483 1.R1040
Contig ID
5'-most EST
                   zsg701121157.hl
                  BLASTX
Method
NCBI GI
                  g1679658
BLAST score
                  1661
```

0.0e + 00

Match length

```
Match length
                   342
% identity
                   93
NCBI Description
                   (U63726) gamma glutamyl hydrolase [Glycine max]
                   943
Seq. No.
                   483 2.R1040
Contig ID
5'-most EST
                   ncj700975264.hl
                   BLASTN
Method
NCBI GI
                   g1680711
BLAST score
                   132
E value
                   3.0e-68
Match length
                   274
                   98
% identity
NCBI Description
                  Glycine max gamma glutamyl hydrolase mRNA, complete cds
Seq. No.
Contig ID
                   483 3.R1040
5'-most EST
                  hyd700725162.hl
Method
                   BLASTN
NCBI GI
                   q1680711
BLAST score
                   136
E value
                   2.0e-70
Match length
                   188
% identity
                   98
NCBI Description
                  Glycine max gamma glutamyl hydrolase mRNA, complete cds
                   945
Seq. No.
                   484 1.R1040
Contig ID
5'-most EST
                   g1518156 FL
Method
                  BLASTX
NCBI GI
                   g3219787
BLAST score
                   1743
                   0.0e+00
E value
Match length
                   345
% identity
                   100
                  MEIOTIC RECOMBINATION PROTEIN DMC1 HOMOLOG >gi 1518157
NCBI Description
                   (U66836) RecA/Rad51/DMC1-like protein [Glycine max]
                   946
Seq. No.
                   486 1.R1040
Contig ID
5'-most EST
                  LIB3049-048-Q1-E1-H6
Method
                  BLASTN
NCBI GI
                  g1575726
BLAST score
                  811
E value
                   0.0e+00
Match length
                  967
                   96
% identity
                  Glycine max 14-3-3 related protein SGF14B mRNA, partial cds
NCBI Description
Seq. No.
                   486 2.R1040
Contig ID
5'-most EST
                  LIB\overline{3}106-069-P1-K1-H4
Method
                  BLASTN
                  g169069
NCBI GI
BLAST score
                  256
E value
                  1.0e-141
```

% identity

```
% identity
                   Pea Cu-Zn superoxide dismutase mRNA, complete cds
NCBI Description
Seq. No.
                   486 5.R1040
Contig ID
                   pxt700946009.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3860328
BLAST score
                   37
E value
                   2.0e-11
                   139
Match length
                   84
% identity
                   Cicer arietinum mRNA for superoxide dismutase
NCBI Description
                   949
Seq. No.
                   486 6.R1040
Contig ID
5'-most EST
                   jC-gmle01810004h01a1
Method
                   BLASTN
NCBI GI
                   g169069
BLAST score
                   93
E value
                   1.0e-44
Match length
                   289
                   83
% identity
                   Pea Cu-Zn superoxide dismutase mRNA, complete cds.
NCBI Description
Seq. No.
                   486 8.R1040
Contig ID
5'-most EST
                   fC-gmf1700905524r4
Method
                   BLASTN
NCBI GI
                   g169069
BLAST score
                   57
E value
                   2.0e-23
Match length
                   85
                   93
% identity
                   Pea Cu-Zn superoxide dismutase mRNA, complete cds
NCBI Description
                   951·
Seq. No.
                   488 1.R1040
Contig ID
5'-most EST
                   bth700846059.h1
Method
                   BLASTN
NCBI GI
                   g1575730
                   1079
BLAST score
E value
                   0.0e+00
Match length
                   1130
% identity
                   99
                  Glycine max 14-3-3 related protein SGF14D mRNA, complete
NCBI Description
                   952
Seq. No.
Contig ID
                   488 2.R1040
5'-most EST
                   jC-gmf102220057d03a1
Method
                   BLASTN
NCBI GI
                   g1575730
BLAST score
                   233
E value
                   1.0e-128
Match length
                   257
```

```
NCBI Description
                  Glycine max 14-3-3 related protein SGF14D mRNA, complete
Seq. No.
                   953
                   489 2.R1040
Contig ID
5'-most EST
                   q55\overline{1}0318
Method
                  BLASTN
NCBI GI
                   q1619904
BLAST score
                   151
                  2.0e-79
E value
Match length
                   290
                   89
% identity
                  Glycine max thiol protease isoform A mRNA, partial cds
NCBI Description
Seq. No.
                   954
                   489 3.R1040
Contig ID
5'-most EST
                  LIB3106-070-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q1620986
BLAST score
                   327
E value
                   3.0e-30
Match length
                   78
% identity
                   79
                   (Y08858) 40S ribosomal protein S17 [Nicotiana
NCBI Description
                  plumbaginifolia]
Seq. No.
                   955
Contig ID
                   489 4.R1040
5'-most EST
                  jC-gmro02910023g10d1
Method
                  BLASTN
NCBI GI
                  g2511690
BLAST score
                  131
E value
                  2.0e-67
Match length
                  325
% identity
                  89
NCBI Description
                  Phaseolus vulgaris Moldavian encoding cysteine proteinase
                  precursor (clone cp41).
                  956
Seq. No.
                  489 5.R1040
Contig ID
5'-most EST
                  leu701156563.hl
                  957
Seq. No.
                  489 6.R1040
Contig ID
5'-most EST
                  zzp700830691.hl
Method
                  BLASTX
NCBI GI
                  g1172874
                  236
BLAST score
E value
                  3.0e-41
Match length
                  215
% identity
                  41
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                  >gi 479589 pir S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                   [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
```

[Arabidopsis thaliana]

```
958
Seq. No.
                   489 7.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy276g11b1
Method
                   BLASTX
NCBI GI
                   g2511691
BLAST score
                   539
                   1.0e-129
E value
Match length
                   330
% identity
                   74
                   (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   489_8.R1040
Contig ID
5'-most EST
                   uC-gmropic034b07b1
Method
                   BLASTN
NCBI GI
                   g2257597
BLAST score
                   436
                   0.0e+00
E value
Match length
                   684
% identity
                   91
                  Robinia pseudoacacia mRNA for phosphoglycerate kinase,
NCBI Description
                  partial cds
Seq. No.
                   960
                   489 9.R1040
Contig ID
                  LIB3138-009-Q1-N1-B11
5'-most EST
Method
                  BLASTN
NCBI GI
                   g1619904
                  827
BLAST score
E value
                  0.0e+00
                  1190
Match length
                   94
% identity
                  Glycine max thiol protease isoform A mRNA, partial cds
NCBI Description
Seq. No.
                   961
                   491 1.R1040
Contig ID
5'-most EST
                  LIB3093-002-Q1-K1-E6
                  BLASTN
Method
NCBI GI
                   g456713
BLAST score
                  1118
                   0.0e+00
E value
                  1160
Match length
                   100
% identity
NCBI Description
                  Glycine max gene for ubiquitin, complete cds
Seq. No.
                   491 2.R1040
Contig ID
5'-most EST
                  LIB3093-036-Q1-K1-E8
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                   680
E value
                  0.0e+00
Match length
                  755
% identity
                   46
NCBI Description
                  Soybean gene for ubiquitin, complete cds
```

963

Seq. No.

5'-most EST

```
Contig ID
                   491 4.R1040
5'-most EST
                   rca701000445.h1
                   BLASTN
Method
NCBI GI
                   g456713
BLAST score
                   160
                   7.0e-85
E value
                   196
Match length
                   72
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                   964
Seq. No.
                   491 5.R1040
Contig ID
                   LIB3106-092-Q1-K1-E11
5'-most EST
Method
                   BLASTN
                   g456713
NCBI GI
                   209
BLAST score
E value
                   1.0e-114
Match length
                   257
                   95
% identity
NCBI Description
                   Glycine max gene for ubiquitin, complete cds
Seq. No.
                   492 1.R1040
Contig ID
5'-most EST
                   leu701145206.hl
                   BLASTN
Method
NCBI GI
                   q18781
BLAST score
                   403
                   0.0e+00
E value
Match length
                   403
                   100
% identity
NCBI Description G.max win gene encoding wound-induced protein
Seq. No.
                   966
Contig ID
                   492 2.R1040
5'-most EST
                   fC-gmro700848126a1
                   BLASTN
Method
NCBI GI
                   g18781
BLAST score
                   177
E value
                   1.0e-94
                   249
Match length
                   93
% identity
                   G.max win gene encoding wound-induced protein
NCBI Description
                 967
Seq. No.
Contig ID
                   493 1.R1040
5'-most EST
                   g872115_FL
Method
                   BLASTX
NCBI GI
                   g872116
BLAST score
                   2461
E value
                   0.0e + 00
Match length
                   569
% identity
                   (X79770) sti (stress inducible protein) [Glycine max]
NCBI Description
Seq. No.
                   968
Contig ID
                   494 1.R1040
```

pxt700946118.h1

NCBI GI

BLAST score

```
Method
                  BLASTX
NCBI GI
                   q1076498
BLAST score
                   1980
E value
                   0.0e + 00
Match length
                   389
% identity
                   96
                   zinc-finger protein (C-terminal) - soybean
NCBI Description
                   >gi 558543 emb CAA85320 (Z36749) C-terminal zinc-finger
                   [Glycine max]
Seq. No.
                   969
                   497 1.R1040
Contig ID
5'-most EST
                  LIB3139-045-P1-N1-G1
Method
                  BLASTX
NCBI GI
                   q129585
BLAST score
                   3399
E value
                   0.0e + 00
Match length
                   706
% identity
                   93
                   PHENYLALANINE AMMONIA-LYASE CLASS II >gi_81877_pir__S04127
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) class II - kidney
                  bean >gi_228614_prf__1807329A Phe ammonia lyase [Phaseolus
                  vulgaris]
Seq. No.
                   970
                   497 2.R1040
Contig ID
5'-most EST
                   fC-gmro700807584e1
Method
                  BLASTN
                   g18376
NCBI GI
BLAST score
                   572
                   0.0e + 00
E value
Match length
                   592
                   99
% identity
NCBI Description
                  Glycine max PAL1 gene for phenylalanine ammonia lyase (EC
                   4.3.1.5
                   971
Seq. No.
                   497 3.R1040
Contig ID
                  uC-gmrominsoy056b10b1
5'-most EST
Method
                  BLASTX
                  g266731
NCBI GI
BLAST score
                   622
E value
                   7.0e-65
Match length
                   144
% identity
                   85
                  PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea
                  >gi 217980 dbj BAA00885 (D10001) phenylalanine
                  ammonia-lyase [Pisum sativum] >gi 217982 dbj BAA00886
                   (D10002) phenylalanine ammonia-lyase [Pisum sativum]
                   972
Seq. No.
                   498 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy123d08b1
Method
                  BLASTX
```

g231799

Method

BLASTX

```
0.0e + 00
E value
                  379
Match length
                  99
% identity
                  CHALCONE SYNTHASE 7 (NARINGENIN-CHALCONE SYNTHASE 7)
NCBI Description
                  >gi_478407_pir__JQ2250 naringenin-chalcone synthase (EC
                  2.3.1.74) - soybean >gi_169937 (M98871) chalcone synthase
                  [Glycine max]
                  973
Seq. No.
                  498 2.R1040
Contig ID
                  q4300400
5'-most EST
Method
                  BLASTN
NCBI GI
                  q169936
BLAST score
                  860
                  0.0e+00
E value
                  999
Match length
                  97
% identity
                  Glycine max chalcone synthase (chs7) gene, complete cds
NCBI Description
Seq. No.
                  498 3.R1040
Contig ID
                  uC-gmropic108h09b1
5'-most EST
Method
                  BLASTN
NCBI GI .
                  g218012
BLAST score
                  385
                  0.0e + 00
E value
                  513
Match length
                  95
% identity
                  Pueraria lobata mRNA for chalocone synthase, complete cds
NCBI Description
                  975
Seq. No.
                  498 6.R1040
Contig ID
                  uC-gmronoir028c02b1
5'-most EST
                  BLASTN
Method
                  g169936
NCBI GI
BLAST score
                  301
                  1.0e-169
E value
Match length
                  334
% identity
                  99
                  Glycine max chalcone synthase (chs7) gene, complete cds
NCBI Description
Seq. No.
                  499 1.R1040
Contig ID
5'-most EST
                  g545762_FL
Method
                  BLASTN
NCBI GI
                  g545762
BLAST score
                  518
                  0.0e+00
E value
Match length
                  526
% identity
                  100
                  Eu4=urease {clone 5E5} [Glycine max=soybeans, cv. Dare,
NCBI Description
                  mid-maturation embryos, mRNA Partial, 540 nt]
Seq. No.
Contig ID
                  500 1.R1040
5'-most EST
                  LIB3170-038-Q1-K1-E6
```

E value

makan ing

```
q3309269
NCBI GI
BLAST score
                   1810
                   0.0e+00
E value
Match length
                   501
                   97
% identity
                   (AF074940) ferric leghemoglobin reductase-2 precursor
NCBI Description
                   [Glycine max]
                   978
Seq. No.
                   500 3.R1040
Contig ID
                   LIB\overline{3}087-008-Q1-K1-B10
5'-most EST
Method
                   BLASTN
NCBI GI
                   q546359
                   279
BLAST score
                   1.0e-155
E value
                   327
Match length
                   96
% identity
NCBI Description
                   ferric leghemoglobin reductase [Glycine max=soybeans, Merr,
                   nodules, mRNA, 1740 nt]
                   979
Seq. No.
                   504 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy062a07b1
                   BLASTX
Method
                   q1706522
NCBI GI
BLAST score
                   2613
                   0.0e + 00
E value
                   521
Match length
% identity
                   94
                   DIHYDROFOLATE REDUCTASE / THYMIDYLATE SYNTHASE (DHFR-TS)
NCBI Description
                   >gi_1362048_pir__S55683 dihydrofolate reductase-thymidylate
                   synthase - soybean >gi_999190_bbs_166832 (S78087)
                   dihydrofolate reductase-thymidylate synthase,
                   DHFR-TS=bifunctional enzyme {EC 1.5.1.3} [Glycine max,
                   seedling, Peptide, 530 aa] [Glycine max]
                   >gi 1096144 prf 2111237A dihydrofolate
                   reductase-thymidylate synthase [Glycine max]
                   980
Seq. No.
                   504 2.R1040
Contig ID
5'-most EST
                   fC-gmst700656887r1
Method
                   BLASTN
                   g999189
NCBI GI
BLAST score
                   146
E value
                   3.0e-76
Match length
                   166
                   97
% identity
                   dihydrofolate reductase-thymidylate synthase=bifunctional
NCBI Description
                   enzyme [Glycine max, seedling, mRNA, 1794 nt]
                   981
Seq. No.
Contig ID
                   504 4.R1040
5'-most EST
                   fC-gmro7000746445a1
                   BLASTN
Method
NCBI GI
                   g999189
BLAST score
                   169
```

4.0e-90

```
257
Match length
% identity
                   91
NCBI Description
                  dihydrofolate reductase-thymidylate synthase=bifunctional
                  enzyme [Glycine max, seedling, mRNA, 1794 nt]
Seq. No.
                  507 1.R1040
Contig ID
5'-most EST
                  LIB3065-026-Q1-N1-B7
Method
                  BLASTN
NCBI GI
                  g498167
BLAST score
                  525
E value
                  0.0e+00
Match length
                  545
                  99
% identity
                  Soybean mRNA for leginsulin, complete cds
NCBI Description
Seq. No.
                   983
                  517 1.R1040
Contig ID
5'-most EST
                  g218259 FL
Method
                  BLASTX
NCBI GI
                  g730164
BLAST score
                  2436
E value
                  0.0e + 00
Match length
                  482
% identity
                  100
                  EARLY NODULIN 70 >gi 486678 pir S34800 sulfate transport
NCBI Description
                  protein homolog (clone GmN70) - soybean
                  >gi 218260 dbj BAA02723 (D13505) early nodulin [Glycine
                  \max >gi 4\overline{47137} prf 19\overline{13422C} nodulin [Glycine max]
                  984
Seq. No.
                  518 2.R1040
Contig ID
                  LIB3040-044-Q1-E1-C8
5'-most EST
Method
                  BLASTN
NCBI GI
                  g218261
BLAST score
                  121
                  2.0e-61
E value
Match length
                  229
                  88
% identity
NCBI Description
                  Soybean mRNA for early nodulin
                  985
Seq. No.
                  521 1.R1040
Contig ID
5'-most EST
                  seb700650013.hl
Method
                  BLASTX
NCBI GI
                  g485495
BLAST score
                  2326
                  0.0e + 00
E value
                  463
Match length
% identity
                  aspartate transaminase (EC 2.6.1.1) AAT5 precursor -
NCBI Description
                  soybean >gi_169915 (L09702) aspartate aminotransferase
                  [Glycine max] >gi_300419_bbs_132011 (S60967) aspartate
                  aminotransferase isozyme 5, AAT5 {EC 2.6.1.1} [Glycine
                  max=soybeans, cv. Century, Peptide Chloroplast, 463 aa]
```

[Glycine max]

% identity

100

```
986
Seq. No.
                   521 2.R1040
Contig ID
5'-most EST
                   LIB3049-021-Q1-E1-C8
Method
                   BLASTN
NCBI GI
                   g300418
                   290
BLAST score
                   1.0e-162
E value
Match length
                   342
                   96
% identity
                   aspartate aminotransferase isozyme 5 [Glycine max=soybeans,
NCBI Description
                   cv. Century, mRNA, 1755 nt]
Seq. No.
                   987
                   521 3.R1040
Contig ID
5'-most EST
                   gsv701055975.hl
Method
                   BLASTN
                   g169914
NCBI GI
BLAST score
                   123
E value
                   7.0e-63
Match length
                   123
                   100
% identity
                   Glycine max (clone pSAT17) aspartate aminotransferase mRNA,
NCBI Description
                   complete cds
                   988
Seq. No.
                   522 1.R1040
Contig ID
5'-most EST
                   g169918 FL
Method
                   BLASTN
NCBI GI
                   g169918
BLAST score
                   1735
                   0.0e+00
E value
                   1924
Match length
                   99
% identity
                   Soybean auxin-regulated protein (Aux22) mRNA, complete cds
NCBI Description
Seq. No.
                   522 2.R1040
Contig ID
5'-most EST
                   rlr700901873.hl
                   BLASTN
Method
NCBI GI
                   g169918
BLAST score
                   144
E value
                   3.0e-75
                   316
Match length
                   88
% identity
NCBI Description
                  Soybean auxin-regulated protein (Aux22) mRNA, complete cds
                   990
Seq. No.
                   523_1.R1040
Contig ID
5'-most EST
                   g169920 FL
Method
                   BLASTN
NCBI GI
                   g169920
BLAST score
                   1780
                   0.0e+00
E value
                   1784
Match length
```

NCBI Description Soybean auxin-regulated protein (Aux28) mRNA, complete cds

Match length

```
991
Seq. No.
                   523 2.R1040
Contig ID
                   leu701151952.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   q169920
BLAST score
                   213
                   1.0e-116
E value
Match length
                   531
% identity
                   87
NCBI Description
                  Soybean auxin-regulated protein (Aux28) mRNA, complete cds
Seq. No.
                   523 3.R1040
Contig ID
5'-most EST
                   jC-qmf102220103g11d1
Method
                  BLASTN
NCBI GI
                  g169920
BLAST score
                  103
E value
                   1.0e-50
Match length
                  285
                  87
% identity
                  Soybean auxin-regulated protein (Aux28) mRNA, complete cds
NCBI Description
                   993
Seq. No.
                  523 4.R1040
Contig ID
5'-most EST
                  seb700653443.h1
Method
                  BLASTX
NCBI GI
                  g114734
BLAST score
                  192
E value
                  2.0e-14
Match length
                  113
                   47
% identity
                  AUXIN-INDUCED PROTEIN AUX28 >gi_81759_pir__A28993 aux28
NCBI Description
                  protein - soybean >gi 169921 (J03919) auxin-regulated
                  protein (Aux28) [Glycine max]
                  994
Seq. No.
                  524 1.R1040
Contig ID
                  zsg701127613.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1706546
BLAST score
                  1791
                  0.0e+00
E value
                  347
Match length
                  100
% identity
NCBI Description
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1, 3-ENDOGLUCANASE) >gi 169923 (M37753)
                  beta-1,3-endoglucanase (EC 3.2.1.39) [Glycine max]
                  995
Seq. No.
                  524 2.R1040
Contig ID
5'-most EST
                  zzp700832021.h1
                  BLASTX
Method
NCBI GI
                  g1403675
BLAST score
                  760
E value
                  7.0e-81
```

```
% identity
NCBI Description
                   (U41323) beta-1,3-glucanase [Glycine max]
Seq. No.
                   524 3.R1040
Contig ID
5'-most EST
                   jC-gmst02400051f12a1
Method
                   BLASTN
NCBI GI
                   q1403674
BLAST score
                   273
E value
                   1.0e-152
Match length
                   449
                   90
% identity
NCBI Description
                  Glycine max beta-1,3-glucanase (SGN1) gene, complete cds
                   997
Seq. No.
                   524 4.R1040
Contig ID
5'-most EST
                  LIB3139-048-P1-N1-H7
                  BLASTX
Method
NCBI GI
                   g1403675
BLAST score
                   528
E value
                   7.0e-54
Match length
                  139
                   75
% identity
NCBI Description
                   (U41323) beta-1,3-glucanase [Glycine max]
Seq. No.
                   528 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy264f06b1
Method
                  BLASTX
NCBI GI
                  g116054
BLAST score
                   2564
E value
                  0.0e + 00
                   492
Match length
% identity
                   100
                  CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)
NCBI Description
                  >gi 280393 pir A43713 calcium-dependent protein kinase (EC
                   2.7.1.-) - soybean >gi 169931 (M64987) Glycine max calcium
                  dependent protein kinase mRNA. [Glycine max]
                   999
Seq. No.
                   528_2.R1040
Contig ID
5'-most EST
                   fua701040310.h1
Method
                  BLASTN
NCBI GI
                  g169930
                  279
BLAST score
E value
                  1.0e-155
Match length
                   423
% identity
NCBI Description
                  Glycine max calcium dependent protein kinase mRNA
                  1000
Seq. No.
Contig ID
                   528 3.R1040
5'-most EST
                   fC-gmse700674513d3
Method
                  BLASTN
NCBI GI
                  q169930
BLAST score
                  187
                  1.0e-101
```

E value

Contig ID

Seq. No.

5'-most EST

```
331
Match length
                    89
% identity
NCBI Description
                   Glycine max calcium dependent protein kinase mRNA
                    1001
Seq. No.
                    531 1.R1040
Contig ID
5'-most EST
                    jC-gmst02400047f05a1
Method
                   BLASTX
NCBI GI
                    g3096935
BLAST score
                   195
E value
                    8.0e-15
Match length
                   102
% identity
                    42
NCBI Description
                    (AL023094) putative protein [Arabidopsis thaliana]
Seq. No.
                   531 2.R1040
Contig ID
                   g5752719
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1617206
BLAST score
                   275
E value
                    4.0e-24
                   129
Match length
% identity
                    48
NCBI Description
                   (Z72489) CP12 [Pisum sativum]
                   1003
Seq. No.
                   531 3.R1040
Contig ID
5'-most EST
                   LIB3170-045-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3334150
                   1870
BLAST score
E value
                   0.0e+00
Match length
                   421
% identity
                   90
                   MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
NCBI Description
                    (MG-PROTOPORPHYRIN IX CHELATASE) >gi 2129847.pir JC4312
                   chlorophyll magnesium chelatase (\overline{EC} \overline{4}.99.-.-) - \overline{soy}bean
                   chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase
                   subunit (46 kD) [Glycine max]
                   1004
Seq. No.
                   531 4.R1040
Contig ID
5'-most EST
                   LIB3028-039-Q1-B2-B2
Method
                   BLASTN
NCBI GI
                   g1732468
BLAST score
                   82
                   5.0e-38
E value
Match length
                   86
                   99
% identity
                   Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
NCBI Description
Seq. No.
                   1005
```

531\_5.R1040 g5510205

5'-most EST

```
Contig ID
                   531 6.R1040
5'-most EST
                   LIB3107-014-Q1-K1-D9
Method
                   BLASTN
NCBI GI
                   g1732468
BLAST score
                   133
E value
                   3.0e-68
Match length
                   439
                   91
% identity
NCBI Description
                   Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
Seq. No.
                   1007
                   531 7.R1040
Contig ID
5'-most EST
                   LIB3074-011-Q1-E1-E12
Method
                   BLASTN
NCBI GI
                   q1732468
BLAST score
                   82
E value
                   3.0e-38
Match length
                   86
                   99
% identity
                   Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
NCBI Description
Seq. No.
Contig ID
                   531_8.R1040
                   g5677965
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1617206.
BLAST score
                   244
E value
                   1.0e-20
                   79
Match length
% identity
                   57
                   (Z72489) CP12 [Pisum sativum]
NCBI Description
                   1009
Seq. No.
Contig ID
                   531 9.R1040
5'-most EST
                   uC-gmropic110e07b1
Method
                   BLASTN
NCBI GI
                   g1732468
BLAST score
                   189
E value
                   1.0e-102
                   257
Match length
% identity
                   93
                   Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
NCBI Description
                   1010
Seq. No.
                   531 10.R1040
Contig ID
5'-most EST
                   g5752984
Method
                   BLASTN
NCBI GI
                   g1732468
BLAST score
                   144
                   4.0e-75
E value
Match length
                   432
                   98
% identity
                   Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
NCBI Description
Seq. No.
                   1011
Contig ID
                   531 14.R1040
```

ssr700557049.hl

```
Method
                   BLASTN
NCBI GI
                   g1732468
BLAST score
                   180
                   7.0e-97
E value
                   244
Match length
                   93
% identity
                  Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
NCBI Description
Seq. No.
                   1012
Contig ID
                   534 1.R1040
5'-most EST
                   jC-qmf102220070f11a1
Method
                   BLASTX
NCBI GI
                   g1351410
BLAST score
                   2477
                   0.0e+00
E value
Match length
                   495
% identity
                   94
                   VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                   >gi 511938 dbj BAA06030 (D28876) cysteine proteinase
                   [Glycine max]
                                        1013
Seq. No.
                   534 2.R1040
Contig ID
5'-most EST
                  LIB3107-004-Q1-K1-D4
Method
                  BLASTN
NCBI GI
                   q511937
                   244
BLAST score
                   1.0e-135
E value
Match length
                   326
                   94
% identity
                  Soybean mRNA for cysteine proteinase, complete cds
NCBI Description
Seq. No.
                   1014
Contig ID
                   534 3.R1040
5'-most EST
                  uC-gmropic103c05b1
Method
                  BLASTN
NCBI GI
                   g511937
BLAST score
                   267
E value
                   1.0e-148
Match length
                   279
                   99
% identity
                  Soybean mRNA for cysteine proteinase, complete cds
NCBI Description
                                                             16. . .
Seq. No.
                   1015
                   535 1.R1040
Contig ID
5'-most EST
                   seb700653014.h1
Method
                  BLASTX
                   q2494415
NCBI GI
BLAST score
                   1914
                   0.0e + 00
E value
                   394
Match length
% identity
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >qi 515747. (L34841) fructose-1,6-bisphosphatase [Glycine
                  maxl
```

```
1016
Seq. No.
                   535 2.R1040
Contig ID
5'-most EST
                   vzy700755037.hl
                   BLASTN
Method
NCBI GI
                   g20716
BLAST score
                   155
E value
                   9.0e-82
                   294
Match length
                   88
% identity
                   P.sativum mRNA for fructose 1,6 biphosphatase
NCBI Description
                   1017
Seq. No.
                   535 3.R1040
Contig ID
5'-most EST
                   fde700872212.h1
Method
                   BLASTN
NCBI GI
                   g515746
BLAST score
                   166
E value
                   2.0e-88
                   187
Match length
                   97
% identity
                   Soybean chloroplast fructose-1,6-bisphosphatase (FBP) mRNA,
NCBI Description
                   complete cds
                   1018
Seq. No.
Contig ID
                   537 1.R1040
5'-most EST
                   LIB3040-043-Q1-E1-C11
Method
                   BLASTN
NCBI GI
                   g548320
BLAST score
                   944
E value
                   0.0e + 00
Match length
                   984
% identity
                   99
NCBI Description
                   Glycine max dihydrodipicolinate synthase (dapA) mRNA,
                   complete cds
Seq. No.
                   1019
                   537 2.R1040
Contig ID
5'-most EST
                   ncj700981542.h1
                   BLASTN
Method
NCBI GI
                   g548320
BLAST score
                   126
E value
                   2.0e-64
Match length
                   138
% identity 4
NCBI Description
                   Glycine max dihydrodipicolinate synthase (dapA) mRNA,
                   complete cds
                   1020
Seq. No.
Contig ID
                   539 1.R1040
5'-most EST
                   jC-gmf102220138d09a1
Method
                   BLASTN
NCBI GI
                   g457569
BLAST score
                   958
E value
                   0.0e + 00
Match length
                   962
% identity
                   100
                   Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
```

5'-most EST

```
1021
Seq. No.
                   539 2.R1040
Contig ID
                   leu701153112.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g457569
BLAST score
                   373
                   0.0e + 00
E value
Match length
                   780
                   88
% identity
                   Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
Seq. No.
                   1022
                   539 3.R1040
Contig ID
5'-most EST
                   LIB3028-050-Q1-B1-A12
                   BLASTX
Method
NCBI GI
                   g2813966
BLAST score
                   234
E value
                   6.0e-19
                   200
Match length
% identity
                   41
                   (Z97053) placental protein Diff33 [Homo sapiens]
NCBI Description
                   >gi 4545219 gb AAD22448.1 (AF112227) TDE homolog [Homo
                   sapiens]
                   1023
Seq. No.
                   539 4.R1040
Contig ID
5'-most EST
                  ncj700981722.hl
                  BLASTX
Method
NCBI GI
                   g2813966
                   255
BLAST score
E value
                   2.0e-21
Match length
                   150
% identity
                   35
NCBI Description
                   (297053) placental protein Diff33 [Homo sapiens]
                  >gi 4545219 gb AAD22448.1 (AF112227) TDE homolog [Homo
                   sapiens]
Seq. No.
                   1024
                   539 5.R1040
Contig ID
                   leu701144894.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q457572
BLAST score
                   631
                   0.0e + 00
E value
                   905
Match length
% identity
                  V.angularis mRNA for endo-xyloglucan transferase, complete
NCBI Description
                   1025
Seq. No.
Contig ID
                   539 6.R1040
5'-most EST
                   zhf700959501.h1
Seq. No.
                   1026
Contig ID
                   539 8.R1040
```

jC-gmst02400018d10d1

```
BLASTN
Method
NCBI GI
                  g457569
BLAST score
                  250
                   1.0e-138
E value
Match length
                  250
                   100
% identity
NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds
Seq. No.
                  1027
                  539 9.R1040
Contig ID
5'-most EST
                  LIB3028-006-Q1-B1-C3
Method
                  BLASTN
NCBI GI
                  g457569
BLAST score
                  206
                   1.0e-112
E value
Match length
                  298
                   93
% identity
                  Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
Seq. No.
                  539 11.R1040
Contig ID
                  zzp700832821.hl
5'-most EST .
                  1029
Seq. No.
                  539 12.R1040
Contig ID
5'-most EST
                  LIB3028-024-Q1-B1-D8
Method
                  BLASTN
                  g457569
NCBI GI
BLAST score
                  273
                  1.0e-152
E value
                  297
Match length
                   98
% identity
                  Soybean mRNA for endo-xyloglucan transferase, partial cds
NCBI Description
Seq. No.
                  1030
                  539 13.R1040
Contig ID
5'-most EST
                   jC-gmf102220082h12a1
                  BLASTN
Method
NCBI GI
                  g457572
BLAST score
                   387
                   0.0e+00
E value
Match length
                   666
                  91
% identity
NCBI Description
                  V.angularis mRNA for endo-xyloglucan transferase, complete
                  1031
Seq. No.
                  540 1.R1040
Contig ID
5'-most EST
                  pxt700944790.h1
Method
                  BLASTN
NCBI GI
                  g169952
BLAST score
                  1024
                  0.0e+00
E value
Match length
                  1044
% identity
                  100
```

NCBI Description Glycine max ferritin mRNA, complete cds

Match length

```
Seq. No.
                   1032
                   540 2.R1040
Contig ID
                   LIB3170-037-Q1-K1-H5
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170077
BLAST score
                   287
E value
                   1.0e-160
Match length
                   311
% identity
                  Soybean ferritin (SOF-H2) mRNA, partial cds
NCBI Description
Seq. No.
                   1033
                   542 1.R1040
Contig ID
5'-most EST
                   LIB3138-079-P1-N1-B2
Method
                   BLASTN
NCBI GI
                   g169954
BLAST score
                   1048
E value
                   0.0e+00
Match length
                   1048
                   100
% identity
                  Glycine max iron superoxide dismutase (FeSOD) mRNA,
NCBI Description
                   complete cds
                   1034
Seq. No.
                   542 3.R1040
Contig ID
                   wrg700792105.hl
5'-most EST
Method
                   BLASTX
                   g134646
NCBI GI
BLAST score
                   220
                   7.0e-18
E value
                   49
Match length
                   73
% identity
NCBI Description
                  SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) >gi 169955
                   (M64267) Fe-superoxide dismutase [Glycine max]
                   >gi 228415 prf 1803527A Fe superoxide dismutase [Glycine
                  max]
Seq. No.
                   1035
                   542 5.R1040
Contig ID
5'-most EST
                   rca701001755.hl
                   BLASTN
Method
NCBI GI
                   q169954
BLAST score
                   147
E value
                   4.0e-77
Match length
                   213
% identity
                  Glycine max iron superoxide dismutase (FeSOD) mRNA,
NCBI Description
                  complete cds
                   1036
Seq. No.
Contig ID
                   544 1.R1040
5'-most EST
                   uC-gmropic022d09b1
Method
                   BLASTN
NCBI GI
                   q169956
BLAST score
                   1266
E value
                   0.0e + 00
```

```
% identity
NCBI Description Glycine max G-box binding factor (GBF1) mRNA, complete cds
                  1037
Seq. No.
                  545 1.R1040
Contig ID
5'-most EST
                  LIB3051-047-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q169959
BLAST score
                  1989
                  0.0e+00
E value
Match length
                  423
                  94
% identity
NCBI Description (L01448) G-box binding factor [Glycine max]
                  1038
Seq. No.
                  545 2.R1040
Contig ID
5'-most EST
                  LIB3138-082-P1-N1-H1
Method
                  BLASTX
NCBI GI
                  g169961
BLAST score
                  1837
                  0.0e + 00
E value
Match length
                  365
                  100
% identity
                  (L01449) G-box binding factor [Glycine max]
NCBI Description
                  1039
Seq. No.
                  545 3.R1040
Contig ID
5'-most EST
                  LIB3093-025-Q1-K1-F3
Method
                  BLASTN
NCBI GI
                  g169958
BLAST score
                  191
                  1.0e-103
E value
Match length
                  358
                  90
% identity
NCBI Description Glycine max G-box binding factor (GBF2A) mRNA, 3' end
                  1040
Seq. No.
                  545 4.R1040
Contig ID
5'-most EST
                  g5688140
                  BLASTX
Method
NCBI GI
                  g1155054
BLAST score
                  278
                  9.0e-44
E value
Match length
                  133
% identity
                  (U41817) regulator of MAT2 [Phaseolus vulgaris]
NCBI Description
Seq. No.
                  1041
Contig ID
                  545 6.R1040
5'-most EST
                  uC-gmropic110b11b1
Method
                  BLASTN
NCBI GI
                  g169958
BLAST score
                  47
E value
                  3.0e-17
Match length
                  118
% identity
                  Glycine max G-box binding factor (GBF2A) mRNA, 3' end
NCBI Description
```

NCBI GI

. .

```
1042
Seq. No.
Contig ID
                  547 1.R1040
                  uC-gmropic074d11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1346192
BLAST score
                  2517
E value
                  0.0e + 00
Match length
                  525
% identity
                  94
                  GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
NCBI Description
                  >gi_169965 (L11632) glutathione reductase [Glycine max]
Seq. No.
                  547 2.R1040
Contig ID
                  fde700872675.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  q169964
BLAST score
                  100
                  7.0e-49
E value
Match length
                  415
% identity
                  88
                  Soybean glutathione reductase (GR) mRNA, complete cds
NCBI Description
                  1044
Seq. No.
                  552 1.R1040
Contig ID
5'-most EST
                  g438898 FL
Method
                  BLASTX
NCBI GI
                  g1709918
BLAST score
                  2776
E value
                  0.0e + 00
Match length
                  548
                  98
% identity
NCBI Description
                  AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE
                  PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE)
                  (GPAT) >gi 438899 (L23833) glutamine.
                  phosphoribosylpyrophosphate amidotransferase [Glycine max]
Seq. No.
                  1045
Contig ID
                  552 2.R1040
5'-most EST
                  g4303654
Method
                  BLASTX
NCBI GI
                  g1709918
BLAST score
                  1084
E value
                  1.0e-118
Match length
                  269
% identity
                  85
                  AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE
NCBI Description
                  PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE)
                  (GPAT) >gi 438899 (L23833) glutamine
                  phosphoribosylpyrophosphate amidotransferase [Glycine max]
                  1046
Seq. No.
Contig ID
                  553 1.R1040
5'-most EST
                  jC-gmro02910062f11a1
Method
                  BLASTX
```

q1346105

```
1978
BLAST score
                   0.0e+00
E value
                   385
Match length
                   99
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT
NCBI Description
                   (GP-ALPHA-1) >gi_439617 (L27418) G protein alpha subunit
                   [Glycine max]
Seq. No.
                  1047
                  554 1.R1040
Contig ID
                  LIB3049-032-Q1-E1-A12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1170031
BLAST score
                  2323
E value
                  0.0e + 00
Match length
                   466
                   97
% identity
NCBI Description
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
                   (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                  >gi 541940 pir JQ2263 glutamate 1-semialdehyde
                  aminotransferase (EC 2.6.1.-) precursor - soybean
                  >gi 310567 (L12453) glutamate 1-semialdehyde
                  aminotransferase [Glycine max] >gi 747968 (U20260)
                  glutamate 1-semialdehyde aminotransferase [Glycine max]
                  1048
Seq. No.
                  554 2.R1040
Contig ID
5'-most EST
                  LIB3138-061-Q1-N1-G9
Method
                  BLASTN
NCBI GI
                  g310566
BLAST score
                  300
E value
                  1.0e-168
                  419
Match length
% identity
                  95
                  Soybean glutamate 1-semialdehyde aminotransferase mRNA,
NCBI Description
                  complete cds
                  1049
Seq. No.
                  555 1.R1040
Contig ID
5'-most EST
                  LIB3055-006-Q1-N1-B8
                  BLASTN
Method
NCBI GI
                  g450634
BLAST score
                  954
E value
                  0.0e+00
Match length
                  998
% identity
                  99
NCBI Description
                  Soybean GTP binding protein mRNA, complete cds
                  1050
Seq. No.
Contiq ID
                  555 2.R1040
5'-most EST
                  g1381677 FL
Method
                  BLASTN
NCBI GI
                  q1381677
BLAST score
                  706
E value
                  0.0e + 00
                  888
Match length
```

95

% identity

Match length

```
NCBI Description
                  Glycine max small GTP-binding protein (sra2) mRNA, complete
                  cds
                                                                     1845 - 1
Seq. No.
                   1051
                   555 3.R1040
Contig ID
5'-most EST
                  uC-gmropic054b10b1
Method
                  BLASTN
NCBI GI
                  g303731
BLAST score
                   4.56
E value
                  0.0e+00
                  723
Match length
                   92
% identity
NCBI Description Pea mRNA for GTP-binding protein, complete cds
                  1052
Seq. No.
                   555 4.R1040
Contig ID
5'-most EST
                  LIB3050-014-Q1-E1-C4
Method
                  BLASTN
NCBI GI
                  g1381677
BLAST score
                  336
E value
                   0.0e + 00
Match length
                   443
                   97
% identity
                  Glycine max small GTP-binding protein (sra2) mRNA, complete
NCBI Description
                                                            A .
                  1053
Seq. No.
                  556 1.R1040
Contig ID
5'-most EST
                  LIB3109-016-Q1-K1-B2
Method
                  BLASTX
                  g1170312
NCBI GI
BLAST score
                  1640
E value
                  0.0e + 00
Match length
                  379
% identity
                  82
                  HOMEOBOX PROTEIN SBH1 >qi 629614 pir S42543 hypothetical
NCBI Description
                  protein - soybean >gi 485406 (L13663) SBH1 [Glycine max]
Seq. No.
                  1054
                  556 2.R1040
Contig ID
5'-most EST
                  g5666882
                  BLASTN
Method
NCBI GI
                  g310568
BLAST score
                  279
E value
                  1.0e-155
Match length
                  455
                  91
% identity
                  Glycine max homeobox-containing (Sbh1) mRNA, complete cds
NCBI Description
                  1055
Seq. No.
                  557 1.R1040
Contig ID
5'-most EST
                  g4313302
Method
                  BLASTN
NCBI GI
                  g170048
BLAST score
                  393
E value
                  0.0e + 00
```

BLAST score

```
% identity
NCBI Description
                   Glycine max SbPRP1 gene encoding a proline-rich protein,
                   complete cds
                   1056
Seq. No.
                   558 1.R1040
Contig ID
5'-most EST
                   g43<u>1</u>3671
Method
                   BLASTN
NCBI GI
                   g347452
BLAST score
                   507 ·
E value
                   0.0e + 00
Match length
                   876
                   20
% identity
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP3) mRNA,
NCBI Description
                   partial cds
                   1057
Seq. No.
                   558_2.R1040
Contig ID
5'-most EST
                   g5606931
Method
                   BLASTN
NCBI GI
                   g1165321
BLAST score
                   146
E value
                   4.0e-76
Match length
                   560
                   25
% identity
                   Glycine max extensin (SbHRGP3) gene, complete cds
NCBI Description
                   1058
Seq. No.
                   559 1.R1040
Contig ID
5'-most EST
                   g4314026
Method
                   BLASTN
NCBI GI
                   g347454
BLAST score
                   573
E value
                   0.0e + 00
                   736
Match length
                   74
% identity
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
NCBI Description
                   end
                   1059
Seq. No.
                   559 2.R1040
Contig ID
5'-most EST
                   LIB3107-063-Q1-K1-C2
Method
                   BLASTN
NCBI GI
                   q2677823
BLAST score
                   117
E value
                   1.0e-58
Match length
                   287
                   87
% identity
                   Prunus armeniaca abscisic stress ripening protein homolog
NCBI Description
                   mRNA, complete cds
Seq. No.
                   1060
Contig ID
                   559 3.R1040
5'-most EST
                   jC-gmro02910061a12a1
Method
                   BLASTN
NCBI GI
                   g2677823
```

```
4.0e-45
E value
Match length
                  254
% identity
                  .84
                  Prunus armeniaca abscisic stress ripening protein homolog
NCBI Description
                  mRNA, complete cds
                  1061
Seq. No.
Contig ID
                  559 4.R1040
                  rca701000967.hl
5'-most EST
Method
                  BLASTN
                  q2677823
NCBI GI
BLAST score
                  38
                  9.0e-12
E value
Match length
                  46
                  96
% identity
                  Prunus armeniaca abscisic stress ripening protein homolog
NCBI Description
                  mRNA, complete cds
Seq. No.
                  1062
                  559 5.R1040
Contig ID
                  sat701009243.hl
5'-most EST
Method
                  BLASTN
                  q2677823
NCBI GI
BLAST score
                  90
                  6.0e-43
E value
                  254
Match length
                  84
% identity
                  Prunus armeniaca abscisic stress ripening protein homolog
NCBI Description
                  mRNA, complete cds
                  1063
Seq. No.
                  559 6.R1040
Contig ID
                  uC-gmflminsoy063c10b1
5'-most EST
Method
                  BLASTX
                  g4544436
NCBI GI
BLAST score
                  273
                  4.0e-24
E value
Match length
                  114
                  50
% identity
                  (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,
NCBI Description
                  3' partial [Arabidopsis thaliana]
                  1064
Seq. No.
Contig ID
                  559 9.R1040
5'-most EST
                  jC-gmst02400033b01a1
Seq. No.
                  1065
                  559 11.R1040
Contiq ID
5'-most EST
                  q4277016
Seq. No.
                  1066
Contig ID
                  559 13.R1040
                  pmv700889430.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2677823
BLAST score
                  83
```

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5.0e-39

E value

5'-most EST

```
Match length
                   194
                   90
% identity
                   Prunus armeniaca abscisic stress ripening protein homolog
NCBI Description
                   mRNA, complete cds
                   1067
Seq. No.
                   559 19.R1040
Contig ID
5'-most EST
                   pmv700890409.h1
Method
                   BLASTN
NCBI GI
                   q2677823
BLAST score
                   48
                   4.0e-18
E value
Match length
                   143
% identity
NCBI Description
                   Prunus armeniaca abscisic stress ripening protein homolog
                   mRNA, complete cds
                   1068
Seq. No.
                   561 1.R1040
Contig ID
5'-most EST
                   taw700658110.hl
Method
                   BLASTX
NCBI GI
                   q1168290
BLAST score
                   2732
E value
                   0.0e + 00
Match length
                   550
% identity
                   95
                   ISOCITRATE LYASE 2 (ISOCITRASE 2) (ISOCITRATASE 2) (ICL 2)
NCBI Description
                   >gi 349329 (L02330) glyoxysomal isocitrate lyase [Glycine
                   max]
                   1069
Seq. No.
                   561 2.R1040
Contig ID
                   fC-gmse700657704f5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1168289
BLAST score
                   2740
                   0.0e + 00
E value
Match length
                   549
                   96
% identity
                   ISOCITRATE LYASE 1 (ISOCITRASE 1) (ISOCITRATASE 1) (ICL 1)
NCBI Description
                   >gi 349327 (L02329) glyoxysomal isocitrate lyase [Glycine
                   max]
                   1070
Seq. No.
                   564 1.R1040
Contig ID
5'-most EST
                   g310579 FL
Method
                   BLASTX
                   g310580
NCBI GI
                   1761
BLAST score
E value
                   0.0e+00
                   339
Match length
% identity
                   (L19360) protein kinase 2 [Glycine max]
NCBI Description
                   1071
Seq. No.
Contig ID
                   564 2.R1040
```

g169990 FL

Contiq ID

5'-most EST

```
Method
                   BLASTX
NCBI GI
                   q1362050
BLAST score
                   1771
E value
                   0.0e + 00
Match length
                   339
                   100
% identity
NCBI Description
                   protein kinase 1 - soybean >gi 169991 (L01453) protein
                   kinase [Glycine max]
                   1072
Seq. No.
                   564 4.R1040
Contig ID
                   hrw701060550.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q310579
BLAST score
                   498
E value
                   0.0e + 00
Match length
                   1118
                   95
% identity
NCBI Description
                  Glycine max protein kinase 2 (SPK-2) mRNA, complete cds
Seq. No.
                   1073
Contig ID
                   564 5.R1040
                   ssr700560617.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g310579
BLAST score
                   230
E value
                   1.0e-126
                   242
Match length
                   99
% identity
                  Glycine max protein kinase 2 (SPK-2) mRNA, complete cds
NCBI Description
Seq. No.
                   564 7.R1040
Contig ID
5'-most EST
                   LIB3093-053-Q1-K1-G5
Method
                   BLASTN
                   q169990
NCBI GI
BLAST score
                   154
                   5.0e-81
E value
Match length
                   229
% identity
                   98
                  Soybean protein kinase (SPK-1) mRNA, complete cds
NCBI Description
                   1075
Seq. No.
                   567 1.R1040
Contig ID
5'-most EST
                   LIB3051-090-Q1-K1-A2
Method
                   BLASTN
NCBI GI
                   q170009
BLAST score
                   1494
                   0.0e+00
E value
Match length
                   1727
                   99
% identity
                  Soybean late embryogenesis abundant (LEA) protein mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1076
```

A

567 2.R1040

LIB3029-001-Q1-B1-F8

```
BLASTN
Method
NCBI GI
                   g170009
BLAST score
                   369
                   0.0e+00
E value
Match length
                   799
                   61
% identity
NCBI Description
                   Soybean late embryogenesis abundant (LEA) protein mRNA,
                   complete cds
                   1077
Seq. No.
                   567 4.R1040
Contig ID
5'-most EST
                   LIB3065-004-Q1-N1-F2
Method
                   BLASTN
NCBI GI
                   q170009
BLAST score
                   86
E value
                   1.0e-40
Match length
                   342
% identity
                   61
NCBI Description
                   Soybean late embryogenesis abundant (LEA) protein mRNA,
                   complete cds
Seq. No.
                   1078
Contig ID
                   567 5.R1040
5'-most EST
                  LIB3029-006-Q1-B1-G3
Method
                   BLASTN
NCBI GI
                   g170009
BLAST score
                   127
E value
                   5.0e-65
Match length
                   359
                   84
% identity
                   Soybean late embryogenesis abundant (LEA) protein mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1079
                   567 7.R1040
Contig ID
5'-most EST
                   crh700850265.hl
Method
                   BLASTN
NCBI GI
                   g170009
BLAST score
                   144
                   5.0e-75
E value
                   495
Match length
% identity
                   62
NCBI Description
                   Soybean late embryogenesis abundant (LEA) protein mRNA,
                   complete cds
                   1080
Seq. No.
                   567 8.R1040
Contiq ID
5'-most EST
                   awf700839939.hl
Method
                   BLASTN
                   g170009
NCBI GI
BLAST score
                   123
E value
                   9.0e-63
Match length
                   301
% identity
NCBI Description
                   Soybean late embryogenesis abundant (LEA) protein mRNA,
```

. .

complete cds

NCBI Description

```
1081
Seq. No.
Contig ID
                   571 1.R1040
5'-most EST
                   uC-gmropic057g04b1
                   BLASTX
Method
NCBI GI
                   g1362046
BLAST score
                   1888
E value
                   0.0e + 00
                   426
Match length
                   99
% identity
                   aspartate transaminase (EC 2.6.1.1) precursor - soybean
NCBI Description
                   >gi 710596 (L40579) mitochondrial aspartate
                   aminotransferase [Glycine max]
                   1082
Seq. No.
                   576 1.R1040
Contig ID
5'-most EST
                   g857396_FL
                   BLASTX
Method
NCBI GI
                   g857397
BLAST score
                   2283
                   0.0e + 00
E value
                   484
Match length
                   92
% identity
                  (D50870) mitotic cyclin a2-type [Glycine max]
NCBI Description
                   1083
Seq. No.
Contig ID
                   576 2.R1040
5'-most EST
                   ncj700988646.h1
Method
                   BLASTN
NCBI GI
                   g857396
BLAST score
                   124
E value
                   2.0e-63
Match length
                   220
% identity
                  Glycine max mRNA for mitotic cyclin a2-type, complete cds
NCBI Description
Seq. No.
                   577 1.R1040
Contig ID
5'-most EST
                   LIB3049-047-Q1-E1-A4
Method
                   BLASTX.
NCBI GI
                   g857399
BLAST score
                   2091
E value
                   0.0e + 00
Match length
                   427
% identity
                   (D50871) mitotic cyclin b1-type [Glycine max]
NCBI Description
                   1085
Seq. No.
Contig ID
                   577 2.R1040
5'-most EST
                   jC-gmf102220070f12a1
                   BLASTN
Method
NCBI GI
                   q857398
BLAST score
                   306
E value
                   1.0e-171
Match length
                   354
% identity
                   97
```

Glycine max mRNA for mitotic cyclin b1-type, complete cds

```
Seq. No.
                   1086
                   578 1.R1040
Contig ID
                   LIB3056-001-Q1-B1-H5
5'-most EST
Method
                   BLASTN
NCBI GI
                   g347458
BLAST score
                   1016
E value
                   0.0e + 00
Match length
                   1048
                   99
% identity
NCBI Description
                   Glycine max brassinosteroid-regulated protein mRNA,
                   complete cds
                   1087
Seq. No.
Contig ID
                   578 2.R1040
5'-most EST
                   fua701043403.hl
                   BLASTN
Method
NCBI GI
                   g347458
BLAST score
                   361
E value
                   0.0e + 00
Match length
                   712
                   90
% identity
                   Glycine max brassinosteroid-regulated protein mRNA,
NCBI Description
                   complete cds
                   1088
Seq. No.
Contig ID
                   578 6.R1040
5'-most EST
                   LIB3139-015-P1-N1-H4
Method
                   BLASTN
NCBI GI
                   g347458
BLAST score
                   216
                   1.0e-118
E value
Match length
                   365
                   94
% identity
NCBI Description
                   Glycine max brassinosteroid-regulated protein mRNA,
                   complete cds
                   1089
Seq. No.
Contig ID
                   579 1.R1040
5'-most EST
                   txt700731909.h1
Method
                   BLASTX
                   g1345976
NCBI GI
BLAST score
                   2058
E value
                   0.0e + 00
Match length
                   387
                   97
% identity
                   OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   ISOZYME 1 >gi 904152 (L43920) microsomal omega-6 desaturase
                   [Glycine max]
                   1090
Seq. No.
                   579 2.R1040
Contig ID
5'-most EST
                   zpv700757037.h1
Method
                   BLASTN
NCBI GI
                   g904151
BLAST score
                   375
E value
                   0.0e + 00
```

560

Match length

5'-most EST

```
% identity
                  Glycine max FAD2-1 microsomal omega-6 desaturase mRNA,
NCBI Description
                  complete cds
Seq. No.
                  1091
                  579 4.R1040
Contig ID
5'-most EST
                  uC-gmropic066c08b1
                  1092
Seq. No.
                  579 5.R1040
Contig ID
                  wwf700675911.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q904151
BLAST score
                  151
                  3.0e-79
E value
                  229
Match length
                  100
% identity
NCBI Description
                  Glycine max FAD2-1 microsomal omega-6 desaturase mRNA,
                  complete cds
Seq. No.
                  1093
                  579 7.R1040
Contig ID
5'-most EST
                  vwf700678878.h1
Method
                  BLASTN
                  q904151
NCBI GI
BLAST score
                  86
                  9.0e-41
E value
Match length
                  236
% identity
                  94
                  Glycine max FAD2-1 microsomal omega-6 desaturase mRNA,
NCBI Description
                  complete cds
                  1094
Seq. No.
Contig ID
                  582 1.R1040
5'-most EST
                  gsv701045761.hl
Method
                  BLASTX
NCBI GI
                  q1906002
BLAST score
                  2837
E value
                  0.0e+00
Match length
                  612
                  91
% identity
                  (U90429) nitrite reductase [Glycine max].
NCBI Description
Seq. No.
                  1095
Contig ID
                  582 2.R1040
5'-most EST
                  LIB3138-051-Q1-N1-F12
Method
                  BLASTN
NCBI GI
                  g1906001
BLAST score
                  276
E value
                  1.0e-154
Match length
                  518
                  93
% identity
NCBI Description Glycine max nitrite reductase gene, complete cds
Seq. No.
                  1096
Contig ID
                  582 3.R1040
```

jC-gmle01810077g08d1

Method

NCBI GI

BLASTN

g409368

```
Method
                   BLASTN
NCBI GI
                   g1906001
BLAST score
                   189
                   1.0e-102
E value
Match length
                   189
                   100
% identity
NCBI Description Glycine max nitrite reductase gene, complete cds
Seq. No.
                   1097
                   582 5.R1040
Contig ID
                   ssr700556787.h1
5'-most EST
                   BLASTN
Method
                   g1906001
NCBI GI
BLAST score
                   285
                   1.0e-159
E value
Match length
                   373
% identity
                   96
NCBI Description
                  Glycine max nitrite reductase gene, complete cds
                   1098
Seq. No.
                   585 1.R1040
Contig ID
5'-most EST
                   LIB3049-002-Q1-E1-B9
Method
                   BLASTN
NCBI GI
                   g310575
BLAST score
                   180
                   3.0e-96
E value
Match length
                   844
                   88
% identity
NCBI Description
                  Glycine max nodulin-26 mRNA, complete cds
                   1099
Seq. No.
                   585 2.R1040
Contig ID
5'-most EST
                   LIB3039-023-Q1-E1-A3
Method
                   BLASTN
NCBI GI
                   g310575
BLAST score
                   209
E value
                   1.0e-113
Match length
                   1016
                   90
% identity
NCBI Description
                  Glycine max nodulin-26 mRNA, complete cds
                   1100
Seq. No.
                   587 1.R1040
Contig ID
5'-most EST
                   leu701153015.h1
Method
                   BLASTN
NCBI GI
                   g310577
BLAST score
                   918
                   0.0e + 00
E value
                   963
Match length
                   99
% identity
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
Seq. No.
                   1101
Contig ID
                   588 1.R1040
5'-most EST
                   g409368 FL
```

Seq. No.

Contig ID

1106

592 1.R1040

```
BLAST score
                   715
                   0.0e + 00
E value
Match length
                   867
                   98
% identity
                   Glycine max mutant nitrate reductase mRNA, 3' end
NCBI Description
Seq. No.
                   1102
Contig ID
                   588 2.R1040
5'-most EST
                   LIB3138-056-Q1-N1-G10
Method
                   BLASTX
NCBI GI
                   g730142
                   657
BLAST score
E value
                   5.0e-69
Match length
                   141
% identity
                   91
                   NITRATE REDUCTASE 2 (NR-2) >gi 392992 (U01029) nitrate
NCBI Description
                   reductase [Phaseolus vulgaris]
Seq. No.
                   1103
                   588 3.R1040
Contig ID
                   smc700749263.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g392991
BLAST score
                   124
E value
                   5.0e-63
Match length
                   396
                   83
% identity
                   Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete
NCBI Description
                   1104
Seq. No.
                   589 1.R1040
Contig ID
                   LIB3109-035-Q1-K1-B8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1345979
BLAST score
                   2322
                   0.0e+00 .
E value
Match length
                   424
                   99
% identity
                   OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 459962 (L29215) plastid omega-6 desaturase [Glycine
                   max]
                   1105
Seq. No.
                   589_5.R1040
Contig ID
                   jC-gmle01810089d01a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q459961
BLAST score
                   259
                   1.0e-144
E value
Match length
                   352
                   98
% identity
                  Glycine max proplastid omega-6 desaturase mRNA, complete
NCBI Description
                   cds
```

Seq. No.

Contig ID

1111

596\_1.R1040

```
5'-most EST
                   LIB3109-037-Q1-K1-D4
Method
                   BLASTN
NCBI GI
                   g170041
BLAST score
                   920
                   0.0e+00
E value
Match length
                   1093
% identity
                   97
NCBI Description
                   Glycine max cv Prize protein kinase mRNA
Seq. No.
                   1107
                   592 2.R1040
Contig ID
5'-most EST
                   LIB3109-013-Q1-K1-A1
Method
                   BLASTN
NCBI GI
                   g170042
BLAST score
                   1216
                   0.0e+00
E value
                   1216
Match length
                   100
% identity
NCBI Description
                   Glycine max cv Prize protein kinase mRNA
                   1108
Seq. No.
                   592 3.R1040
Contig ID
5'-most EST
                   uaw700665730.h1
Method
                   BLASTN
                  q170041
NCBI GI
BLAST score
                   255
E value
                   1.0e-141
                   259
Match length
% identity
                   100
NCBI Description
                   Glycine max cv Prize protein kinase mRNA
                   1109
Seq. No.
                   592 4.R1040
Contig ID
5'-most EST
                   leu701155312.h1
Method
                   BLASTN
NCBI GI
                   g170042
BLAST score
                   246
E value
                   1.0e-136
Match length
                   341
% identity
                   96
NCBI Description
                  Glycine max cv Prize protein kinase mRNA
                   1110
Seq. No.
                   594 1.R1040
Contig ID
5'-most EST
                   g736338_FL
Method
                   BLASTX
NCBI GI
                   g1171965
BLAST score
                   4069
                   0.0e + 00
E value
Match length
                   814
                   97
% identity
                   PHOSPHATIDYLINOSITOL 3-KINASE, ROOT ISOFORM (PI3-KINASE)
NCBI Description
                   (PTDINS-3-KINASE) (PI3K) (SPI3K-5) >gi 736339 (L27265)
                   phosphatidylinositol 3-kinase [Glycine max]
```

```
5'-most EST
                  g515750 FL
Method
                  BLASTX
NCBI GI
                  q1172495
BLAST score
                   3387
E value
                  0.0e+00
Match length
                  1106
                   94
% identity
NCBI Description
                  PHYTOCHROME A >gi_515749 (L34842) phytochrome A [Glycine
                  max] >gi 515751 (L34844) phytochrome A [Glycine max]
Seq. No.
                  1112
                  596 2.R1040
Contig ID
5'-most EST
                  fC-qmse700654835a6
Method
                  BLASTN
NCBI GI
                  q515748
BLAST score
                  219
E value
                   1.0e-120
Match length
                   435
% identity
                  94
                  Soybean chloroplast phytochrome A (phyA) gene, complete cds
NCBI Description
Seq. No.
Contig ID
                  596 3.R1040
                  uC-qmflminsoy012f11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3953465
BLAST score
                   452
E value
                  1.0e-44
Match length
                  160
% identity
                   55
                   (AC002328) F20N2.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  1114
                  596 4.R1040
Contig ID
5'-most EST
                  fC-gmst700660709a4
Method
                  BLASTN
                  g515750
NCBI GI
                  320
BLAST score
                   1.0e-180
E value
                  719
Match length
% identity
                   91
                  Soybean phytochrome A (phyA) mRNA, complete cds
NCBI Description
Seq. No.
                  1115
                  597 1.R1040
Contig ID
                  g170043 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g117519
BLAST score
                  2972
                  0.0e+00
E value
Match length
                  570
% identity
                  100
                  PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
NCBI Description
                  >gi 99945 pir A39597 phytoene dehydrogenase (EC 1.3.-.-) -
```

max]

soybean >gi\_170044 (M64704) phytoene desaturase [Glycine

```
Seq. No.
                   1116
                   597 2.R1040
Contig ID
                   fua701041583.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170043
BLAST score
                   143
E value
                   9.0e-75
Match length
                   219
% identity
                   94
                  Soybean phytoene desaturase mRNA, complete cds
NCBI Description
                   1117
Seq. No.
                   599 1.R1040
Contig ID
5'-most EST
                   ssr700560806.h1
Method
                   BLASTX
NCBI GI
                   g478809
BLAST score
                   2356
E value
                   0.0e+00
Match length
                   462
% identity
                   97
                  protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449)
NCBI Description
                  protein kinase [Glycine max] >gi 444789 prf__1908223A
                  protein kinase [Glycine max]
Seq. No.
                   1118
                                                                . .
                   599 2.R1040
Contig ID
5'-most EST
                   LIB3093-030-Q1-K1-E1
Method
                   BLASTN
                   g170046
NCBI GI
BLAST score
                   177
                   1.0e-94
E value
                   345
Match length
                   92
% identity
NCBI Description
                  Glycine max protein kinase (PK6) mRNA, complete cds
Seq. No.
                   1119
                   600 1.R1040
Contig ID
                  hrw701060433.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2497538
BLAST score
                   2531
                   0.0e+00
E value
Match length
                   511
                   98
% identity
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
NCBI Description
                  pyruvate kinase [Glycine max]
Seq. No.
                   1120
                   600 3.R1040
Contig ID
5'-most EST
                   uC-gmropic054f07b1
Method
                  BLASTN
NCBI GI
                   g170050
BLAST score
                   314
                   1.0e-176
E value
Match length
                   318
% identity
                   100
                  Soybean pyruvate kinase mRNA, complete cds
NCBI Description
```

```
1121
Seq. No.
                   600 5.R1040
Contig ID
5'-most EST
                   uC-qmropic047d08b1
                   BLASTN
Method
NCBI GI
                   q170050
BLAST score
                   301
                   1.0e-169
E value
Match length
                   434
                   94
% identity
NCBI Description
                   Soybean pyruvate kinase mRNA, complete cds
                   1122
Seq. No.
                   600 8.R1040
Contig ID
5'-most EST
                   ncj700975678.h1
                   BLASTN
Method
NCBI GI
                   q170050
BLAST score
                   147
                   5.0e-77
E value
Match length
                   233
                   98
% identity
                   Soybean pyruvate kinase mRNA, complete cds
NCBI Description
Seq. No.
Contig ID
                   601 1.R1040
5'-most EST
                   LIB3109-036-Q1-K1-C10
Method
                   BLASTN
NCBI GI
                   q414831
BLAST score
                   776
E value
                   0.0e+00
Match length
                   815
% identity
                   99
NCBI Description Glycine max (Rablp) mRNA, complete cds
Seq. No.
                   1124
Contig ID
                   602 1.R1040
5'-most EST
                   g414833 FL
Method
                   BLASTN
NCBI GI
                   g414833
BLAST score
                   1076
E value
                   0.0e+00
Match length
                   1118
% identity
                   100
                  Glycine max (Rab7p) mRNA, complete cds
NCBI Description
Seq. No.
                   1125
                   602 2.R1040
Contig ID
5'-most EST
                   fua701039675.hl
Method
                   BLASTN
NCBI GI
                   q414833
BLAST score
                   195
                   1.0e-106
E value
                   227
Match length
                   96
% identity
NCBI Description Glycine max (Rab7p) mRNA, complete cds
Seq. No.
                   1126
```

Seq. No.

1131

```
603 1.R1040
Contig ID
5'-most EST
                   awf700838208.hl
Method
                   BLASTN
NCBI GI
                   q170051
BLAST score
                   851
                   0.0e + 00
E value
Match length
                   884
                   99
% identity
NCBI Description
                   Glycine max RNA polymerase II fifth largest subunit mRNA,
                   complete cds
                                                            ٠,٠.
                   1127
Seq. No.
                   603 2.R1040
Contig ID
5'-most EST
                   uC-qmropic009q08b1
Method
                   BLASTN
NCBI GI
                   g170051
BLAST score
                   354
                   0.0e + 00
E value
Match length
                   433
% identity
                   Glycine max RNA polymerase II fifth largest subunit mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1128
                   604 1.R1040
Contig ID
5'-most EST
                   LIB3107-038-Q1-K1-E12
Method
                   BLASTN
NCBI GI
                   q170053
BLAST score
                   545
E value
                   0.0e + 00
Match length
                   682
% identity
                   95
NCBI Description
                   Soybean ribosomal protein S11 mRNA, 3' end
Seq. No.
                   1129
Contig ID
                   604 2.R1040
5'-most EST
                   LIB3039-047-Q1-E1-E3
Method
                   BLASTN
NCBI GI
                   g170053
BLAST score
                   224
E value
                   1.0e-122
Match length
                   416
% identity
                   88
                   Soybean ribosomal protein S11 mRNA, 3' end
NCBI Description
Seq. No.
                   1130
Contig ID
                   604 3.R1040
5'-most EST
                   LIB3049-056-Q1-E1-F10
Method
                   BLASTN
NCBI GI
                   g170053
BLAST score
                   432
E value
                   0.0e+00
                   579
Match length
                   94
% identity
                   Soybean ribosomal protein S11 mRNA, 3' end
NCBI Description
```

```
604 5.R1040
Contig ID
                   LIB3039-015-Q1-E1-H4
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170053
BLAST score
                   175
E value
                   1.0e-93
Match length
                   211
                   96
% identity
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                   1132
Seq. No.
                   604 9.R1040
Contig ID
                   LIB3040-029-Q1-E1-H5
5'-most EST
Method
                   BLASTN
                   q170053
NCBI GI
                   91
BLAST score
                   1.0e-43
E value
                   195
Match length
                   87
% identity
NCBI Description
                   Soybean ribosomal protein S11 mRNA, 3' end
                   1133
Seq. No.
Contig ID
                   605 1.R1040
5'-most EST
                   ssr700553763.hl
Method
                   BLASTN
NCBI GI
                   q454178
BLAST score
                   1264
E value
                   0.0e + 00
Match length
                   1285
                   99
% identity
                  Glycine max rubisco-associated protein mRNA, complete cds
NCBI Description
Seq. No.
                   1134
Contig ID
                   606 1.R1040
5'-most EST
                   LIB3040-030-Q1-E1-B7
Method
                   BLASTX
NCBI GI
                   g3915032
BLAST score
                   1814
E value
                   0.0e + 00
Match length
                   411
% identity
                   86
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                   (STEAROYL-ACP DESATURASE) >gi_508603 (L34346) stearoyl-acyl
                   carrier protein desaturase [Glycine max]
Seq. No.
                   1135
Contig ID
                   606 2..R1040
5'-most EST
                   uC-gmflminsoy028f03b1
Method
                   BLASTN
NCBI GI
                   q508602
BLAST score
                   268
                  1.0e-149
E value
Match length
                   348
                   94
% identity
                  Glycine max stearoyl-acyl carrier protein desaturase
NCBI Description
```

(SACPD) mRNA, complete cds

1.4

Match length

829

```
Seq. No.
                   1136
                   607 1.R1040
Contig ID
5'-most EST
                   uxk700671927.hl
Method
                   BLASTX
NCBI GI
                   g530207
BLAST score
                   4384
E value
                   0.0e + 00
Match length
                   896
% identity
NCBI Description
                   (L35272) heat shock protein [Glycine max]
                   1137
Seq. No.
Contig ID
                   608 1.R1040
5'-most EST
                   zpv700757989.h1
Method
                   BLASTX
NCBI GI
                   g548900
BLAST score
                   1973
E value
                   0.0e + 00
Match length
                   504
% identity
                   78
                   SUCROSE-BINDING PROTEIN PRECURSOR (SBP)
NCBI Description
                   >gi_322691_pir__JQ1730 62K sucrose-binding protein
                   precursor - soybean >gi 170064 (L06038) glucose binding
                   protein [Glycine max]
Seq. No.
                   1138
                   608 2.R1040
Contig ID
                   zpv700763038.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1431744
BLAST score
                   392
                   0.0e + 00
E value
                   737
Match length
% identity
                   98
NCBI Description
                   Glycine max sucrose binding protein (sbp) mRNA, complete
                   cds
                   1139
Seq. No.
                   608 3.R1040
Contig ID
5'-most EST
                   uaw700662248.hl
Method
                   BLASTN
NCBI GI
                   g1431744
                   155
BLAST score
E value
                   1.0e-81
Match length
                   519
% identity
                   Glycine max sucrose binding protein (sbp) mRNA, complete
NCBI Description
                   cds
                   1140
Seq. No.
                   609 1.R1040
Contig ID
5'-most EST
                   wrg700785963.h2
                   BLASTN
Method
NCBI GI
                   g170073
BLAST score
                   433
E value
                   0.0e+00
```

```
% identity
                   Soybean calmodulin (SCaM-3) mRNA, complete cds
NCBI Description
Seq. No.
                   609 2.R1040
Contig ID
5'-most EST
                   LIB3072-053-Q1-E1-E12
Method
                   BLASTN
NCBI GI
                   g170069
                   705
BLAST score
                   0.0e + 00
E value
Match length
                   738
% identity
                   99.
NCBI Description Soybean calmodulin (SCaM-1) mRNA, complete cds
Seq. No.
                   1142
Contig ID
                   609 3.R1040
5'-most EST
                   LIB3106-104-Q1-K1-F4
Method
                   BLASTN
NCBI GI
                   g170073
BLAST score
                   431
E value
                   0.0e+00
Match length
                   435
                   100
% identity
NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds
                   1143
Seq. No.
                   609_5.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy118b07b1
Method
                   BLASTN ,
NCBI GI
                   g170069
BLAST score
                   265
E value
                   1.0e-147
Match length
                   321
                   96
% identity
NCBI Description Soybean calmodulin (SCaM-1) mRNA, complete cds
Seq. No.
                   1144
Contig ID
                   610 1.R1040
5'-most EST
                   LIB3049-024-Q1-E1-H5
Method
                   BLASTN
NCBI GI
                   g170071
BLAST score
                   668
                   0.0e+00
E value
Match length
                   839
% identity
                   97
                   Soybean calmodulin (SCaM-2) mRNA, complete cds
NCBI Description
Seq. No.
                   1145
Contig ID
                   610 2.R1040
                   k11701205314.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4103958
BLAST score
                   460
                   0.0e+00
E value
Match length
                   788
% identity
                   92
```

NCBI Description Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele,

.

## complete cds

```
Seq. No.
                   1146
Contig ID
                   612 1.R1040
5'-most EST
                   g170075 FL
Method
                   BLASTN
NCBI GI
                   q170075
BLAST score
                   764
E value
                   0.0e + 00
Match length
                   1352
% identity
                   100
NCBI Description
                   Soybean calmodulin (SCaM-4) mRNA, complete cds
Seq. No.
Contig ID
                   612 3.R1040
5'-most EST
                   LIB3053-012-Q1-N1-F1
Method
                   BLASTN
NCBI GI
                   g170075
BLAST score
                   105
E value
                   6.0e-52
Match length
                   201
                   100
% identity
NCBI Description
                  Soybean calmodulin (SCaM-4) mRNA, complete cds
                   1148
Seq. No.
Contig ID
                   613 1.R1040
                   g532289_FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2492792
BLAST score
                   2806
E value
                   0.0e+00
Match length
                   549
% identity
                   100
NCBI Description
                   LATE NODULIN 56 (N-56) >qi 532290 dbj BAA07212 (D38015)
                   soybean late nodulin [Glycine max]
Seq. No.
                   1149
                   614 1.R1040
Contig ID
5'-most EST
                   LIB3049-004-Q1-E1-G9
Method
                   BLASTN
NCBI GI
                   g1161251
BLAST score
                   852
E value,
                   0.0e+00
Match length
                   1364
                   98
% identity
NCBI Description
                   Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
                   complete cds
                   1150
Seq. No.
                   614 2.R1040
Contig ID
                   leu701157276.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1161251
BLAST score
                   291
E value
                   1.0e-162
Match length
                   901
```

87

% identity

NCBI GI

BLAST score

121

```
NCBI Description Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
                   complete cds
Seq. No.
                   1151
                   614 4.R1040
Contig ID
                   uC-gmflminsoy043h04b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1161251
BLAST score
                   120
E value
                   6.0e-61
Match length
                   219
% identity
                   94
                   Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1152
                   614 7.R1040
Contig ID
5'-most EST
                   crh700850781.hl
Method
                   BLASTN
NCBI GI
                   g1161251
BLAST score
                   130
E value
                   6.0e-67
Match length
                   200
% identity
                   93
                   Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1153
                   617 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy203b07b1
Method
                   BLASTN
NCBI GI
                   g1220521
                   953
BLAST score
E value
                   0.0e + 00
                   1070
Match length
% identity
                   96
                   Glycine max TATA-box binding protein (STBP1) mRNA, complete
NCBI Description
                   cds
                   1154
Seq. No.
                   617 2.R1040
Contig ID
                   zhf700952839.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1220521
BLAST score
                   123
E value
                   1.0e-62
                   223
Match length
                   89
% identity
                   Glycine max TATA-box binding protein (STBP1) mRNA, complete
NCBI Description
                   cds
                   1155
Seq. No.
                   617 3.R1040
Contig ID
                   LIB3087-005-Q1-K1-B7
5'-most EST
Method
                   BLASTN
                   g1220521
```

```
E value
                   2.0e-61
Match length
                   228
                   96
% identity
                  Glycine max TATA-box binding protein (STBP1) mRNA, complete
NCBI Description
                   1156
Seq. No.
                   617 4.R1040
Contig ID
5'-most EST
                  uxk700669017.h1
Seq. No.
                  1157
                   617 5.R1040
Contig ID
5'-most EST
                   ssr700560377.hl
                  BLASTN
Method
NCBI GI
                   g1220521
BLAST score
                   131
E value
                   1.0e-67
Match length
                   240
                   100
% identity
                  Glycine max TATA-box binding protein (STBP1) mRNA, complete
NCBI Description
Seq. No.
                  1158
                   618 1.R1040
Contig ID
5'-most EST
                  wvk700685392.hl
Method
                  BLASTX
NCBI GI
                  q986969
BLAST score
                  1765
E value
                   0.0e + 00
Match length
                   362
% identity
                   96
                   (L28005) TGACG-motif-binding protein [Glycine max]
NCBI Description
Seq. No.
Contig ID
                   618 3.R1040
5'-most EST
                  ary700764344.hl
Method
                  BLASTN
                  q986968
NCBI GI
BLAST score
                  167
                   6.0e-89
E value
Match length
                  296
% identity
                  Glycine max TGACG-motif binding protein (STGA1) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  1160
                   622 1.R1040
Contig ID
5'-most EST
                  LIB3028-049-Q1-B1-F5
Method
                  BLASTN
NCBI GI
                  q4100432
                  258
BLAST score
                  1.0e-142
E value
Match length
                  524
                  97
% identity
                  Glycine max beta-glucosidase mRNA, partial cds
NCBI Description
```

1161

Seq. No.

Contig ID

```
Contig ID
                   624 1.R1040
5'-most EST
                   awf700838867.h1
Method
                   BLASTN
NCBI GI
                   g2270987
BLAST score
                   798
E value
                   0.0e+00
Match length
                   798
                   100
% identity
NCBI Description
                   Glycine max Em protein mRNA, complete cds
Seq. No.
                   1162
                   624 2.R1040
Contig ID
5'-most EST
                   awf700839943.hl
Method
                   BLASTN
NCBI GI
                   q2270987
BLAST score
                   228
E value
                   1.0e-125
Match length
                   394
% identity
                   92
                   Glycine max Em protein mRNA, complete cds
NCBI Description
Seq. No.
Contig ID
                   625 1.R1040
5'-most EST
                   g4102689 FL
Method
                   BLASTN
NCBI GI
                   g4102689
BLAST score
                   885
E value
                   0.0e + 00
Match length
                   885
% identity
                   100
                   Glycine max 24 kDa seed maturation protein mRNA, complete
NCBI Description
                   cds
Seq. No.
                   1164
Contig ID
                   626 1.R1040
5'-most EST
                   LIB3094-100-Q1-K1-F2
Method
                   BLASTN
NCBI GI
                   q2270989
BLAST score
                   729
E value
                   0.0e + 00
Match length
                   729
                   100
% identity
                  Glycine max dehydrin (GmPM12) mRNA, complete cds
NCBI Description
Seq. No.
                   1165
Contig ID
                   626 2.R1040
5'-most EST
                   LIB3051-006-Q1-K1-F3
Method
                   BLASTN
NCBI GI
                   g2270989
BLAST score
                   293
E value
                   1.0e-164
Match length
                   384
                   99
% identity
                   Glycine max dehydrin (GmPM12) mRNA, complete cds
NCBI Description
Seq. No.
                   1166
```

627\_1.R1040

Seq. No.

1171

```
LIB3072-017-Q1-E1-G4
5'-most EST
Method
                  BLASTN
NCBI GI
                   g2306978
BLAST score
                   490
                   0.0e+00
E value
Match length
                   502
% identity
                   99
                  Glycine max metallothionein-II protein (PGMPM19) mRNA,
NCBI Description
                  complete cds
Seq. No.
                   1167
                   627 2.R1040
Contig ID
                  LIB3072-028-Q1-E1-G2
5'-most EST
Method
                  BLASTN
                  g2270991
NCBI GI
BLAST score
                  287
                   1.0e-160
E value
Match length
                  386
                   100
% identity
                  Glycine max metallothionein-II protein mRNA, complete cds
NCBI Description
Seq. No.
                  1168
                   627 3.R1040
Contig ID
5'-most EST
                  LIB3072-059-Q1-K1-G7
Method
                  BLASTN
NCBI GI
                  q2270991
BLAST score
                  413
                  0.0e+00
E value
Match length
                  413
                  100
% identity
NCBI Description Glycine max metallothionein-II protein mRNA, complete cds
Seq. No.
                  1169
Contig ID
                  628 1.R1040
5'-most EST
                  uxk700668563.hl
Method
                  BLASTN
                  q2270993
NCBI GI
BLAST score
                  819
E value
                  0.0e+00
                  964
Match length
                  99
% identity
                  Glycine max Ca+2-binding EF hand protein (GmPM13) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  1170
Contig ID
                  629 1.R1040
                  awf700843103.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  g4102691
BLAST score
                  633
E value
                  0.0e + 00
Match length
                  633
                  100
% identity
                  Glycine max late-embryogenesis abundant protein mRNA,
NCBI Description
                  complete cds
```

```
629 2.R1040
Contig ID
                   crh700854653.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4102691
BLAST score
                   275
                   1.0e-153
E value
Match length
                   532
% identity
                   91
NCBI Description
                   Glycine max late-embryogenesis abundant protein mRNA,
                   complete cds
Seq. No.
                   1172
                   629 3.R1040
Contig ID
5'-most EST
                   LIB3170-004-Q1-K1-E10
Method
                   BLASTN
NCBI GI
                   g4102691
BLAST score
                   240
                   1.0e-132
E value
Match length
                   519
                   93
% identity
                   Glycine max late-embryogenesis abundant protein mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1173
Contig ID
                   630 1.R1040
5'-most EST
                   zpv700757378.h1
Method
                   BLASTN
NCBI GI
                   q4097895
BLAST score
                   728
E value
                   0.0e + 00
                   728
Match length
                   100
% identity
                   Glycine max napin-type 2S albumin 3 mRNA, complete cds
NCBI Description
Seq. No.
                   1174
                   630 2.R1040
Contig ID
5'-most EST
                   uC-gmropic066f10b1
Method
                   BLASTX
NCBI GI
                   q4063749
BLAST score
                   239
E value
                   6.0e-20
Match length
                   92
% identity
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1175
                   630 4.R1040
Contig ID
5'-most EST
                   LIB3073-008-Q1-K1-G3
Method
                   BLASTN
NCBI GI
                   q4097895
BLAST score
                   129
                   8.0e-66
E value
                   241
Match length
                   98
% identity
                   Glycine max napin-type 2S albumin 3 mRNA, complete cds
NCBI Description
```

1176

Seq. No.

```
Contig ID
                    630 6.R1040
5'-most EST
                    vwf700678862.hl
Method
                   BLASTN
NCBI GI
                    g2305019
BLAST score
                    172
E value
                    6.0e-92
Match length
                    176
                    99
% identity
NCBI Description
                   Glycine max 2S albumin pre-propeptide mRNA, complete cds
Seq. No.
                    1177
                    631 1.R1040
Contig ID
5'-most EST
                   LIB3051-110-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                    q2253384
BLAST score
                    2739
E value
                    0.0e + 00
Match length
                    539
                    99
% identity
NCBI Description
                    (AF007100) biotin carboxylase precursor [Glycine max]
Seq. No.
                    1178
Contig ID
                    631_2.R1040
5'-most EST
                    fua701040021.hl
Method
                   BLASTX
NCBI GI
                   q134892
BLAST score
                    654
E value
                    2.0e-68
Match length
                   194
% identity
                    68
                   SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
NCBI Description
                    (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                   >gi 88607 pir A29440 signal recognition particle receptor
                   - human >gi_30866_emb_CAA29608_ (X06272) docking protein [Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal
                   recognition particle receptor ('docking protein')
Seq. No.
                    1179
                    631 3.R1040
Contig ID
5'-most EST
                    g3219360 FL
Method
                   BLASTX
NCBI GI
                   g3219361
BLAST score
                   2741
                   0.0e+00
E value
Match length
                   539
% identity
                    (AF068249) biotin carboxylase precursor [Glycine max]
NCBI Description
Seq. No.
                   1180
                   631 6.R1040
Contig ID
5'-most EST
                   LIB3055-001-Q1-B1-F6
Method
                   BLASTN
                   g3219360
NCBI GI
BLAST score
                   182
                   5.0e-98
E value
Match length
                   262
```

93

% identity

E value

```
Glycine max biotin carboxylase precursor (accC-3) mRNA,
 NCBI Description
                    nuclear gene encoding chloroplast protein, complete cds
 Seq. No.
                    632 1.R1040
 Contig ID
                    uC-gmropic022d10b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q2245683
 BLAST score
                    1680
 E value
                    0.0e+00
 Match length
                    339
 % identity
                    99
                    (AF007211) peroxidase precursor [Glycine max]
 NCBI Description
 Seq. No.
                    1182
                    632 2.R1040
 Contig ID
                    trc700563017.h1
 5'-most EST
 Method
                    BLASTN
NCBI GI
                    q2245682
 BLAST score
                    289
 E value
                    1.0e-161
 Match length
                    341
 % identity
                    96
                   Glycine max peroxidase precursor (GMIPER1) mRNA, complete
 NCBI Description
 Seq. No.
                    1183
                    633 1.R1040
 Contig ID
 5'-most EST
                    g4102189 FL
 Method
                    BLASTN
 NCBI GI
                    q4102189
 BLAST score
                    1208
                    0.0e + 00
 E value
 Match length
                    1220
 % identity
                    98
                    Glycine max 35 kDa seed maturation protein (pGmPM18) mRNA,
 NCBI Description
                    complete cds
 Seq. No.
                    1184
 Contig ID
                    633 2.R1040
                    6HA-02-Q1-B1-G6
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    g4102189
 BLAST score
                    267
 E value
                    1.0e-148
 Match length
                    461
 % identity
                    86
                   Glycine max 35 kDa seed maturation protein (pGmPM18) mRNA,
 NCBI Description
                    complete cds
 Seq. No.
                    1185
                    635 1.R1040
 Contig ID
 5'-most EST
                    LIB3167-042-P1-K1-G11
 Method
                    BLASTN
 NCBI GI
                    g2738559
 BLAST score
                    715
```

0.0e + 00

E value

```
730
Match length
                   100
% identity
                   Glycine max ribosomal protein L22 mRNA, nuclear gene
NCBI Description
                   encoding chloroplast protein, partial cds
                   1186
Seq. No.
                   635 2.R1040
Contig ID
                   epx701105174.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2738559
BLAST score
                   264
                   1.0e-146
E value
Match length
                   347
% identity
NCBI Description
                   Glycine max ribosomal protein L22 mRNA, nuclear gene
                   encoding chloroplast protein, partial cds
                   1187
Seq. No.
Contig ID
                   636 1.R1040
5'-most EST
                   zhf700952296.hl
Method
                   BLASTN
NCBI GI
                   g2388688
BLAST score
                   958
E value
                   0.0e + 00
                   1105
Match length
% identity
                   97
                  Glycine max GH1 protein (GH1) mRNA, partial cds
NCBI Description
                   1188
Seq. No.
                   636 2.R1040
Contig ID
5'-most EST
                   LIB3107-063-Q1-K1-B2
                   BLASTN
Method
NCBI GI
                   q2388688
BLAST score
                   308
E value
                   1.0e-172
Match length
                   825
% identity
                   90
                  Glycine max GH1 protein (GH1) mRNA, partial cds
NCBI Description
Seq. No.
                   1189
Contig ID
                   636 3.R1040
5'-most EST
                   LIB3109-031-Q1-K1-E12
Method
                   BLASTN
NCBI GI
                   g2388688
BLAST score
                   214
E value
                   1.0e-116
Match length
                   385
                   89
% identity
                  Glycine max GH1 protein (GH1) mRNA, partial cds
NCBI Description
                   1190
Seq. No.
                   636 4.R1040
Contig ID
                   fua701040689.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2388688
                  71
BLAST score
```

2.0e-31

```
143
Match length
                  87
% identity
NCBI Description Glycine max GH1 protein (GH1) mRNA, partial cds
Seq. No.
                   1191
                   636 6.R1040
Contig ID
5'-most EST
                   jC-gmro02910006g06d1
Seq. No.
                  1192
                   636 9.R1040
Contig ID
5'-most EST
                  LIB3039-041-Q1-E1-H8
Seq. No.
                   1193
                   637 1.R1040
Contig ID
5'-most EST
                  g2565258 FL
Method
                  BLASTX
NCBI GI
                  q2565259
BLAST score
                   1641
                   0.0e + 00
E value
Match length
                   329
                   100
% identity
NCBI Description
                   (AF019115) putative cadmium-transporting ATPase [Glycine
Seq. No.
                   1194
Contig ID
                   638_1.R1040
5'-most EST
                   jC-qmro02910069c06a1
Method
                  BLASTN
NCBI GI
                  g3789722
BLAST score
                   1223
E value
                   0.0e+00
Match length
                   1324
% identity
                   99
                  Glycine max peroxidase (PC7) mRNA, complete cds
NCBI Description
Seq. No.
                   639_1.R1040
Contig ID
                   jex700903127.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4432860
BLAST score
                   1158
                   0.0e+00
E value
Match length
                   637
% identity
                   (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
                   1196
Seq. No.
                   639 2.R1040
Contig ID
5'-most EST
                  LIB3028-042-Q1-B1-F1
Method
                  BLASTX
NCBI GI
                  g4432860
BLAST score
                  1160
                  1.0e-127
E value
Match length
                  368
% identity
                  (AC006300) putative glucose-induced repressor protein
NCBI Description
```

Seq. No.

## 639 3.R1040 Contig ID uC-gmrominsoy026h10b1 5'-most EST Method BLASTX NCBI GI g4432860 BLAST score 522 E value 7.0e-53 Match length 197 % identity 59 (AC006300) putative glucose-induced repressor protein NCBI Description [Arabidopsis thaliana] Seq. No. 1198 639 4.R1040 Contig ID jC-gmst02400023g06a1 5'-most EST Method BLASTX NCBI GI g2407790 BLAST score 174 E value 2.0e-12 Match length 87 % identity 47 (AF019910) grr1 [Glycine max] NCBI Description Seq. No. 1199 639 5.R1040 Contig ID LIB3170-046-Q1-K1-G11 5'-most EST Method BLASTN NCBI GI g2407789 BLAST score 242 1.0e-134 E value 261 Match length % identity 99 NCBI Description Glycine max grr1 (grr1) mRNA, complete cds 1200 Seq. No. 641\_1.R1040 Contig ID 5'-most EST g2895197 FL Method BLASTX g3913525 NCBI GI BLAST score 5544 0.0e+00E value 1088 Match length 99 % identity DNA POLYMERASE DELTA CATALYTIC CHAIN >gi 2895198 (AF020193) NCBI Description DNA polymerase delta [Glycine max] Seq. No. 1201 641 3.R1040 Contig ID leu701151641.hl 5'-most EST BLASTN Method NCBI GI g2895197 BLAST score 140 E value 5.0e-73 Match length 156 % identity 97

[Arabidopsis thaliana]

1197

BLAST score

176

```
NCBI Description Glycine max DNA polymerase delta (Pol delta) mRNA, complete
                  cds
                   1202
Seq. No.
                   642 1.R1040
Contig ID
                  LIB3170-048-Q1-J1-E7
5'-most EST
Method
                  BLASTN
NCBI GI
                   g2444419
BLAST score
                   1114
E value
                   0.0e + 00
Match length
                   1141
                   99
% identity
                  Glycine max ribosome-associated protein p40 mRNA, complete
NCBI Description
                  cds
                   1203
Seq. No.
                   642 2.R1040
Contig ID
5'-most EST
                  LIB3170-036-Q1-K2-F2
Method
                   BLASTN
NCBI GI
                   g2815245
BLAST score
                   94
                   4.0e-45
E value
Match length
                  289
                  85
% identity
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                  CanMT-2)
                   1204
Seq. No.
                   642 3.R1040
Contig ID
5'-most EST
                   jC-gmst02400076g08a1
Method
                  BLASTN
NCBI GI
                  g2815245
BLAST score
                  86
                   2.0e-40
E value
Match length
                  242
                  84
% identity
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                  CanMT-2)
Seq. No.
                   1205
                   642 4.R1040
Contig ID
5'-most EST
                   zhf700957326.h1
Method
                  BLASTN
NCBI GI
                   g2444419
BLAST score
                   386
                  0.0e+00
E value
                   494
Match length
                   95
% identity
                  Glycine max ribosome-associated protein p40 mRNA, complete
NCBI Description
                  cds
                  1206
Seq. No.
                   642 7.R1040
Contig ID
5'-most EST
                  LIB3170-019-Q1-J1-H3
Method
                  BLASTN
NCBI GI
                  g2444419
```

. . .



E value 3.0e-94
Match length 297
% identity 92

NCBI Description Glycine max ribosome-associated protein p40 mRNA, complete

cds

Seq. No. 1207

Contig ID 642 8.R1040

5'-most EST LIB3107-010-Q1-K1-A2

Seq. No. 1208

Contig ID 642\_9.R1040 5'-most EST gsv701054621.h1

Seq. No. 1209

Contig ID 643\_1.R1040 5'-most EST wvk700684093.h1

Method BLASTX
NCBI GI g2738982
BLAST score 2518
E value 0.0e+00
Match length 514
% identity 95

NCBI Description (AF022157) CYP71A10 [Glycine max]

Seq. No. 1210

644 1.R1040 Contig ID 5'-most EST g5509129 Method BLASTX NCBI GI g2738996 BLAST score 2907 E value 0.0e+00Match length 561 % identity 100

NCBI Description (AF022457) CYP97B2p [Glycine max]

Seq. No. 1211

Contig ID 645 1.R1040

5'-most EST LIB3139-049-P1-N1-H10

Method BLASTX
NCBI GI g2738998
BLAST score 2669
E value 0.0e+00
Match length 509
% identity 99

NCBI Description (AF022458) CYP98A2p [Glycine max]

Seq. No. 1212

Contig ID 646\_1.R1040 5'-most EST leu701146357.h1

Method BLASTX
NCBI GI g2739000
BLAST score 2388
E value 0.0e+00
Match length 510
% identity 92

NCBI Description (AF022459) CYP71D10p [Glycine max]

NCBI Description

```
1213
Seq. No.
                   647 1.R1040
Contiq ID
5'-most EST
                  LIB3049-016-Q1-E1-A5
                  BLASTX
Method
                  g2739002
NCBI GI
BLAST score
                  2331
E value
                   0.0e+00
Match length
                   499
% identity
                   91
                   (AF022460) CYP83D1p [Glycine max]
NCBI Description
                  1214
Seq. No.
                   647 2.R1040
Contig ID
5'-most EST
                  uC-qmronoir004e08b1
Method
                  BLASTN
                  g2739001
NCBI GI
BLAST score
                  145
E value
                  2.0e-75
                  249
Match length
                   90
% identity
NCBI Description Glycine max cytochrome P450 monooxygenase CYP83D1p
                   (CYP83D1) mRNA, partial cds
Seq. No.
                  1215
                  648 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810086g05a1
Method
                  BLASTX
                  g2739004
NCBI GI
                  2805
BLAST score
                  0.0e+00
E value
Match length
                  532
% identity
                  100
NCBI Description
                   (AF022461) CYP82Clp [Glycine max]
                  1216
Seq. No.
                  649 1.R1040
Contig ID
5'-most EST
                  txt700733671.h1
Method
                  BLASTX
NCBI GI
                  g2739006
BLAST score
                  2248
                  0.0e+00
E value
                  498
Match length
                  89
% identity
NCBI Description
                  (AF022462) CYP93Clp [Glycine max]
                  1217
Seq. No.
Contig ID
                  649 2.R1040
5'-most EST
                  g5230725 FL
Method
                  BLASTX
NCBI GI
                  g2739006
BLAST score
                  2152
E value
                  0.0e + 00
Match length
                  518
% identity
```

(AF022462) CYP93Clp [Glycine max]

E value

```
1218
Seq. No.
                   649 3.R1040
Contig ID
5'-most EST
                   jC-gmst02400030a06d1
                   BLASTX
Method
                   g2739371
NCBI GI
BLAST score
                   476
E value
                   1.0e-47
Match length
                   141
                   70
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   649 4.R1040
Contig ID
5'-most EST
                   LIB3138-019-Q1-N1-E7
Seq. No.
                   1220
                   649 7.R1040
Contig ID
5'-most EST
                   jC-gmle01810071g04a1
Method
                   BLASTN
NCBI GI
                   g2739005
BLAST score
                   370
E value
                   0.0e + 00
Match length
                   525
                   93
% identity
                   Glycine max cytochrome P450 monooxygenase CYP93C1p
NCBI Description
                   (CYP93C1) mRNA, complete cds
Seq. No.
                   1221
                   649 8.R1040
Contig ID
5'-most EST
                   sat701015083.hl
Method
                   BLASTN
NCBI GI
                   g2739005
BLAST score
                   121
E value
                   1.0e-61
Match length
                   189
                   92
% identity
NCBI Description
                   Glycine max cytochrome P450 monooxygenase CYP93Clp
                   (CYP93C1) mRNA, complete cds
Seq. No.
                   1222
                   651 1.R1040
Contig ID
5'-most EST
                   ncj700984140.h1
Method
                   BLASTX
NCBI GI
                   g2739010
BLAST score
                   2560
E value
                   0.0e + 00
Match length
                   513
% identity
                   (AF022464) CYP77A3p [Glycine max]
NCBI Description
Seq. No.
                   1223
Contig ID
                   653 1.R1040
5'-most EST
                   g2739043 FL
Method
                   BLASTN
NCBI GI
                   q2739043
BLAST score
                   1422
```

0.0e + 00

```
1426
Match length
% identity
                   100
NCBI Description
                  Glycine max polyphosphoinositide binding protein Sshlp
                   (SSH1) mRNA, complete cds
Seq. No.
                   1224
Contig ID
                   653 3.R1040
5'-most EST
                   leu701149472.h1
Method
                  BLASTN
NCBI GI
                  q2739043
BLAST score
                   128
E value
                  8.0e-66
Match length
                  153
                   96
% identity
                  Glycine max polyphosphoinositide binding protein Sshlp
NCBI Description
                   (SSH1) mRNA, complete cds
Seq. No.
                  1225
Contig ID
                   653 5.R1040
5'-most EST
                  LIB3028-044-Q1-B1-G1
Method
                  BLASTN
NCBI GI
                  q2739043
BLAST score
                  139
E value
                  2.0e-72
Match length
                  209
% identity
                  91
                  Glycine max polyphosphoinositide binding protein Sshlp
NCBI Description
                   (SSH1) mRNA, complete cds
Seq. No.
                  1226
                  655 3.R1040
Contig ID
5'-most EST
                  uC-gmropic059d06b1
Method
                  BLASTN
                  g3169543
NCBI GI
BLAST score
                  461
E value
                  0.0e + 00
                  2275
Match length
                  84
% identity
                  Medicago sativa sucrose synthase mRNA, complete cds
NCBI Description
Seq. No.
                  1227
                  655 4.R1040
Contig ID
                  jC-gmro02910073c10a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3915046
                  679
BLAST score
                  0.0e + 00
E value
                  791
Match length
                  80
% identity
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                  >gi 3169544 (AF049487) sucrose synthase [Medicago sativa]
                  1228
Seq. No.
                  657 1.R1040
Contig ID
5'-most EST
                  g2654093 FL
Method
                  BLASTX
```

g2654094

NCBI GI

5'-most EST

```
BLAST score
                   2186
E value
                   0.0e+00
Match length
                   456
                   93
% identity
                   (AF034210) aspartate aminotransferase glyoxysomal isozyme
NCBI Description
                   AAT1 precursor [Glycine max]
Seq. No.
                   1229
                   658 1.R1040
Contig ID
5'-most EST
                   LIB3049-014-Q1-E1-B12
Method
                   BLASTN
NCBI GI
                   g3377793
BLAST score
                   929
                   0.0e+00
E value
Match length
                   965
                   99
% identity
                   Glycine max proteasome IOTA subunit mRNA, complete cds
NCBI Description
                   1230
Seq. No.
                   658 2.R1040
Contig ID
                   942\overline{9}1492
5'-most EST
                   BLASTN
Method
                   g3377793
NCBI GI
                   330
BLAST score
                   0.0e+00
E value
                   390
Match length
                   96
% identity
NCBI Description
                   Glycine max proteasome IOTA subunit mRNA, complete cds
Seq. No.
                   1231
                   659 1.R1040
Contig ID
5'-most EST
                   LIB3030-005-Q1-B1-A12
Method
                   BLASTX
NCBI GI
                   g231695
BLAST score
                   2683
                   0.0e + 00
E value
                   492
Match length
                   100
% identity
NCBI Description
                   CATALASE >gi 66299 pir CSSY catalase (EC 1.11.1.6) -
                   soybean >gi_18560_emb_CAA78056_ (Z12021) catalase [Glycine
                   max] >gi_2661015 (AF035252) catalase [Glycine max]
                   >gi_2661\overline{0}17 (AF035253) catalase [Glycine max]
Seq. No.
                   1232
Contig ID
                   659 2.R1040
5'-most EST
                   LIB3051-080-Q1-K1-F12
Method
                   BLASTN
NCBI GI
                   g2661014
BLAST score
                   121
E value
                   1.0e-61
Match length
                   167
                   96
% identity
                   Glycine max catalase (cat1) mRNA, complete cds
NCBI Description
Seq. No.
                   1233
                   659 4.R1040
Contig ID
```

LIB3107-016-Q1-K1-G1

NCBI GI

```
Method
                    BLASTN
 NCBI GI
                    q2661018
 BLAST score
                    294
 E value
                    1.0e-164
Match length
                    302
 % identity
                    99
 NCBI Description
                   Glycine max catalase (cat3) mRNA, complete cds
 Seq. No.
                    1234
                    659 6.R1040
 Contig ID
 5'-most EST
                    zsg701119529.hl
                    BLASTN
Method
 NCBI GI
                    q18559
 BLAST score
                    258
 E value
                    1.0e-143
Match length
                    390
                    98
 % identity
NCBI Description
                   G.max gene for catalase
 Seq. No.
                    1235
                    662_1.R1040
 Contig ID
 5'-most EST
                    jC-gmle01810020g04a1
Method
                    BLASTX
 NCBI GI
                    q2661021
BLAST score
                    2689
E value
                    0.0e + 00
Match length
                    492
 % identity
                    100
NCBI Description
                    (AF035255) catalase [Glycine max]
                    1236
Seq. No.
                    662 2.R1040
 Contig ID
 5'-most EST
                    fC-gmst700889880r1
 Method
                    BLASTN
 NCBI GI
                    g2661022
 BLAST score
                    388
 E value
                    0.0e+00
Match length
                    388 [
                    100
 % identity
                   Glycine max catalase (cat5) mRNA, partial cds
 NCBI Description
 Seq. No.
                    662 3.R1040
 Contig ID
 5'-most EST
                    LIB3051-025-Q1-K1-A8
Method
                    BLASTN
NCBI GI
                    g2661020
BLAST score
                    241
                    1.0e-133
E value
                    337
Match length
                    99
 % identity
                   Glycine max catalase (cat4) mRNA, complete cds
NCBI Description
                    1238
Seq. No.
                    662 5.R1040
 Contig ID
                    jC-gmle01810082c02d1
 5'-most EST
Method
                    BLASTN
```

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g2661020

Method

BLASTN

```
337
BLAST score
E value
                   0.0e+00
Match length
                   341
                   100
% identity
NCBI Description
                  Glycine max catalase (cat4) mRNA, complete cds
                   1239
Seq. No.
                   662 8.R1040
Contig ID
5'-most EST
                   awf700838945.hl
Method
                   BLASTN
NCBI GI
                   g2661020
BLAST score
                   175
E value
                   6.0e-94
Match length
                   251
                   97
% identity
NCBI Description
                   Glycine max catalase (cat4) mRNA, complete cds
                   1240
Seq. No.
                   664 1.R1040
Contig ID
5'-most EST
                   asn701139293.h1
Method
                   BLASTX
NCBI GI
                   g3334122
BLAST score
                   1767
E value
                   0.0e+00
Match length
                   350
                   98
% identity
NCBI Description
                  ARGINASE >gi 2661128 (AF035671) arginase [Glycine max]
                   1241
Seq. No.
                   664 2.R1040
Contig ID
5'-most EST
                   kl1701203871.h1
Method
                   BLASTX
NCBI GI
                   g1168493
BLAST score
                   1464
                   1.0e-163
E value
Match length
                   330
% identity
                   87
                  ARGINASE >gi_602422 (U15019) arginase [Arabidopsis
NCBI Description
                   thaliana] >gi_4325373_gb_AAD17369_ (AF128396) Arabidopsis
                   thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,
                   E=3.7e-142 N=1) [Arabidopsis thaliana]
                   1242
Seq. No.
                   665 1.R1040
Contig ID
5'-most EST
                   zhf700960949.hl
Method
                   BLASTX
NCBI GI
                   q4104561
BLAST score
                   1689
E value
                   0.0e + 00
Match length
                   370
% identity
NCBI Description
                   (AF036960) subtilisin-like protease [Glycine max]
Seq. No.
                   1243
Contig ID
                   666 1.R1040
5'-most EST
                   g5002233 FL
```

```
g3982595
NCBI GI
BLAST score
                    884
E value
                    0.0e + 00
Match length
                    1252
% identity
                    95
NCBI Description
                   Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
Contig ID
                    666 2.R1040
5'-most EST
                   LIB3109-045-Q1-K1-A9
                   BLASTX
Method
NCBI GI
                   g3982596
BLAST score
                   1680
                   0.0e + 00
E value
Match length
                   331
% identity
                    96
NCBI Description
                    (AF039027) cationic peroxidase 2 [Glycine max]
                   1245
Seq. No.
                   666 3.R1040
Contig ID
5'-most EST
                   LIB3107-063-Q1-K1-A3
                   1246
Seq. No.
                   666 4.R1040
Contig ID
                   asn701138013.h1
5'-most EST
Method
                   BLASTN
                   g3982595
NCBI GI
                   67
BLAST score
E value
                   3.0e-29
                   250
Match length
% identity
                   87
                   Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
NCBI Description
                   1247
Seq. No.
                   667_1.R1040
Contig ID
5'-most EST
                   jC-qmle01810025e03a1
Method
                   BLASTX
NCBI GI
                   g2773270
BLAST score
                   5249
                   0.0e + 00
E value
Match length
                   1023
% identity
                   100
NCBI Description
                    (AF039851) ferredoxin-dependent glutamate synthase [Glycine
                   max]
                   1248
Seq. No.
Contig ID
                   667 2.R1040
5'-most EST
                   bth700845893.h1
Method
                   BLASTX
NCBI GI
                   q2494793
BLAST score
                   689
E value
                   8.0e-73
Match length
                   159
% identity
                   [Segment 2 of 2] FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE
NCBI Description
                   (FD-GOGAT) >gi_2146724_pir__S67496 ferredoxin-dependent glutamate synthase (EC 1.4.7.1) - spinach (fragment)
```

Method

BLASTN

```
>qi 414979 (U03006) ferredoxin-dependent glutamate synthase
                   [Spinacia oleracea]
Seq. No.
                   1249
                   668 1.R1040
Contig ID
5'-most EST
                   LIB3052-015-Q1-N1-A6
Method
                   BLASTX
NCBI GI
                   g120680
BLAST score
                   233
                   2.0e-19
E value
Match length
                   53
                   79
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66010_pir__DEBHG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - barley
                   >gi_18978_emb_CAA42901_ (X60343) glyceraldehyde 3-phosphate
                   dehydrogenase [Hordeum vulgare]
                   1250
Seq. No.
Contig ID
                   668 2.R1040
                   LIB3139-002-Q1-N1-B6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q462137
BLAST score
                   589
                   1.0e-60
E value
Match length
                   186
                   68
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
Seq. No.
                   1251
Contig ID
                   668 3.R1040
5'-most EST
                   LIB3028-045-Q1-B1-D7
Method
                   BLASTN
NCBI GI
                   q169090
BLAST score
                   160
E value
                   2.0e-84
Match length
                   466
% identity
NCBI Description
                   Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA,
                   complete cds
Seq. No.
Contig ID
                   668 4.R1040
5'-most EST
                   kl1701209936.h1
Method
                   BLASTN
NCBI GI
                   g169090
BLAST score
                   186
                   1.0e-100
E value
                   477
Match length
% identity
                   Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA,
NCBI Description
                   complete cds
                   1253
Seq. No.
                   668 5.R1040
Contig ID
5'-most EST
                   LIB3087-006-Q1-K1-G1
```

5'-most EST

```
g166705
NCBI GI
BLAST score
                   224
E value
                   1.0e-122
Match length
                   951
% identity
                   83
NCBI Description
                  Arabidopsis thaliana glyceraldehyde-3-phosphate
                   dehydrogenase C subunit (GapC) gene, complete cds
                   1254
Seq. No.
                   668_6.R1040
Contig ID
5'-most EST
                   jC-gmf102220103a05a1
Method
                   BLASTN
                  g169090
NCBI GI
BLAST score
                   262
E value
                   1.0e-145
Match length
                   698
                   85
% identity
                  Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1255
                   670 1.R1040
Contig ID
5'-most EST
                  LIB3139-017-P1-N1-H1
Method
                  BLASTX
                   g4056457
NCBI GI
BLAST score
                   343
                   1.0e-53
E value
Match length
                  135
% identity
                   81
                   (AC005990) ESTs gb 234051 and gb F13722 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   1256
Seq. No.
Contig ID
                   670 2.R1040
5'-most EST
                  LIB3073-025-Q1-K1-E5
Method
                  BLASTN
NCBI GI
                   q2905777
BLAST score
                   182
E value
                   8.0e-98
Match length
                  266
% identity
                   92
NCBI Description
                  Glycine max ribosomal protein L41 mRNA, partial cds
                   1257
Seq. No.
                   670 3.R1040
Contig ID
5'-most EST
                  sat701010357.hl
Method
                  BLASTN
NCBI GI
                  g2905777
BLAST score
                  239
E value
                   1.0e-131
                  340
Match length
% identity
                  Glycine max ribosomal protein L41 mRNA, partial cds
NCBI Description
Seq. No.
                   1258
                   670 4.R1040
Contig ID
```

uC-gmropic018h03b1

BLAST score

E value

163 2.0e-86

```
Method
                   BLASTN
NCBI GI
                   q2905777
BLAST score
                   167
E value
                   7.0e-89
Match length
                   243
% identity
                   92
                   Glycine max ribosomal protein L41 mRNA, partial cds
NCBI Description
Seq. No.
                   1259
Contig ID
                   670 5.R1040
5'-most EST
                   LIB3049-044-Q1-E1-C3
Method
                   BLASTN
NCBI GI
                   q2905777
BLAST score
                   160
E value
                   1.0e-84
Match length
                   244
                   92
% identity
                   Glycine max ribosomal protein L41 mRNA, partial cds
NCBI Description
Seq. No.
Contig ID
                   670_7.R1040
5'-most EST
                   q56\overline{0}5749
Method
                   BLASTN
NCBI GI
                   g2905777
BLAST score
                   167
E value
                   1.0e-88
Match length
                   243
                   92
% identity
                   Glycine max ribosomal protein L41 mRNA, partial cds
NCBI Description
                   1261
Seq. No.
                   670 10.R1040
Contig ID
5'-most EST
                   epx701109978.h1
Seq. No.
                   1262
Contig ID
                   671 1.R1040
5'-most EST
                   LIB3170-056-Q1-K1-B7
                   1263
Seq. No.
                   671 2.R1040
Contig ID
                   g4397284
5'-most EST
Method
                   BLASTN
                   ģ2905779
NCBI GI
BLAST score
                   257
E value
                   1.0e-142
Match length
                   343
                   98
% identity
                   Glycine max hydroxyproline-rich glycoprotein (hrgp) mRNA,
NCBI Description
                   partial cds
Seq. No.
                   1264
                   671 3.R1040
Contig ID
5'-most EST
                   g4396481
                   BLASTN
Method
NCBI GI
                   g2905779
```

:-

E value

```
206
Match length
% identity
                   96
                  Glycine max hydroxyproline-rich glycoprotein (hrgp) mRNA,
NCBI Description
                  partial cds
                   1265
Seq. No.
                   673 1.R1040
Contig ID
5'-most EST
                  LIB3170-074-Q1-K1-G8
Seq. No.
                   673 2.R1040
Contig ID
                  LIB3073-020-Q1-K1-F7
5'-most EST
Seq. No.
                   673 3.R1040
Contig ID
5'-most EST
                   g3005575 FL
Method
                  BLASTX
NCBI GI
                   g3005576
BLAST score
                   2576
E value
                   0.0e+00
Match length
                   516
% identity
                   9.7
                   (AF047718) putative high affinity nitrate transporter;
NCBI Description
                  GmNRT2 [Glycine max]
Seq. No.
                   673 4.R1040
Contig ID
5'-most EST
                   jC-gmro02800043e01a1
Method -
                  BLASTN
NCBI GI
                   g3005575
BLAST score
                   310
                   1.0e-174
E value
                  370
Match length
% identity
NCBI Description
                  Glycine max putative high affinity nitrate transporter
                   (NRT2) mRNA, complete cds
                  1269
Seq. No.
                   678 1.R1040
Contig ID
5'-most EST
                   vwf700676019.h1
Method
                  BLASTN
                  g2827079
NCBI GI
BLAST score
                   351
E value
                   0.0e + 00
Match length
                  803
% identity
                  86
                  Medicago sativa mitochondrial malate dehydrogenase
NCBI Description
                  precursor (mmdh) mRNA, nuclear gene encoding mitochondrial
                  protein, complete cds
Seq. No.
                  1270
                   678 3.R1040
Contig ID
                  kl1701208643.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2827079
BLAST score
                  63
```

5.0e-27

Contig ID

```
Match length
                   115
% identity
                   89
NCBI Description
                  Medicago sativa mitochondrial malate dehydrogenase
                  precursor (mmdh) mRNA, nuclear gene encoding mitochondrial
                  protein, complete cds
Seq. No.
                   1271
Contig ID
                   678 4.R1040
5'-most EST
                   zsq701125938.h1
Method
                  BLASTN
NCBI GI
                   g2827079
BLAST score
                   44
E value
                   1.0e-15
Match length
                   96
% identity
                   86
                  Medicago sativa mitochondrial malate dehydrogenase
NCBI Description
                  precursor (mmdh) mRNA, nuclear gene encoding mitochondrial
                  protein, complete cds
Seq. No.
                   1272
Contig ID
                   679 1.R1040
5'-most EST
                  pxt700942053.h1
Method
                  BLASTN
NCBI GI
                   q3193221
BLAST score
                   318
E value
                   1.0e-179
Match length
                   516
                  93
% identity
                  Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene
NCBI Description
                  encoding mitochondrial protein, partial cds
                   1273
Seq. No.
                   680 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy067d03b1
Method
                  BLASTX
NCBI GI
                  q3399777
                  1700
BLAST score
                  0.0e + 00
E value
                  347
Match length
                   97
% identity
                   (AF069738) symbiotic ammonium transporter; nodulin [Glycine
NCBI Description
                  max]
                  1274
Seq. No.
                   682 1.R1040
Contig ID
5'-most EST
                  zhf700956708.h1
Method
                  BLASTN
NCBI GI
                  g3552012
BLAST score
                  1260
E value
                  0.0e + 00
                  1304
Match length
                  99
% identity
NCBI Description
                  Glycine max proline-rich protein precursor, mRNA, complete
                  cds
Seq. No.
                  1275
```

682 3.R1040

NCBI Description

```
jC-gmst02400067c05a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3552012.
BLAST score
                   145
                   1.0e-75
E value
Match length
                   504
% identity
                   88
                  Glycine max proline-rich protein precursor, mRNA, complete
NCBI Description
                   1276
Seq. No.
Contig ID
                   683 1.R1040
5'-most EST
                   q957422
Method
                   BLASTX
NCBI GI
                   g1076511
BLAST score
                   2415
                   0.0e + 00
E value
Match length
                   522
                   90
% identity
NCBI Description
                   H+-transporting ATPase (EC 3.6.1.35) - kidney bean
                   >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
                   [Phaseolus vulgaris]
                   1277
Seq. No.
                   683_2.R1040
Contig ID
5'-most EST
                   jC-qmst02400039q11a1
Method
                   BLASTN
NCBI GI
                   a3644031
BLAST score
                   175
                   2.0e-93
E value
Match length
                   183
                   99
% identity
                  Glycine max plasma membrane proton-ATPase mRNA, partial cds
NCBI Description
Seq. No.
                   1278
Contig ID
                   683 3.R1040
5'-most EST
                  LIB3051-064-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1076511
BLAST score
                   1765
E value
                   0.0e+00
Match length
                   371
% identity
                   94
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                   >gi 758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
                   [Phaseolus vulgaris]
                   1279
Seq. No.
                   683 5.R1040
Contig ID
5'-most EST
                   jC-qmf102220060a11d1
Method
                  BLASTN
NCBI GI
                   g3644031
BLAST score
                   180
                   1.0e-96
E value
Match length
                  180
                   100
% identity
                  Glycine max plasma membrane proton-ATPase mRNA, partial cds
```

```
Seq. No.
                     1280
  Contig ID
                     683 6.R1040
                     uC-gmflminsoy037a02b1
  5'-most EST
  Method
                     BLASTN
  NCBI GI
                     g758249
  BLAST score
                     200
  E value
                     1.0e-108
  Match length
                     396
  % identity
                     88
                     P.vulgaris mRNA for plasma membrane H+ ATPase
  NCBI Description
                     1281
  Seq. No.
  Contig ID
                     683 8.R1040
  5'-most EST
                     q5508913
  Method
                     BLASTN
  NCBI GI
                     g758249
  BLAST score
                     116
  E value
                     1.0e-58
  Match length
                     254
  % identity
                     94
  NCBI Description
                     P.vulgaris mRNA for plasma membrane H+ ATPase
  Seq. No.
  Contig ID
                     684 1.R1040
                     uC-qmflminsoy014b09b1
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     g2275219
  BLAST score
                     1852
  E value
                     0.0e+00
  Match length
                     418
  % identity
                     83
                     (AC002337) unknown protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     1283
                     684 2.R1040
  Contig ID
  5'-most EST
                     LIB3051-006-Q1-E1-F11
                     BLASTX
  Method
                     g2275219
  NCBI GI
  BLAST score
                     371
                     1.0e-35
  E value
  Match length
                     138
                     61
  % identity
                     (AC002337) unknown protein [Arabidopsis thaliana]
NCBI Description
  Seq. No.
                     1284
                     685 1.R1040
  Contig ID
  5'-most EST
                     rlr700895815.h1
                     BLASTX
  Method
  NCBI GI
                     g123506
  BLAST score
                     336
                     4.0e-31
  E value
  Match length
                     80
  % identity
                     81
  NCBI Description
                     HYDROPHOBIC SEED PROTEIN (HPS) >gi 99917 pir A29385
                     hydrophobic seed protein - soybean >gi 349888 pdb 1HYP
```

Hydrophobic Protein From Soybean

Seq. No.

```
1285
Seq. No.
Contig ID
                   685 2.R1040
5'-most EST
                   rlr700895643.h1
Method
                   BLASTX
NCBI GI
                   q123506
BLAST score
                   249
                   3.0e-21
E value
Match length
                   66
% identity
                   74
NCBI Description
                   HYDROPHOBIC SEED PROTEIN (HPS) >gi_99917_pir__A29385
                   hydrophobic seed protein - soybean >gi 349888 pdb 1HYP
                   Hydrophobic Protein From Soybean
                   1286
Seq. No.
                   685 3.R1040
Contig ID
                   rlr700897394.hl
5'-most EST
                   1287
Seq. No.
                   686 1.R1040
Contig ID
                   uxk700672239.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3832527
BLAST score
                   1500
                   0.0e + 00
E value
Match length
                   1521
                   100
% identity
                  Glycine max unknown mRNA
NCBI Description
Seq. No.
Contig ID
                   686_2.R1040
5'-most EST
                   uC-gmflminsoy042g06b1
Method
                   BLASTN
NCBI GI
                   g3832527
BLAST score
                   73
E value
                   8.0e-33
Match length
                   73
% identity
                   100
NCBI Description
                  Glycine max unknown mRNA
Seq. No.
                   1289
                   689 3.R1040
Contig ID
5'-most EST
                   eep700863946.hl
                   1290
Seq. No.
Contig ID
                   689 4.R1040
5'-most EST
                   uC-gmrominsoy081g04b1
Method
                  BLASTX
NCBI GI
                   g3831470
BLAST score
                   184
E value
                   2.0e-13
Match length
                   92
% identity
                   (AC005700) unknown protein, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
```

5'-most EST

```
Contig ID
                   689 5.R1040
5'-most EST
                   LIB3050-017-Q1-E1-C9
Method
                   BLASTX
NCBI GI
                   g3851670
BLAST score
                   285
E value
                   3.0e-25
Match length
                   111
% identity
                   56
NCBI Description
                   (AF099906) J8 [Arabidopsis thaliana]
Seq. No.
                   1292
Contig ID
                   689 6.R1040
5'-most EST
                   LIB3051-011-Q1-E1-A7
Method
                   BLASTX
NCBI GI
                   q1388078
BLAST score
                   244
E value
                   9.0e-22
                   96
Match length
% identity
                   50
NCBI Description
                   (U35826) thioredoxin h [Arabidopsis thaliana]
Seq. No.
                   689 7.R1040
Contig ID
5'-most EST
                   LIB3049-029-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                   g4455358
BLAST score
                   487
E value
                   8.0e-49
                   184
Match length
% identity
                   61
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   1294
Seq. No.
                   689 8.R1040
Contig ID
5'-most EST
                   LIB3055-008-Q1-N1-B9
Method
                   BLASTX
NCBI GI
                   q3269293
BLAST score
                   272
                   2.0e-49
E value
Match length
                   213
% identity
                   55
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   689 9.R1040
5'-most EST
                   jC-gmst02400052b03a1
                   BLASTX
Method
                   g3851670
NCBI GI
                   281
BLAST score
                   1.0e-24
E value
                  112
Match length
% identity
                   51
                  (AF099906) J8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1296
Contig ID
                   689 10.R1040
```

jC-gmst02400004g01a1

```
BLASTX
Method
                   q3269293
NCBI GI
                   472
BLAST score
E value
                   6.0e-47
                   179
Match length
% identity
                   56
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   1297
Seq. No.
                   689 11.R1040
Contig ID
5'-most EST
                   rlr700900707.h1
Method
                   BLASTN
                   q2687435
NCBI GI
BLAST score
                   449
E value
                   0.0e + 00
                   645
Match length
                   93
% identity
                   Hamamelis virginiana large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
                   1298
Seq. No.
                   689 12.R1040
Contig ID
5'-most EST
                   LIB3050-008-Q1-E1-E9
Method
                   BLASTX
                   q2129752
NCBI GI
BLAST score ·
                   437
                   5.0e-43
E value
Match length
                   104
                   75
% identity
NCBI Description
                   thioredoxin - Arabidopsis thaliana >gi 992964 emb CAA84612
                   (Z35475) thioredoxin [Arabidopsis thaliana]
                   1299
Seq. No.
                   689 13.R1040
Contig ID
5'-most EST
                   LIB3170-046-Q1-J1-B4
Method
                   BLASTN
NCBI GI
                   q2852442
BLAST score
                   224
E value
                   1.0e-122
Match length
                   510
% identity
                   86
                   Salix bakko mRNA for ADP-ribosylation factor, complete cds
NCBI Description
Seq. No.
                   689 14.R1040
Contig ID
5'-most EST
                   jC-gmro02910071a04a1
Method
                   BLASTX
NCBI GI
                   g1708236
BLAST score
                   1265
E value
                   0.0e + 00
Match length
                   462
% identity
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
NCBI Description
                   (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase
(EC 4.1.3.5) - Arabidopsis thaliana
                   >gi 1143390 emb CAA58763_ (X83882)
```

```
hydroxymethylqlutaryl-CoA synthase [Arabidopsis thaliana]
>gi_1586548_prf__2204245A hydroxy methylglutaryl CoA
synthase [Arabidopsis thaliana]
```

Seq. No. 1301 Contig ID 689 15.R1040 5'-most EST uC-gmropic080b12b1 Method BLASTN NCBI GI g2852442 BLAST score 221 E value 1.0e-120 485 Match length 86 % identity Salix bakko mRNA for ADP-ribosylation factor, complete cds NCBI Description Seq. No. 689 16.R1040 Contig ID leu701156547.h1 5'-most EST Method BLASTN NCBI GI q2852442 BLAST score 224 1.0e-122 E value Match length 480 % identity 87 Salix bakko mRNA for ADP-ribosylation factor, complete cds NCBI Description Seq. No. 1303 Contiq ID 689 17.R1040 5'-most EST jex700909370.h1

Method BLASTX NCBI GI q1708236

BLAST score 1544 E value 1.0e-179 Match length 464 % identity 67

NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)

(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)

>gi\_2129617\_pir\_\_JC4567 hydroxymethylglutaryl-CoA synthase

(EC 4.1.3.5) - Arabidopsis thaliana

>gi\_1143390\_emb\_CAA58763\_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA

synthase [Arabidopsis thaliana]

Seq. No. 1304

Contig ID 689 18.R1040

5'-most EST LIB3050-023-Q1-K1-C8

Method BLASTN NCBI GI g4324966 BLAST score 349 E value 0.0e+00Match length 610 🚓 % identity 96

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No. 1305

Contig ID 690 1.R1040

% identity

....

```
5'-most EST
                   crh700852726.h1
Method
                   BLASTN
                   g472849
NCBI GI
BLAST score
                   180
E value
                   2.0e-96
                   460
Match length
                   85
% identity
NCBI Description
                   Glycine max Essex desiccation protectant protein Lea14
                   homolog mRNA, complete cds
                   1306
Seq. No.
Contig ID
                   691 1.R1040
5'-most EST
                  LIB3051-047-Q1-K1-E6
                   1307
Seq. No.
                   691 2.R1040
Contig ID
5'-most EST
                   all700863202.hl
                   1308
Seq. No.
                   692 1.R1040 -
Contig ID
5'-most EST
                   LIB3027-008-Q1-B1-H3
                   1309
Seq. No.
Contig ID
                   694_1.R1040
5'-most EST
                   LIB3072-017-Q1-E1-E5
Method
                   BLASTX
                   g2909422
NCBI GI
BLAST score
                   395
                   6.0e-38
E value
                   135
Match length
% identity
                   62
                   (AJ224519) LEA PROTEIN [Cicer arietinum]
NCBI Description
                   1310
Seq. No.
                   694 2.R1040
Contig ID
5'-most EST
                   LIB3106-072-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g2245062
BLAST score
                   185
E value
                   2.0e-13
Match length
                   44
% identity
NCBI Description
                   (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   1311
Contig ID
                   694 4.R1040
5'-most EST
                   q5688020
Seq. No.
                   1312
Contig ID
                   695 1.R1040
                   crh700853905.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g169101
BLAST score
                   407
                   2.0e-39
E value
                   127
Match length
```

```
NCBI Description
                   (M33900) 17.9 kDa heat shock protein (hsp17.9) [Pisum
                   sativum]
                   1313
Seq. No.
Contig ID
                   696 1.R1040
5'-most EST
                   g4559291 FL
Method
                   BLASTX
                   g4559292
NCBI GI
BLAST score
                   2962
E value .
                   0.0e+00
                   557
Match length
                   100
% identity
                   (AF124148) trehalase 1 GMTRE1 [Glycine max]
NCBI Description
                   1314
Seq. No.
Contig ID
                   698 1.R1040
5'-most EST
                   LIB3109-042-Q1-K1-D5
                   BLASTX
Method
                   g4567091
NCBI GI
BLAST score
                   2104
E value
                   0.0e + 00
Match length
                   507
                   96
% identity
NCBI Description
                   (AF128443) SNF-1-like serine/threonine protein kinase
                   [Glycine max]
                   1315
Seq. No.
Contig ID
                   698 2.R1040
                   LIB\overline{3}051-030-Q1-K1-G7
5'-most EST
Method
                   BLASTN
                   g4567090
NCBI GI
BLAST score
                   105
                   1.0e-51
E value
Match length
                   205
                   91
% identity
NCBI Description
                  Glycine max SNF-1-like serine/threonine protein kinase
                   mRNA, complete cds
Seq. No.
                   1316
                   698 3.R1040
Contig ID
5'-most EST
                   jex700907708.h1
Seq. No.
                   1317
Contig ID
                   698 4.R1040
                   seb700651919.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4567090
BLAST score
                   137
E value
                   6.0e-71
                   277
Match length
                   87
% identity
NCBI Description
                  Glycine max SNF-1-like serine/threonine protein kinase
                  mRNA, complete cds
Seq. No.
                   1318
                   698 5.R1040
Contig ID
```

zsg701128474.h1

5'-most EST

```
Method
                   BLASTN
NCBI GI
                   g4567090
BLAST score
                   137
                   7.0e-71
E value
                   407
Match length
% identity
                   86
                   Glycine max SNF-1-like serine/threonine protein kinase
NCBI Description
                   mRNA, complete cds
                   1319
Seq. No.
                   699 1.R1040
Contig ID
5'-most EST
                   xpa700793223.hl
Method
                   BLASTX
                   g130846
NCBI GI
BLAST score
                   494
E value
                   1.0e-49
Match length
                   161
                   57
% identity
                   BASIC FORM OF PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PRP
NCBI Description
                   1) >gi_82185_pir__S04728 pathogenesis-related protein
                   homolog precursor - common tobacco >gi_19972_emb_CAA32228_
                   (X14065) PRP 1 precursor (AA -23 to 15\overline{4}) [Nicotiana
                   tabacum] >gi_228620_prf__1807333A pathogenesis-related
                   protein 1 [Nicotiana tabacum]
                   1320
Seq. No.
Contig ID
                   702_1.R1040
5'-most EST
                   g5002235_FL
Method
                   BLASTX
NCBI GI
                   q4538927
BLAST score
                   1138
                   1.0e-125
E value
Match length
                   302
% identity
                   (ALO49483) putative peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1321
Contig ID
                   703 1.R1040
5'-most EST
                   zzp700834588.hl
Method
                   BLASTX
NCBI GI
                   q478409
BLAST score
                   1020
E value
                   1.0e-111
Match length
                   320
% identity
                   62
NCBI Description
                   peroxidase (EC 1.11.1.7), cationic - adzuki bean
                   >gi 218328_dbj_BAA01950_ (D11337) peroxidase [Vigna
                   angularis]
Seq. No.
                   1322
                   704 1.R1040
Contig ID
5'-most EST
                   zhf700962226.h1
Method
                   BLASTX
NCBI GI
                   g4512617
BLAST score
                   255
```

2.0e-21

157

E value Match length

```
% identity
                   (AC004793) F28K20.16 [Arabidopsis thaliana]
NCBI Description
                   1323
Seq. No.
                   705 1.R1040
Contig ID
                   sat701002940.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1938226
BLAST score
                   290
                   1.0e-162
E value
Match length
                   745
% identity
                  85
NCBI Description M.sativa mRNA for carbonic anhydrase
                   1324
Seq. No.
                   706 1.R1040
Contig ID
                  LIB3093-024-Q1-K1-B2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3413473
BLAST score
                   1781
                   0.0e+00
E value
Match length
                   338
% identity
                   100
NCBI Description
                   (AJ006308) tyrosine phosphatase 1 [Glycine max]
                   1325
Seq. No.
                   707 1.R1040
Contig ID
5'-most EST
                  LIB3170-084-Q1-K1-A6
                   BLASTN
Method
NCBI GI
                   q533691
BLAST score
                   483
E value
                   0.0e+00
Match length
                  502
                   95
% identity
NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds
Seq. No.
                   1326
                   708 1.R1040
Contig ID
5'-most EST
                  LIB3170-086-Q1-J1-B5
Method
                  BLASTX
NCBI GI
                   g905361
BLAST score
                   3108
E value
                   0.0e+00
Match length
                  640
% identity
                   93
NCBI Description
                  (U22103) gag-protease polyprotein [Glycine max]
                   1327
Seq. No.
                   710 1.R1040
Contig ID
5'-most EST
                  LIB3170-007-Q1-K1-D8
Method
                  BLASTX
                  g3915009
NCBI GI
                   3105
BLAST score
E value
                   0.0e+00
Match length
                  691
                   87
% identity
```

NCBI Description ARGININE DECARBOXYLASE (ARGDC) (ADC) >gi 1163181 (U35367)

## arginine decarboxylase [Glycine max]

```
Seq. No.
                  1328
                   710 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy165f06b1
Method
                   BLASTN
                   g1163180
NCBI GI
BLAST score
                   278
E value
                   1.0e-155
Match length
                   316
                   97
% identity
                   Glycine max arginine decarboxylase mRNA, complete cds
NCBI Description
Seq. No.
                   715 1.R1040
Contig ID
                   kl1701212945.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2832629
BLAST score
                   342
                   1.0e-31
E value
                   221
Match length
% identity
                   35
                   (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   1330
                   715 2.R1040
Contig ID
                   g1143318_FL
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1143318
BLAST score
                   1067
                   0.0e + 00
E value
                   1129
Match length
% identity
                   99
NCBI Description
                   Glycine max biotin carboxyl carrier protein precursor
                   (accB-1) mRNA, complete cds
                   1331
Seq. No.
                   716 1.R1040
Contig ID
5'-most EST
                   g1335861 FL
Method
                   BLASTX
NCBI GI
                   g1335862
BLAST score
                   8090
                   0.0e + 00
E value
Match length
                   1656
% identity
                   96
                   (U42608) clathrin heavy chain [Glycine max]
NCBI Description
Seq. No.
                   1332
                   717 1.R1040
Contig ID
5'-most EST
                   leu701156669.hl
Method
                   BLASTN
NCBI GI
                   g758693
BLAST score
                   88
E value
                   2.0e-41
Match length
                   152
                   95
% identity
```

BLAST score

```
Catharanthus roseus S-adenosyl-L-methionine decarboxylase
NCBI Description
                   proenzyme mRNA, complete cds
Seq. No.
                   717 2.R1040
Contig ID
5'-most EST
                   g1438880 FL
Method
                   BLASTX
NCBI GI
                   q1438881
BLAST score
                   1912
                   0.0e + 00
E value
Match length
                   362
                   100
% identity
                   (U43839) GmCK2p [Glycine max]
NCBI Description
Seq. No.
                   1334
                   717 3.R1040
Contig ID
5'-most EST
                   LIB3028-005-Q1-B1-B4
Method
                   BLASTX
NCBI GI
                   q3913420
BLAST score
                   1508
                   1.0e-168
E value
Match length
                   346
% identity
                   83
NCBI Description
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine
                   decarboxylase [Pisum sativum]
Seq. No.
Contig ID
                   717 4.R1040
5'-most EST
                   rca700998660.h1
Method
                   BLASTX
NCBI GI
                   q3913420
BLAST score
                   1495
E value
                   1.0e-166
Match length
                   347
% identity
                   81
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine
                   decarboxylase [Pisum sativum]
Seq. No.
                   1336
                   717 5.R1040
Contig ID
5'-most EST
                   q14\overline{3}8878 FL
Method
                   BLASTX
NCBI GI
                   q1438879
BLAST score
                   1900
E value
                   0.0e + 00
Match length
                   359
% identity
                   100
NCBI Description
                   (U43838) GmCK1p [Glycine max]
Seq. No.
Contig ID
                   717 6.R1040
5'-most EST
                   LIB3051-043-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   q3860274
```

Contig ID

```
2.0e-46
E value
Match length
                   158
% identity
                   57
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
                   >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
                   protein [Arabidopsis thaliana]
                   1338
Seq. No.
                   717 7.R1040
Contig ID
                   rca701002512.hl
5'-most EST
                   BLASTN'
Method
                   g1438878
NCBI GI
BLAST score
                   303
E value
                   1.0e-170
Match length
                   360
% identity
                   100
                  Glycine max choline kinase GmCK1p mRNA, complete cds
NCBI Description
                   1339
Seq. No.
                   717 8.R1040
Contig ID
5'-most EST
                   g5606823
                   BLASTX
Method
                   g3860274
NCBI GI
BLAST score
                   216
E value
                   3.0e-17
Match length
                   54
% identity
                   74
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
                   >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
Seq. No.
                   1340
                   717 9.R1040
Contig ID
                   epx701105723.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1438878
BLAST score
                   430
                   0.0e + 00
E value
                   448
Match length
% identity
                  Glycine max choline kinase GmCK1p mRNA, complete cds
NCBI Description
Seq. No.
                   1341
                   717.10.R1040
Contig ID
5'-most EST
                   q50\overline{5}7990
Method
                   BLASTX
NCBI GI
                   q3860274
BLAST score
                   410
E value
                   7.0e-40
Match length
                   147
                   54
% identity
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
                  >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
Seq. No.
```

717\_11.R1040

Seq. No.

1347

```
uC-gmronoir054h11b1
5'-most EST
Method
                  BLASTX
                  g3860274..
NCBI GI
                   292
BLAST score
                   4.0e-26
E value
Match length
                   118
% identity
                   51
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4314397_gb_AAD15607_ (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
                   1343
Seq. No.
                  717 12.R1040
Contig ID
                  rca700997186.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                   g1438878
BLAST score
                   345
                   0.0e + 00
E value
                   345
Match length
                   100
% identity
                  Glycine max choline kinase GmCK1p mRNA, complete cds
NCBI Description
                   1344
Seq. No.
                  717_14.R1040
Contig ID
                   jC-gmro02910026f07a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1438880
BLAST score
                   256
                   1.0e-142
E value
                   372
Match length
                   95
% identity
                  Glycine max choline kinase GmCK2p mRNA, complete cds
NCBI Description
Seq. No.
                   1345
                   717 21.R1040
Contig ID
                   jC-gmst02400055f08d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1134881
                   33
BLAST score
                   6.0e-09
E value
                   92
Match length
                   92
% identity
                  P.sativum mRNA for cysteine protease
NCBI Description
                   1346
Seq. No.
                   717_23.R1040
Contig ID
                  LIB3106-102-Q1-K1-E2
5'-most EST
Method
                  BLASTN
                   g758693
NCBI GI
BLAST score
                   75
E value
                   6.0e - 34
Match length
                   147
                   93
% identity
NCBI Description
                  Catharanthus roseus S-adenosyl-L-methionine decarboxylase
                  proenzyme mRNA, complete cds
```

5'-most EST

```
717 26.R1040
Contig ID
                   jC-gmro02910026d07d1
5'-most EST
                   BLASTN
Method
                   g1438880
NCBI GI
                   272
BLAST score
E value
                   1.0e-151
                   363
Match length
                   96
% identity
                   Glycine max choline kinase GmCK2p mRNA, complete cds
NCBI Description
                   1348
Seq. No.
                   719 1.R1040
Contig ID
                   g1438882 FL
5'-most EST
Method
                   BLASTX
                   g1438883
NCBI GI
BLAST score
                   2586
E value
                   0.0e+00
Match length
                   497
                   100
% identity
NCBI Description
                   (U43840) GmCK3p [Glycine max]
                   1349
Seq. No.
Contig ID
                   722 1.R1040
                   LIB3109-042-Q1-K1-G7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4204759
BLAST score
                   1722
E value
                   0.0e+00
                   354
Match length
                   95
% identity
                   (U51191) peroxidase precursor [Glycine max]
NCBI Description
Seq. No.
                   1350
                   724 1.R1040
Contig ID
                   LIB3107-052-Q1-K1-H12
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4204762
BLAST score
                   1030
E value
                   0.0e + 00
Match length
                   1135
                   98
% identity
                  Glycine max peroxidase (sEPb1) mRNA, partial cds
NCBI Description
Seq. No.
                   1351
                   724 2.R1040
Contig ID
5'-most EST
                   g4204764_FL
Method
                   BLASTX
NCBI GI
                   g4204765
BLAST score
                   1671
E value
                   0.0e+00
                   325
Match length
% identity
                   100
                   (U51194) peroxidase [Glycine max]
NCBI Description
                   1352
Seq. No.
                   726 1.R1040
Contig ID
```

ary700764391.hl

```
Method
                   BLASTX
NCBI GI
                   q1518540
BLAST score
                   2422
E value
                   0.0e + 00
Match length
                   480
% identity
                   97
NCBI Description
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                   1353
Contig ID
                   726_2.R1040
5'-most EST
                   jC-gmst02400027a06d1
                   BLASTN
Method
NCBI GI
                   q1518539
BLAST score
                   109
E value
                   3.0e-54
Match length
                   197
                   89
% identity
NCBI Description
                   Glycine max UDP-glucose dehydrogenase mRNA, complete cds
Seq. No.
Contig ID
                   726 6.R1040
5'-most EST
                   jsh701069261.h1
Method
                   BLASTX
NCBI GI
                   g1518540
BLAST score
                   329
E value
                   5.0e-47
Match length
                   142
% identity
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                   1355
                   727 2.R1040
Contig ID
                   taw700655529.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q1778371
BLAST score
                   158
E value
                   1.0e-83
Match length
                   220
% identity
                   99
                   Glycine max asparagine synthetase 1 (AS1) mRNA, complete
NCBI Description
                   1356
Seq. No.
                   727 3.R1040
Contig ID
5'-most EST
                   fC-gmf1700906171a1
Method
                   BLASTN
NCBI GI
                   g1778371
BLAST score
                   366
E value
                   0.0e + 00
Match length
                   927
% identity
                   97
NCBI Description
                   Glycine max asparagine synthetase 1 (AS1) mRNA, complete
Seq. No.
                   1357
                   727 4.R1040
Contig ID
```

crh700855008.h1

5'-most EST

Contig ID

```
BLASTX
Method
                   q3789911
NCBI GI
BLAST score
                   143
E value
                   6.0e-27
                   192
Match length
% identity
                   43
                   (AF081802) developmental protein DG1118 [Dictyostelium
NCBI Description
                  discoideum]
Seq. No.
                  1358
Contig ID
                   727_5.R1040
                  uC-gmropic067d04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1778372
BLAST score
                   1198
                   0.0e + 00
E value
                   573
Match length
% identity
                   55
                   (U77679) asparagine synthetase 1 [Glycine max]
NCBI Description
Seq. No.
                  1359
                  727 6.R1040
Contig ID
                  LIB3139-049-P1-N1-G6
5'-most EST
Method
                  BLASTX
                  q1778370
NCBI GI
BLAST score
                  804
                   0.0e+00
E value
Match length
                  579
                   42
% identity
NCBI Description
                   (U77678) asparagine synthetase 2 [Glycine max]
Seq. No.
                  1360
                  728 1.R1040
Contig ID
5'-most EST
                  leu701144891.hl
                  BLASTN
Method
NCBI GI
                  g1381675
BLAST score
                  739
E value
                  0.0e + 00
Match length
                  747
                  100
% identity
NCBI Description
                  Glycine max small GTP-binding protein (sra1) mRNA, partial
Seq. No.
                  1361
                  728_2.R1040
Contig ID
5'-most EST
                  jC-gmf102220078d07a1
Method
                  BLASTX
NCBI GI
                  q4262154
BLAST score
                  257
E value
                  1.0e-21
Match length
                  179
% identity
                   (AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
```

728 3.R1040

Match length

```
5'-most EST
                   LIB3039-022-Q1-E1-G3
Method
                   BLASTN
                   g1381675
NCBI GI
BLAST score
                   139
E value
                   5.0e-72
Match length
                   303
                   87
% identity
                   Glycine max small GTP-binding protein (sral) mRNA, partial
NCBI Description
                   1363
Seq. No.
                   728 4.R1040
Contig ID
5'-most EST
                   wrg700786826.h2
                   1364
Seq. No.
                   728 5.R1040
Contig ID
                   gsv701052886.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g1381675
BLAST score
                   119
E value
                   2.0e-60
Match length
                   267
                   86
% identity
                   Glycine max small GTP-binding protein (sra1) mRNA, partial
NCBI Description
Seq. No.
                   1365
                   728 6.R1040
Contig ID
5'-most EST
                   ncj700988106.h1
Method
                   BLASTN
NCBI GI
                   q1381675
BLAST score
                   214
E value
                   1.0e-117
Match length
                   222
                   99
% identity
NCBI Description
                   Glycine max small GTP-binding protein (sral) mRNA, partial
                   1366
Seq. No.
                   730 1.R1040
Contig ID
                   awf700841707.hl
5'-most EST
Method
                   BLASTX
                   g1389897
NCBI GI
BLAST score
                   2704
                   0.0e + 00
E value
Match length
                   643
% identity
                   86
NCBI Description
                   (U59626) LEA protein [Glycine max] -
Seq. No.
                   1367
                   732 1.R1040
Contig ID
5'-most EST
                   g4097568 FL
Method
                   BLASTN
NCBI GI
                   q4097568
BLAST score
                   588
E value
                   0.0e + 00
```

% identity

```
% identity
                   98
                  Glycine max farnesylated protein GMFP4 mRNA, partial cds
NCBI Description
                   1368
Seq. No.
                   733 4.R1040
Contig ID
                  LIB3170-083-Q1-K1-D10
5'-most EST
                   1369
Seq. No.
Contig ID
                   733_5.R1040
                   zpv700761634.hl
5'-most EST
Method
                   BLASTX
                   g3157949
NCBI GI
BLAST score
                   337
E value
                   9.0e-34
Match length
                   89
% identity
                   87
                   (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
NCBI Description
                  precursor gb_Z28697 from Nicotiana tabacum. ESTs gb Z18185
                  and gb AA605362 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   1370
                   733 6.R1040
Contig ID
5'-most EST.
                  jC-gmle01810001b03a1
Seq. No.
                  1371
Contig ID
                  733 7.R1040
                  uC-gmrominsoy283e09b1
5'-most EST
Method
                  BLASTX
                  q4467159
NCBI GI
BLAST score
                  145
E value
                   4.0e-09
Match length
                   47
                   55
% identity
NCBI Description
                   (AL035540) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  1372
Contig ID
                  733 8.R1040 ·
5'-most EST
                  uxk700671427.h1
Method
                  BLASTX
NCBI GI
                   q3157934
BLAST score
                   509
E value
                   6.0e-65
Match length
                   180
% identity
NCBI Description
                   (AC002131) Similar to hypothetical protein F09E5.8
                  gb U37429 from C. elegans. ESTs gb_T42019 and gb_N97000
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  1373
Contig ID
                  733 9.R1040
5'-most EST
                  asn701136839.hl
Method
                  BLASTN
NCBI GI
                  q18729
BLAST score
                  58
                  8.0e-24
E value
Match length
                  62
```

Method

NCBI GI

BLASTN

g455949

```
NCBI Description Soybean (Glycine max) 18S ribosomal RNA
                  1374
Seq. No.
                  733 10.R1040
Contig ID
5'-most EST
                  gsv701055023.hl
Method
                  BLASTN
                   g455949
NCBI GI
                  85
BLAST score
                   6.0e-40
E value
Match length .
                  89
                   99
% identity
                  18S rRNA {3' region} [Glycine max=soybeans, var. Pella 86,
NCBI Description
                  leaves, rRNA Partial, 111 nt]
                   1375
Seq. No.
                  733 11.R1040
Contig ID
                   jsh701069821.h1
5'-most EST
                  1376
Seq. No.
                  733 12.R1040
Contig ID
5'-most EST
                  uxk700672545.h1
                  BLASTX
Method
NCBI GI
                  g4539303
BLAST score
                  153
E value
                  1.0e-20
Match length
                  132
% identity
                   47
                   (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
                  1377
Seq. No.
                  733 13.R1040
Contig ID
                  LIB3106-099-Q1-K1-G12
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4115533
                   63
BLAST score
E value
                   1.0e-26
Match length
                   161
% identity
                  Vigna mungo UFGlyT mRNA for UDP-glycose:flavonoid
NCBI Description
                  glycosyltransferase, complete cds
Seq. No.
                   1378
                   733 14.R1040
Contig ID
5'-most EST
                  LIB3092-040-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                   g2330648
BLAST score
                   549
E value
                  0.0e+00
Match length
                  1076
% identity
                  88
NCBI Description
                  Pisum sativum mRNA for topoisomerase I
Seq. No.
                  1379
                  733 15.R1040
Contig ID
                  leu701145478.hl
5'-most EST
```

```
BLAST score
                   93
                   1.0e-44
E value
                  93
Match length
                  100
% identity
                  18S rRNA {3' region} [Glycine max=soybeans, var. Pella 86,
NCBI Description
                  leaves, rRNA Partial, 111 nt]
                  1380
Seq. No.
                  733 16.R1040
Contig ID
                  LIB3029-002-Q1-B1-B6
5'-most EST
                  BLASTN
Method
                  g3097320
NCBI GI
                  87
BLAST score
E value
                  7.0e-41
                  577
Match length
                  83
% identity
                  Glycine max gene for Bd 30K, complete cds
NCBI Description
                  1381
Seq. No.
                  733 17.R1040
Contig ID
5'-most EST
                  k11701207520.h1
Method
                  BLASTX
NCBI GI
                  g3738230
BLAST score
                  376
                  7.0e-36
E value
Match length
                  141
% identity
                  54
                   (AB007790) DREB2A [Arabidopsis thaliana]
NCBI Description
                  >gi 4126706 dbj BAA36705 (AB016570) DREB2A [Arabidopsis
                  thaliana]
Seq. No.
                  1382
                  733 18.R1040
Contig ID
5'-most EST
                  LIB3049-021-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                  g4455242
BLAST score
                  304
                  1.0e-27
E value
Match length
                  66
% identity
                   (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  1383
                  733 19.R1040
Contig ID
5'-most EST
                  6HA-01-Q1-E1-A2
Seq. No.
                  1384
Contig ID
                  733 20.R1040
5'-most EST
                  LIB3039-052-Q1-E1-E3
Method
                  BLASTN
NCBI GI
                  g455949
BLAST score
                  92
E value
                  9.0e-44
Match length
                  96
% identity
                  99
NCBI Description 18S rRNA {3' region} [Glycine max=soybeans, var. Pella 86,
```

## leaves, rRNA Partial, 111 nt] Seq. No. 1385 Contig ID 733 21.R1040

Contig ID 733\_21.R1040 5'-most EST leu701154457.h1 Method BLASTX

Method BLASTX
NCBI GI g1168548
BLAST score 329
E value 3.0e-30
Match length 110
% identity 59

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN ATHB-7) >gi\_629527\_pir\_\_S47137 homeotic protein Athb-7 - Arabidopsis thaliana >gi\_499164\_emb\_CAA47425\_ (X67032) orf

[Arabidopsis thaliana]

Seq. No. 1386

Contig ID 733 22.R1040

5'-most EST LIB3170-066-Q1-J1-H1

Seq. No. 1387

Contig ID 733\_23.R1040 5'-most EST zhf700960789.h1

Method BLASTX
NCBI GI g2959358
BLAST score 351
E value 4.0e-62
Match length 128
% identity 91

NCBI Description (X96758) clathrin coat assembly protein AP17 [Zea mays]

Seq. No. 1388

Contig ID 733\_24.R1040 5'-most EST zvj700605287.h2

Method BLASTX
NCBI GI g2642448
BLAST score 438
E value 8.0e-43
Match length 251
% identity 29

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 1389

Contig ID 733\_25.R1040 5'-most EST kmv700738553.h1

Method BLASTX
NCBI GI 94530591
BLAST score 720
E value 1.0e-95
Match length 242
% identity 71

NCBI Description (AF132475) heme oxygenase 1 [Arabidopsis thaliana]

>gi\_4530593\_gb\_AAD22108.1\_ (AF132476) heme oxygenase 1

[Arabidopsis thaliana]

```
Seq. No.
                   1390
                   733 26.R1040
Contig ID
5'-most EST
                   LIB3072-019-Q1-E1-F5
Method
                   BLASTN
NCBI GI
                   g343344
BLAST score
                   298
E value
                   1.0e-167
Match length
                   628
% identity
                   96
NCBI Description
                   Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end),
                   Ile-tRNA, and Ala-tRNA genes
Seq. No.
                   1391
Contig ID
                   733 27.R1040
5'-most EST
                   LIB3051-043-Q1-K1-B7
Method
                   BLASTN
NCBI GI
                   g166769
BLAST score
                   182
E value
                   1.0e-97
Match length
                   577
% identity
                   84
NCBI Description
                   A.thaliana heat shock protein 83 mRNA, complete cds
Seq. No.
                   1392
Contig ID
                   733 28.R1040
5'-most EST
                   LIB3107-079-Q1-K1-F4
Method
                   BLASTN
NCBI GI
                   q4097570
BLAST score
                   626
E value
                   0.0e+00
Match length
                   982
                   97
% identity
                  Glycine max farnesylated protein GMFP5 mRNA, partial cds
NCBI Description
Seq. No.
                   1393
Contig ID
                   733 29.R1040
                   asn701140463.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g388206
BLAST score
                   57
E value
                   3.0e-23
                   177
Match length
% identity
                   84
                   Lycopersicon esculentum ubiquitin carrier protein (Ubc)
NCBI Description
                   mRNA, complete cds. >gi 2086269 gb I38279 I38279 Sequence
                   109 from patent US
                   1394
Seq. No.
                   733 30.R1040
Contig ID
5'-most EST
                   gsv701053339.h1
Method
                   BLASTN
NCBI GI
                   g4097570
                   225
BLAST score
E value
                   1.0e-123
                   787
Match length
% identity
                   91
```

NCBI Description Glycine max farnesylated protein GMFP5 mRNA, partial cds

NCBI GI

```
Seq. No.
                  1395
                  733 31.R1040 🕾
Contig ID
                  LIB3094-038-Q1-K1-A5
5'-most EST
Method
                  BLASTN
                  g1326160
NCBI GI
BLAST score
                   66
E value
                   3.0e-28
Match length
                   334
                   94
% identity
                  Phaseolus vulgaris dehydrin mRNA, complete cds
NCBI Description
                  1396
Seq. No.
                  733 32.R1040
Contig ID
                  LIB3073-017-Q1-K1-D5
5'-most EST
                  BLASTN
Method
                  g2104958
NCBI GI
BLAST score
                  144
E value
                   6.0e-75
Match length
                  252
                  91
% identity
                  Vicia faba immunophilin (FKBP12) mRNA, complete cds
NCBI Description
                  1397
Seq. No.
Contig ID
                  733 33.R1040
5'-most EST
                  LIB3074-004-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1350989
BLAST score
                  219
E value
                   6.0e-56
Match length
                  205
% identity
                   67
                  PROBABLE 40S RIBOSOMAL PROTEIN S3 >gi_1055070 (U39851)
NCBI Description
                  coded for by C. elegans cDNA CEMSE13F; coded for by C.
                  elegans cDNA CEMSE13R; coded for by C. elegans cDNA
                  CEMSG70F; coded for by C. elegans cDNA CEESL66F;
                  to ribosomal protein S3 [Caenorhabditis elegans]
                  1398
Seq. No.
                  733 34.R1040
Contig ID
                  LIB3109-038-Q1-K1-A6
5'-most EST
Method
                  BLASTX
NCBI GI
                  q133940
BLAST score
                  278
                  1.0e-41
E value
Match length
                  179
% identity
                  63
NCBI Description
                  40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A
                  ribosomal protein S3a - African clawed frog
                  >gi_65091_emb_CAA40592_ (X57322) ribosomal protein Sla
                   [Xenopus laevis]
Seq. No.
                  1399
Contig ID
                  733 35.R1040
5'-most EST
                  awf700837545.hl
Method
                  BLASTX
```

q1389897

```
BLAST score
                   437
                   3.0e-42
E value
Match length
                   738
% identity
                   29
                   (U59626) LEA protein [Glycine max]
NCBI Description
Seq. No.
                   1400
                   733 36.R1040
Contig ID
5'-most EST
                   hyd700729149.hl
Method
                   BLASTX
NCBI GI
                   q1945447
BLAST score
                   1140
E value
                   0.0e + 00
Match length
                   661
% identity
                   63
                   (U94395) 90-kDa heat shock protein [Sus scrofa]
NCBI Description
                   1401
Seq. No.
                   733 37.R1040
Contig ID
5'-most EST
                   ncj700983392.hl
Method
                   BLASTX
                   g417154
NCBI GI
BLAST score
                   794
E value
                   0.0e + 00
                   630
Match length
% identity
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   1402
Contig ID
                   733 38.R1040
5'-most EST
                   LIB3065-019-Q1-N1-G7
Method
                   BLASTX
NCBI GI
                   q547683
BLAST score
                   998
E value
                   1.0e-177
Match length
                   647
% identity
                   72
NCBI Description
                   HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat
                   shock cognate protein 80 [Solanum lycopersicum]
                   >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
Seq. No.
                   1403
Contig ID
                   733 39.R1040
5'-most EST
                   LIB3040-018-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   g135404
BLAST score
                   817
E value
                   1.0e-114
                   419
Match length
                   54
% identity
                   TUBULIN ALPHA-1/ALPHA-2 CHAIN >gi_81291_pir__S04694 tubulin
NCBI Description
                   alpha chain - Volvox carteri f. nagariensis
```

>gi 22001 emb CAA31326 (X12846) alpha-1 tubulin [Volvox

```
carteri]
Seq. No.
                   1404
                   734 1.R1040
Contig ID
                   LIB3170-037-Q1-K1-H4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4467145
BLAST score
                   657
E value
                   7.0e-69
Match length
                   154
% identity
                   81
                   (AL035540) farnesylated protein (ATFP6) [Arabidopsis
NCBI Description
                   thaliana]
                   1405
Seq. No.
                   734 2.R1040
Contig ID
                   awf700836821.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4097572
                   567
BLAST score
                   0.0e + 00
E value
Match length
                   583
% identity
                   Glycine max farnesylated protein GMFP7 mRNA, partial cds
NCBI Description
                   1406
Seq. No.
Contig ID
                   734 3.R1040
5'-most EST
                   LIB3051-084-Q1-K1-A8
Method
                   BLASTN
NCBI GI
                   q4097572
BLAST score
                   67
E value
                   3.0e-29
Match length
                   178
% identity
                   88
NCBI Description
                   Glycine max farnesylated protein GMFP7 mRNA, partial cds
Seq. No.
                   735 1.R1040
Contig ID
                   awf700837424.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1732555
                   570
BLAST score
E value
                   0.0e + 00
Match length
                   610
% identity
                   98
NCBI Description
                   Glycine max desiccation protective protein LEA5 (Lea5)
                   mRNA, complete cds
Seq. No.
                   1408
                   737 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy047e10b1
Method
                   BLASTN
NCBI GI
                   g1763062
BLAST score
                   955
E value
                   0.0e + 00
Match length
                   981
```

carteri] >gi 404089 (L24546) alpha-2 tubulin [Volvox

```
99
% identity
                   Glycine max putative transcription factor SCOF-1 (scof-1)
NCBI Description
                   mRNA, complete cds
                   1409
Seq. No.
                   737 2.R1040
Contig ID
                   LIB3050-022-Q1-K1-G11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1763063
BLAST score
                   640
E value
                   1.0e-66
Match length
                   233
% identity
                   62
NCBI Description
                   (U68763) SCOF-1 [Glycine max]
                   1410
Seq. No.
Contig ID
                   737 3.R1040
5'-most EST
                   LIB3092-016-Q1-K1-B12
Method
                   BLASTN
NCBI GI
                   q1763062
BLAST score
                   115
E value
                   7.0e-58
Match length
                   281
% identity
                   93
                  Glycine max putative transcription factor SCOF-1 (scof-1)
NCBI Description
                   mRNA, complete cds
Seq. No.
                   1411
                   737 4.R1040
Contig ID
5'-most EST
                   rlr700899402.h1
Method
                   BLASTX
NCBI GI
                   q439493
BLAST score
                   145
E value
                   4.0e-09
Match length
                   64
% identity
                   (D26086) zinc-finger protein [Petunia x hybrida]
NCBI Description
Seq. No.
                   1412
                   737 7.R1040
Contig ID
5'-most EST
                   jC-gmle01810050c10a1
Seq. No.
                   1413
                   738 1.R1040
Contig ID
                   LIB3107-008-Q1-K1-A11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2501764
BLAST score
                   2555
E value
                   0.0e + 00
                   490
Match length
                   100
% identity
                   (U69173) calmodulin-like domain protein kinase isoenzyme
NCBI Description
                   beta [Glycine max]
Seq. No.
                   1414
                   739 4.R1040
Contig ID
```

crh700854956.h1

5'-most EST

Seq. No.

```
Method
                   BLASTN
                   g2501765
NCBI GI
BLAST score
                   136
E value
                   3.0e-70
Match length
                   364
                   84
% identity
                  Glycine max calmodulin-like domain protein kinase isoenzyme
NCBI Description
                   gamma mRNA, complete cds
                   1415
Seq. No.
                   739 5.R1040
Contig ID
                   smc700746856.hl
5'-most EST
Method
                   BLASTN
                   g18764
NCBI GI
BLAST score
                   163
E value
                   2.0e-86
Match length
                   267
                   90
% identity
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
Seq. No.
                   1416
                   739_6.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy207f02b1
Method
                   BLASTN
                   g2501765
NCBI GI
BLAST score
                   287
                   1.0e-160
E value
                   703
Match length
                   93
% identity
                   Glycine max calmodulin-like domain protein kinase isoenzyme
NCBI Description
                   gamma mRNA, complete cds
                   1417
Seq. No.
                   739_7.R1040
Contig ID
                   uC-gmrominsoy049b08b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2501766
BLAST score
                   2789
E value
                   0.0e + 00
Match length
                   538
                   100
% identity
                   (U69174) calmodulin-like domain protein kinase isoenzyme
NCBI Description
                   gamma [Glycine max]
                                                                         4
Seq. No.
                   1418
Contig ID
                   739 8.R1040
5'-most EST
                   LIB3040-013-Q1-E1-C12
Method
                   BLASTX
NCBI GI
                   g1352345
BLAST score
                  1055
E value
                   0.0e + 00
Match length
                   438
                   77
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_18765_emb_CAA40182_ (X56856) eEF-la [Glycine max]
```

Seq. No.

```
Contig ID
                   739 9.R1040
5'-most EST
                   crh700853432.hl
Method
                   BLASTN
NCBI GI
                   g2598656
BLAST score
                   600
                   0.0e+00
E value
Match length
                   1360
                   8.7 ·
% identity
NCBI Description
                   Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
Seq. No.
                   1420
Contig ID
                   739 10.R1040
5'-most EST
                   jC-qmro02910011c12a1
Method
                   BLASTN
                   g2598656
NCBI GI
BLAST score
                   662
E value
                   0.0e + 00
Match length
                   1510
                   88
% identity
                   Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
NCBI Description
                   1421
Seq. No.
Contig ID
                   739_11.R1040
                   jC-gmle01810062e02a1
5'-most EST
                   BLASTN
Method
                   g18764
NCBI GI
BLAST score
                   704
E value
                   0.0e + 00
Match length
                   1440
% identity
NCBI Description
                   G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                   1422
Contig ID
                   740 1.R1040
5'-most EST
                   LIB3029-003-Q1-B1-G2
Method
                   BLASTN
NCBI GI
                   q4097893
BLAST score
                   399
E value
                   0.0e+00
Match length
                   658
% identity
                   96
NCBI Description
                   Glycine max napin-type 2S albumin 1 precursor, mRNA,
                   complete cds
Seq. No.
                   1423
Contig ID
                   744 1.R1040
5'-most EST
                   zhf700956541.h1
Method
                   BLASTN
NCBI GI
                   g1778822
BLAST score
                   745
E value
                   0.0e+00
Match length
                   757
% identity
                   100
                   Glycine max early light-induced protein (ELIP) mRNA,
NCBI Description
                   complete cds
```

```
744 2.R1040
Contig ID
5'-most EST
                  uC-gmropic014a06b1
Method
                  BLASTX
NCBI GI
                  g3650037
BLAST score
                  1336
                  1.0e-180
E value
                  398
Match length
                  80
% identity
                   (AC005396) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  1425
Seq. No.
Contig ID
                  744 3.R1040
                  rlr700902458.h1
5'-most EST
                  BLASTN
Method
                  g1778822
NCBI GI
                  377
BLAST score
                  0.0e + 00
E value
                  449
Match length
                  96
% identity
NCBI Description
                  Glycine max early light-induced protein (ELIP) mRNA,
                  complete cds
                  1426
Seq. No.
Contig ID
                  744 4.R1040
5'-most EST
                  LIB3138-081-P1-N1-C3
Method '
                  BLASTN
NCBI GI
                  g1778822
BLAST score
                  230
E value
                  1.0e-126
Match length
                  340
% identity
                  Glycine max early light-induced protein (ELIP) mRNA,
NCBI Description
                  complete cds
                  1427
Seq. No.
                                                                3\epsilon_2 + \epsilon
Contig ID
                  745_1.R1040
                  uC-gmflminsoy054b09b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2769671
BLAST score
                  1289
E value
                  0.0e + 00
Match length
                  1297
                  100
% identity
                  Glycine max alternative oxidase (Aox2) mRNA, nuclear gene
NCBI Description
                  encoding mitochondrial protein, complete cds
Seq. No.
                  1428
Contig ID
                  746 1.R1040
5'-most EST
                  g1946337 FL
Method
                  BLASTN
NCBI GI
                  g1946337
BLAST score
                  1206
E value
                  0.0e + 00
Match length
                  1220
                  93
% identity
```

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Match length

167

## encoding mitochondrial protein, complete cds

```
1429
Seq. No.
Contig ID
                   746 2.R1040
                   wrq700788036.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1946337
BLAST score
                   164
E value
                   5.0e-87
Match length
                   253
                   84
% identity
                   Glycine max alternative oxidase (Aox3) mRNA, nuclear gene
NCBI Description
                   encoding mitochondrial protein, complete cds
                   1430
Seq. No.
                   748 1.R1040
Contig ID
                   LIB3170-071-Q1-K1-B9
5'-most EST
Method
                   BLASTN .
NCBI GI
                   g18737
BLAST score
                   543
E value
                   0.0e + 00
Match length
                   890
                   14
% identity
NCBI Description
                   Glycine max RPRP3 gene for repetitive proline-rich protein
                   1431
Seq. No.
                   748 2.R1040
Contig ID
                   uC-gmrominsoy088g05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4263704
BLAST score
                   744
                   9.0e-79
E value
Match length
                   246
% identity
                   61
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   1432
                   748 3.R1040
Contig ID
5'-most EST
                   q4289852
Method
                   BLASTX
NCBI GI
                   q4263704
BLAST score
                   205
E value
                   1.0e-15
Match length
                   79
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
                   1433
Seq. No.
Contig ID
                   748 4.R1040
5'-most EST
                   jC-gmst02400023b02a1
Method
                   BLASTX
NCBI GI
                   g4263704
BLAST score
                   501
E value
                   2.0e-50
```

5'-most EST

Method

```
% identity
                   61
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana].
Seq. No.
                   1434
                   748 5.R1040
Contig ID
                   uC-gmropic019e04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4263704
                   495
BLAST score
                   8.0e-50
E value
                   187
Match length
% identity
                   56.
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                   1435
Seq. No.
                   748 6.R1040
Contig ID
                   q4405568
5'-most EST
Method
                   BLASTX
                   g4263704
NCBI GI
BLAST score
                   194
E value
                   2.0e-28
Match length
                   128
                   59
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
                   1436
Seq. No.
                   748 11.R1040
Contig ID
5'-most EST
                   LIB3139-064-P1-N1-C7
                   BLASTN
Method
NCBI GI
                   q255407
BLAST score
                   244
E value
                   1.0e-134
Match length
                   706
% identity
NCBI Description
                   repetitive proline-rich protein {cDNA clone 1A10-2}
                   [Glycine max=soybeans, axes germinated for 31 hours, mRNA,
                   943 ntl
Seq. No.
                   1437
Contig ID
                   748 13.R1040
5'-most EST
                   k11701202974.h1
Method
                   BLASTN
NCBI GI
                   g170048
BLAST score
                   281
E value
                   1.0e-157
Match length
                   400
% identity
                   Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                   complete cds
Seq. No.
                   1438
                   748 16.R1040
Contig ID
```

LIB3051-011-Q1-E1-F1

BLASTN

NCBI GI

```
NCBI GI
                   g170065
                   350
BLAST score
                   0.0e+00
E value
                   825
Match length
                   26
% identity
                   Soybean (G.max) proline-rich cell wall protein (SbPRP2)
NCBI Description
                   gene, complete cds
                   1439
Seq. No.
                   751 1.R1040
Contig ID
                   LIB\overline{3}139-075-P1-N1-D6
5'-most EST
                   BLASTN
Method
                   g1196896
NCBI GI
BLAST score
                   1168
                   0.0e+00
E value
                   1243
Match length
                   99
% identity
                   Glycine max acidic ribosomal protein PO mRNA, complete cds
NCBI Description
                   1440
Seq. No.
                   751 2.R1040
Contig ID
                   uC-gmropic0001e04b1
5'-most EST
                   BLASTN
Method
                   q1196896
NCBI GI
BLAST score
                   491
                   0.0e + 00
E value
Match length
                   848
                   92
% identity
                   Glycine max acidic ribosomal protein PO mRNA, complete cds
NCBI Description
                   1441
Seq. No.
                   751 3.R1040
Contig ID
                   kl1701212451.h1
5'-most EST
Method
                   BLASTN
                   g1196896
NCBI GI
BLAST score
                   227
E value
                   1.0e-124
                   358
Match length
                   95
% identity
                   Glycine max acidic ribosomal protein PO mRNA, complete cds
NCBI Description
                   1442
Seq. No.
                   753 1.R1040
Contig ID
5'-most EST
                   ncj700987283.hl
                   BLASTX
Method
NCBI GI
                   q1346501
BLAST score
                   1517
E value
                   0.0e+00
Match length
                   352
                   95
% identity
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
Seq. No.
                   1443
Contig ID
                   754 1.R1040
5'-most EST
                   g310569_FL
Method
                   BLASTN
```

g310569

5'-most EST

```
932
BLAST score
                   0.0e + 00
E value
                   1004
Match length
                   98
% identity
NCBI Description
                  Glycine max seed maturation protein (GmPM3) mRNA, complete
                   1444
Seq. No.
                   755 1.R1040
Contig ID
5'-most EST
                   LIB3049-009-Q1-E1-F10
Method '
                   BLASTX
NCBI GI
                   g1170878
BLAST score
                   2971
                   0.0e + 00
E value
                   563
Match length
                   100
% identity
                  MALATE SYNTHASE, GLYOXYSOMAL (MS) >gi_170026 (L01629)
NCBI Description
                   malate synthase [Glycine max]
                   1445
Seq. No.
Contig ID
                   755_2.R1040
5'-most EST
                   fC-gmst700653114f4
Method
                   BLASTX
NCBI GI
                   g2708743
BLAST score
                   180 .
                   8.0e-13
E value
Match length
                   184
                   28
% identity
                   (AC003952) putative Tal-1-like reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   1446
Contig ID
                   755_3.R1040
5'-most EST
                   fC-gmst700653647r1
Method
                   BLASTX
NCBI GI
                   g4262236
BLAST score
                   229
E value
                  2.0e-18
                   238
Match length
% identity
                   (AC006200) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
                   1447
Seq. No.
                   755 4.R1040
Contig ID
5'-most EST
                   jC-\overline{g}mst02400054a05a1
Method
                   BLASTN
NCBI GI
                   g170025
BLAST score
                   165
                   1.0e-87
E value
Match length
                   257
% identity
NCBI Description
                  Soybean malate synthase (MS) mRNA, 3' end
Seq. No.
                   1448
                   755 5.R1040
Contig ID
```

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zpv700758222.hl

NCBI GI

```
BLASTN
Method
NCBI GI
                   g170025
BLAST score
                   88
E value
                   7.0e-42
Match length
                   136
                   91
% identity
                   Soybean malate synthase (MS) mRNA, 3' end
NCBI Description
                   1449
Seq. No.
                   755_6.R1040
Contig ID
                   uC-gmflminsoy010h05b1
5'-most EST
Method
                   BLASTN
                   g170025
NCBI GI
                   254
BLAST score
                   1.0e-141
E value
Match length
                   410
                   91
% identity
                   Soybean malate synthase (MS) mRNA, 3' end
NCBI Description
                   1450
Seq. No.
                   755_8.R1040
Contig ID
5'-most EST
                   LIB3170-065-Q1-K1-E5
                   BLASTN
Method
NCBI GI
                   g170025
BLAST score
                   185
                   2.0e-99
E value
Match length
                   188
                   99
% identity
                  Soybean malate synthase (MS) mRNA, 3' end
NCBI Description
                   1451
Seq. No.
                   755_9.R1040
Contig ID
                   txt700736239.h1
5'-most EST
                   BLASTN
Method
                   g170025
NCBI GI
BLAST score
                   407
E value
                   0.0e+00
Match length
                   575
                   93
% identity
                   Soybean malate synthase (MS) mRNA, 3' end
NCBI Description
Seq. No.
                   1452
                   755 10.R1040
Contig ID
                   jC-gmst02400008b12d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170025
BLAST score
                   75
E value
                   5.0e-34
Match length
                   107
                   93
% identity
                  Soybean malate synthase (MS) mRNA, 3' end
NCBI Description
Seq. No.
                   1453
                   756 1.R1040
Contig ID
                   jsh701070153.hl
5'-most EST
Method
                   BLASTX
```

g1362051

```
BLAST score
                   1711
E value
                   0.0e + 00
Match length
                   351
                   94
% identity
                   protein kinase 3 - soybean >gi 310582 (L19361) protein
NCBI Description
                   kinase 3 [Glycine max]
                   1454
Seq. No.
                   756 2.R1040
Contig ID
5'-most EST
                   ncj700982236.hl
Method
                   BLASTX
NCBI GI
                   g1161254
BLAST score
                   1710
E value
                   0.0e+00
Match length
                   349
% identity
                   94
NCBI Description
                   (L38855) protein kinase [Glycine max]
                   1455
Seq. No.
                   756 3.R1040
Contig ID
5'-most EST
                   sat701011327.h1
                   1456
Seq. No.
                   756 4.R1040
Contig ID
5'-most EST
                   LIB3138-101-Q1-N1-G4
Seq. No.
                   1457
Contig ID
                   756 8.R1040
                   eep700869793.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1161253
BLAST score
                   137
                   8.0e-71
E value
Match length
                   137
                   100
% identity
                  Glycine max protein kinase (SPK-4) mRNA, complete cds
NCBI Description
Seq. No.
                   1458
                   756_9.R1040
Contig ID
5'-most EST
                   LIB3138-124-Q1-N1-E11
                   BLASTN
Method
NCBI GI
                   g1161253
BLAST score
                   255
E value
                   1.0e-141
                   295
Match length
% identity
NCBI Description
                  Glycine max protein kinase (SPK-4) mRNA, complete cds
Seq. No.
                   1459
Contig ID
                   758 1.R1040
5'-most EST
                   LIB3109-056-Q1-K1-A4
Method
                   BLASTN
NCBI GI
                   q986966
BLAST score
                   1200
                   0.0e + 00
E value
Match length
                   1265
```

99

% identity

```
NCBI Description Glycine max TGACG-motif binding factor (STF2) mRNA,
                  complete cds
                  1460
Seq. No.
                  758 2.R1040
Contig ID
5'-most EST
                  fde700873235.h1
                  BLASTN
Method
                  g2934883
NCBI GI
BLAST score
                  1215
E value
                  0.0e+00
                  1215
Match length
                  100
% identity
NCBI Description
                  Glycine max TGACG-motif binding protein (STF1) mRNA,
                  complete cds
                  1461
Seq. No.
                  758 5.R1040
Contig ID
5'-most EST
                  hyd700730858.h1
Method
                  BLASTN
                  g986966
NCBI GI
                  151 ,
BLAST score
                  2.0e-79
E value
                  155
Match length
                  99
% identity
                  Glycine max TGACG-motif binding factor (STF2) mRNA,
NCBI Description
                  complete cds
                  1462
Seq. No.
Contig ID
                  760 1.R1040
5'-most EST
                  zpv700761071.hl
Method
                  BLASTX
                  g2353333
NCBI GI
BLAST score
                  211
E value
                  3.0e-16
Match length
                  158
% identity
NCBI Description
                  (AF016513) Ce-LEA [Caenorhabditis elegans]
                  >gi_3924819_emb_CAB05543_ (Z83113) cDNA EST EMBL:D26945
                  comes from this gene; cDNA EST EMBL: D26944 comes from this
                  gene; cDNA EST EMBL: D26943 comes from this gene; cDNA EST
                  EMBL: D26942 comes from this gene; cDNA EST EMBL: D35244
                  comes from this gene; cDN
Seq. No.
                  1463
                  761_1.R1040
Contig ID
                  uC-gmropic112b10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3164115
BLAST score
                  256
E value
                  1.0e-21
Match length
                  145
% identity
NCBI Description
                  (AJ224145) major latex-like protein [Rubus idaeus]
Seq. No.
                  1464
```

761 2.R1040

LIB3139-048-P1-N1-G3

Contig ID 5'-most EST

BLAST score

320

```
Method
                   BLASTX
NCBI GI
                   q2465015
BLAST score
                   273
E value
                   1.0e-23
Match length
                   152
% identity
                   40
                   (AJ001449) ripening-induced protein [Fragaria vesca]
NCBI Description
                   1465
Seq. No.
                   761 3.R1040
Contig ID
5'-most EST
                   LIB3106-006-Q1-K2-C4
Seq. No.
                   1466
                   761 4.R1040
Contig ID
                   LIB3139-079-P1-N1-B2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2465015
BLAST score
                   267
E value
                   6.0e-23
Match length
                   152
% identity
                   40
NCBI Description
                   (AJ001449) ripening-induced protein [Fragaria vesca]
                   1467
Seq. No.
                   761 5.R1040
Contig ID
5'-most EST
                   asn701134581.h1
                   1468
Seq. No.
                   764 1.R1040
Contig ID
                   LIB3093-045-Q1-K1-H7
5'-most EST
Method
                   BLASTN
NCBI GI
                   g21028
                   469
BLAST score
                   0.0e+00
E value
Match length
                   949
% identity
                   87
NCBI Description
                   P.vulgaris pgip gene for polygalacturonase-inhibiting
                  protein
                   1469
Seq. No.
Contig ID
                   765 1.R1040
5'-most EST
                   ncj\overline{7}00979033.h1
Method
                   BLASTX
NCBI GI
                   q3747089
BLAST score
                   2160
E value
                   0.0e + 00
Match length
                   409
% identity
NCBI Description
                   (AF095445) NADP-dependent isocitrate dehydrogenase [Glycine
                   max]
Seq. No.
                   1470
Contig ID
                   765 2.R1040
5'-most EST
                   fua701040651.h1
Method
                   BLASTN
NCBI GI
                   q3747088
```

Contig ID

```
E value
                   1.0e-180
                   532
Match length
                   98
% identity
                  Glycine max NADP-dependent isocitrate dehydrogenase (IDH1)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   1471
                   765 3.R1040
Contig ID
5'-most EST
                   kll701213049.hl
                   BLASTN
Method
                   g3747088
NCBI GI
                   91
BLAST score
E value
                   1.0e-43
                   123
Match length
                   93
% identity
                  Glycine max NADP-dependent isocitrate dehydrogenase (IDH1)
NCBI Description
                   mRNA, complete cds
                   1472
Seq. No.
                   769 1.R1040
Contig ID
                   LIB\overline{3}109-016-Q1-K1-F8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3128220
BLAST score
                   1167
                   1.0e-128
E value
Match length
                   253
% identity
                   (AC004077) putative urease accessory protein [Arabidopsis
NCBI Description
                   thaliana] >gi_3337375 (AC004481) putative urease accessory
                   protein [Arabidopsis thaliana]
                   1473
Seq. No.
                   770 1.R1040
Contig ID
                   sat701011252.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2462753
BLAST score
                   1390
                   1.0e-154
E value
Match length
                   407
% identity
                   (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                   thaliana]
                   1474
Seq. No.
Contig ID
                   773 1.R1040
5'-most EST
                   LIB3139-032-P1-N1-A4
Method
                   BLASTX
NCBI GI
                   q4559342
BLAST score
                   3226
E value
                   0.0e + 00
Match length
                   701
% identity
                   (AC007087) putative copper methylamine oxidase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   1475
```

774 1.R1040

```
LIB3039-044-Q1-E1-C5
5'-most EST
Method
                  BLASTX
                  q3023858
NCBI GI
BLAST score
                  1690
                  0.0e + 00
E value
                  325
Match length
                  98
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 1256608 (U44850) G protein beta subunit
                  [Glycine max]
                  1476
Seq. No.
                  774 3.R1040
Contig ID
                  LIB3138-087-P1-N1-A5
5'-most EST
Method
                  BLASTN
                  q1256607
NCBI GI
BLAST score
                  270
                  1.0e-150
E value
                  290
Match length
% identity
NCBI Description Glycine max G protein beta subunit mRNA, complete cds
Seq. No.
                  1477
Contig ID
                  774 4.R1040
5'-most EST
                  LIB3087-012-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  q1256607
BLAST score
                  166
E value
                  2.0e-88
Match length
                  210
% identity
                  96
                  Glycine max G protein beta subunit mRNA, complete cds
NCBI Description
                  1478
Seq. No.
Contig ID
                  774 5.R1040
5'-most EST
                  LIB3170-039-Q1-K2-G12
Method
                  BLASTX
                  g3023847
NCBI GI
                  144
BLAST score
                  3.0e-09
E value
Match length
                  70
                  57
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                  subunit-like [Medicago sativa]
                  1479
Seq. No.
                  775_1.R1040
Contig ID
                  kll701203226.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  q20562
                  152
BLAST score
                  7.0e-80
E value
                  368
Match length
                  85
% identity
```

NCBI Description P.hybrida myb.Ph3 gene encoding protein

. .:

```
1480
Seq. No.
                   776 1.R1040
Contig ID
                   smc700744417.hl
5'-most EST
Method
                   BLASTX
                   g1002800
NCBI GI
BLAST score
                   586
                   1.0e-60
E value
Match length
                   126
% identity
                   81
                   (U33917) Cpm7 [Craterostigma plantagineum]
NCBI Description
                   1481
Seq. No.
                   777_1.R1040
Contig ID
                   qsv701044385.hl
5'-most EST
Method
                   BLASTX
                   q2605621
NCBI GI
                   402
BLAST score
                   2.0e-39
E value
                   100
Match length
% identity
                   74
                   (D88619) OSMYB3 [Oryza sativa]
NCBI Description
                   1482
Seq. No.
Contig ID
                   779.1.R1040
                   LIB3028-029-Q1-B1-E11
5'-most EST
Method
                   BLASTX
NCBI GI
                   a2129563
BLAST score
                   466
E value
                   1.0e-46
Match length
                   98
% identity
                   88
                   cM4 protein - Arabidopsis thaliana >gi_928928_emb_CAA62030_
NCBI Description
                   (X90382) cM4 [Arabidopsis thaliana]
Seq. No.
                   1483
Contig ID
                   780 1.R1040
5'-most EST
                   fC-qmse700672319f2
Method
                   BLASTX
NCBI GI
                   q1101770
BLAST score
                   566
E value
                   3.0e-58
Match length
                   150
% identity
                   69
                   (U39448) MYB-like transcriptional factor MBF1 [Picea
NCBI Description
                   mariana]
Seq. No.
                   1484
                   783 1.R1040
Contig ID
                   gsv701056550.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3334665
BLAST score
                   1162
E value
                   1.0e-127
Match length
                   502
% identity
                   46
                   (Y10492) putative cytochrome P450 [Glycine max]
NCBI Description
```

NCBI Description

```
1485
Seq. No.
                   783 2.R1040
Contig ID
5'-most EST
                   hyd700730654.h1
Method
                   BLASTX
NCBI GI
                   g4538911
BLAST score
                   676
E value
                   6.0e-71
Match length
                   183
% identity
NCBI Description
                   (AL049482) hypothetical protein [Arabidopsis thaliana]
                   1486
Seq. No.
                   785 1.R1040
Contig ID
                   rca700998785.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3318611
BLAST score
                   1632
E value
                   0.0e + 00
Match length
                   375
% identity
                   86
NCBI Description
                   (AB016063) mitochondrial phosphate transporter [Glycine
                   1487
Seq. No.
                   785 3.R1040
Contig ID
                                                          15
5'-most EST
                   jC-gmro02910075b05a1
Method
                   BLASTN
NCBI GI
                   g3318610
BLAST score
                   257
E value
                   1.0e-142
Match length
                   378
% identity
                   93
                  Glycine max mRNA for mitochondrial phosphate transporter,
NCBI Description
                  complete cds
Seq. No.
                   1488
                   786 1.R1040
Contig ID
5'-most EST
                  rlr700899175.hl
Method
                  BLASTN
                  g2765444
NCBI GI
BLAST score
                   616
E value
                  0.0e+00
Match length
                  730
                  98
% identity
NCBI Description Glycine max mRNA for ferredoxin thioredoxin reductase
                  1489
Seq. No.
Contig ID
                  787 1.R1040
5'-most EST
                  g4294555
Method
                  BLASTX
NCBI GI
                  g1402878
                  208
BLAST score
E value
                  2.0e-16
Match length
                  55
% identity
                  67
```

(X98130) unknown [Arabidopsis thaliana]

Match length

84

```
1490
Seq. No.
                   787_2.R1040
Contig ID
5'-most EST
                   LIB3028-056-Q1-B1-A5
                   1491
Seq. No.
Contig ID
                   787 3.R1040
5'-most EST
                   uC-gmrominsoy200e09b1
                   BLASTX
Method
                   g4455208
NCBI GI
BLAST score
                   280
                   1.0e-24
E value
Match length
                   81
% identity
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   787 4.R1040
Contig ID
5'-most EST
                   uC-gmropic041f08b1
Method
                   BLASTN
NCBI GI
                   g436789
BLAST score
                   49
                   4.0e-18
E value
Match length
                   108
                   86
% identity
NCBI Description Tobacco RNA-binding glycine-rich protein (RGP-1a) mRNA
                   1493
Seq. No.
Contig ID
                   787 5.R1040
                  LIB3051-083-Q1-K1-D8
5'-most EST
Method
                   BLASTN
                   g2267568
NCBI GI
BLAST score
                   56
E value
                   3.0e-22
Match length
                   266
% identity
                   83
                   Pelargonium x hortorum glycine-rich RNA binding protein 2
NCBI Description
                   (GRP2) precursor mRNA, complete cds
                   1494
Seq. No.
Contig ID
                   787 6.R1040
5'-most EST
                   LIB3106-033-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                  q4455208
BLAST score
                   155
E value
                   7.0e-10
Match length
                   101
% identity
NCBI Description
                  (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   787 7.R1040
5'-most EST
                   vwf700678078.hl
Method
                  BLASTX
NCBI GI
                  q544424
BLAST score
                  163
E value
                   7.0e-14
```

```
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir_S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                   [Arabidopsis thaliana] >gi 166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                   1496
Seq. No.
                   787 8.R1040
Contig ID
5'-most EST
                   LIB3106-060-Q1-K1-B10
Method
                   BLASTX
                   g2267567
NCBI GI
BLAST score
                   158
E value
                   4.0e-10
                   91
Match length
% identity
                   (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                   x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding
                   protein 2 [Pelargonium x hortorum]
                   1497
Seq. No.
                   787 9.R1040
Contig ID
                   zhf700956043.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4455208
BLAST score
                   488
                   8.0e-49
E value
                   163
Match length
                   49
% identity
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   1498
Seq. No.
                   788 1.R1040
Contig ID
                   LIB3030-010-Q1-B1-B10
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2244811
BLAST score
                   680
                   1.0e-73
E value
Match length
                   209
                   76
% identity
                   (Z97336) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   1499
Seq. No.
                   788 2.R1040
Contig ID
5'-most EST
                   q42\overline{6}0108
Method
                   BLASTN
NCBI GI
                   g972916
BLAST score
                   122
E value
                   1.0e-61
Match length
                   254
% identity
                   87
                  Arabidopsis thaliana IAA7 (IAA7) gene, complete cds
NCBI Description
```

1500

788 3.R1040

Seq. No. Contig ID

5'-most EST

```
5'-most EST
                  LIB3106-034-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g117290
BLAST score
                  1660
                  0.0e + 00
E value
Match length
                  392
% identity
                  84
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
NCBI Description
                  (P36) (E30) >gi 100071 pir S23774 triose
                  phosphate/3-phosphoglycerate/phosphate translocator
                  precursor - garden pea >gi_20691_emb CAA38451 (X54639)
                  chloroplast import receptor p36 [Pisum sativum]
                  >gi 20853 emb CAA48210 (X68077) phosphate translocator
                  [Pisum sativum] >gi 228551 prf 1805409A phosphate
                  translocator [Pisum sativum]
                  1501
Seq. No.
Contig ID
                  788 5.R1040
                  asn701136914.h1
5'-most EST
                  BLASTX
Method
                  q1363487
NCBI GI
BLAST score
                  326
E value
                  3.0e-30
Match length
                  96
                  71
% identity
                  IAA7 protein - Arabidopsis thaliana >gi 972917 (U18409)
NCBI Description
                  IAA7 [Arabidopsis thaliana]
                  1502
Seq. No.
Contig ID
                  790 1.R1040
5'-most EST
                  LIB3073-002-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1717975
                  279
BLAST score
E value
                  1.0e-24
Match length
                  98
                  49
% identity
                  14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114
NCBI Description
                  ANTIGEN HOMOLOG) >gi 1177435 emb CAA64670 (X95384) 14.5
                  kDa translational inhibitor protein, p14.5 [Homo sapiens]
                  1503
Seq. No.
Contig ID
                  791 1.R1040
5'-most EST
                  kl1701208271.h1
Method
                  BLASTX
                  q3176673
NCBI GI
BLAST score
                  210
                  2.0e-16
E value
Match length
                  76
% identity
                  (AC003671) Similar to serine/threonine kinase gb Y12531
NCBI Description
                  from Brassica oleracea. [Arabidopsis thaliana]
Seq. No.
Contig ID
                  791 5:R1040
```

*3*7.

LIB3170-028-Q1-K1-B10

```
1505
Seq. No.
Contig ID
                   793 1.R1040
                   uxk700667991.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g687844
BLAST score
                   283
E value
                   5.0e-25
Match length
                   172
% identity
NCBI Description
                   (U21320) contains TPR domain-like repeats [Caenorhabditis
                   elegans]
                   1506
Seq. No.
                   793 2.R1040
Contig ID
5'-most EST
                   LIB3049-001-Q1-E1-C7
                   1507
Seq. No.
                   794 1.R1040
Contig ID
5'-most EST
                   LIB3106-104-Q1-K1-G8
                   BLASTX
Method
NCBİ GI
                   g3859570
BLAST score
                   322
E value
                   9.0e-30
Match length
                   132
% identity
                   54
                   (AF098753) unknown [Oryza sativa]
NCBI Description
Seq. No.
                   799 1.R1040
Contig ID
5'-most EST
                   ssr700556237.h1
                   1509
Seq. No.
                   800 1.R1040
Contig ID
5'-most EST
                   2DA-01-Q1-B1-A9
Seq. No.
                   1510
Contig ID
                   801 1.R1040
5'-most EST
                   kmv700738580.h1
Method
                  BLASTX
NCBI GI
                   g4006868
BLAST score
                   201
                   3.0e-15
E value
                  144
Match length
% identity
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                  1511
                  802 1.R1040
Contig ID
5'-most EST
                  g5677474
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  507
                  1.0e-51
E value
Match length
                  127
% identity
NCBI Description
                   (AF091455) translationally controlled tumor protein [Hevea
```

brasiliensis]

E value

```
Seq. No.
                   1512
Contig ID
                   803 1.R1040
5'-most EST
                   LIB3107-017-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   q2623199
BLAST score
                   787
E value
                   3.0e-84
Match length
                   151
                   99
% identity
                   (AF030290) protein phosphatase X isoform 2 [Arabidopsis
NCBI Description
                   thaliana]
                   1513
Seq. No.
Contig ID
                   803 3.R1040
5'-most EST
                   pxt700946264.hl
Method
                   BLASTX
NCBI GI
                   g2623199
BLAST score
                   273
E value
                   2.0e-24
Match length
                   56
% identity
                   95
                   (AF030290) protein phosphatase X isoform 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   1514
                   805 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810062a02a1
Method
                   BLASTN
NCBI GI
                   g3128138
BLAST score
                   59
                   3.0e-24
E value
Match length
                   478
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFO20, complete sequence [Arabidopsis thaliana]
                   1515
Seq. No.
                   808 1.R1040
Contig ID
5'-most EST
                   LIB3093-005-Q1-K1-A11
Method
                   BLASTX
                   g1723562
NCBI GI
BLAST score
                   105
                   5.0e-12
E value
Match length
                   102
% identity
                   42
                   PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03
NCBI Description
                   >qi 1314155 emb CAA97349 (Z73099) probable initiation
                   factor [Schizosaccharomyces pombe]
Seq. No.
                   1516
                   808 2.R1040
Contig ID
5'-most EST
                   2DA-01-Q1-B1-B6
Method
                   BLASTX
NCBI GI
                   g2895097
BLAST score
                   294
```

2.0e-26

BLAST score

477

```
Match length
                   128
% identity
                   47
NCBI Description
                   (AF012072) eIF4GII [Homo sapiens]
                   >gi 4503541 ref NP 003751.1 pEIF4G3 UNKNOWN
Seq. No.
Contig ID
                   809 1.R1040
5'-most EST
                  pcp700990419.h1
Seq. No.
Contig ID
                   810 1.R1040
5'-most EST
                   2DA-01-Q1-B1-B8
Method
                   BLASTX
NCBI GI
                   q3426039
BLAST score
                   324
E value
                   6.0e-30
Match length
                   129
% identity
NCBI Description
                   (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   1519
Contig ID
                   811_1.R1040
5'-most EST
                   2DA-01-Q1-B1-B9
Method
                  BLASTX
NCBI GI
                   g231551
BLAST score
                   158
E value
                   2.0e-10
Match length
                   124
% identity
                   3
NCBI Description
                  ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN,
                  NONERYTHROID)
                  1520
Seq. No.
                  811 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy124b05b1
                  1521
Seq. No.
                  813 1.R1040
Contig ID
5'-most EST
                  LIB3051-065-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g416873
                  260
BLAST score
E value
                  2.0e-22
                  96
Match length
                  53
% identity
NCBI Description
                  3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH)
                  >gi 111295 pir A32867 3-hydroxyisobutyrate dehydrogenase
                   (EC 1.1.1.31) precursor - rat (fragment) >gi_556389
                   (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus
                  norvegicus]
Seq. No.
                  1522
                  815 1.R1040
Contig ID
5'-most EST
                  epx701105596.h1
Method
                  BLASTX
NCBI GI
                  g2832300
```

.....

BLAST score

288

```
9.0e-48
E value
Match length
                  118
% identity
                  75
NCBI Description
                   (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
                  roseusl
                  1523
Seq. No.
Contig ID
                  817 1.R1040
5'-most EST
                  LIB3040-014-Q1-E1-F1
Method
                  BLASTX
                  g4467098
NCBI GI
                  192
BLAST score
                  1.0e-14
E value
Match length
                  58
% identity
                  60
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  1524
Seq. No.
                  818 1.R1040
Contig ID
5'-most EST
                  gsv701046553.h1
Method
                  BLASTX
                  g3881497
NCBI GI
BLAST score
                  176
E value
                  6.0e-12
Match length
                  318
% identity
                   (Z35604) cDNA EST EMBL: Z14593 comes from this gene; cDNA
NCBI Description
                  EST EMBL:T01764 comes from this gene; cDNA EST EMBL:D37668
                  comes from this gene; cDNA EST EMBL: D73892 comes from this
                  gene; cDNA EST EMBL: D71243 comes from this gene; cDN
                  1525
Seq. No.
Contig ID
                  818 2.R1040
5'-most EST
                  uC-gmrominsoy300b04b1
                  1526
Seq. No.
Contig ID /
                  819 5.R1040
                  leu701155872.h1
5'-most EST
Seq. No.
Contig ID
                  819 6.R1040
5'-most EST
                  g4396041
Method
                  BLASTX
NCBI GI
                  g2129577
BLAST score
                  270
E value
                  1.0e-23
Match length
                  64
% identity
                  DnaJ homolog protein - Arabidopsis thaliana >gi_727357
NCBI Description
                  (U22340) DnaJ homolog [Arabidopsis thaliana]
Seq. No.
                  819 7.R1040
Contig ID
5'-most EST
                  jC-gmle01810022f03a1
Method
                  BLASTX
NCBI GI
                  q4263704
```

```
8.0e-26
E value
Match length
                  102
% identity
                   54
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                  1529
Seq. No.
Contig ID
                  819 8.R1040
5'-most EST
                   jC-gmf102220088h01a1
Method
                  BLASTX
                  q4263704
NCBI GI
BLAST score
                  416
                  3.0e-40
E value
                  257
Match length
                  39
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  1530
                  819 9.R1040
Contig ID
                  hrw701060405.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4263704
BLAST score
                  336
                  8.0e-40
E value
                  252
Match length
                  40
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                  1531
Seq. No.
                  819 10.R1040
Contig ID
5'-most EST
                  uC-gmropic067e03b1
                  BLASTX
Method
NCBI GI
                  g1213460
BLAST score
                  568
                  4.0e-58
E value
                  247
Match length
% identity
                  (U03374) C subunit of V-ATPase [Amblyomma americanum]
NCBI Description
                  1532
Seq. No.
                  819 11.R1040
Contig ID
5'-most EST
                  LIB3107-070-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  q461944
                  712
BLAST score
E value
                  1.0e-132
Match length
                  419
% identity
                  54
                  DNAJ PROTEIN HOMOLOG (DNAJ-1) >gi_18260_emb_CAA47925_
NCBI Description
                   (X67695) cs DnaJ-1 [Cucumis sativus]
Seq. No.
Contig ID
                  819 12.R1040
5'-most EST
                  LIB3139-030-P1-N1-F3
```

Method

BLASTN

5'-most EST

```
NCBI GI
                   g609222
BLAST score
                   297
                   1.0e-166
E value
                   1048
Match length
                   83
% identity
NCBI Description
                  P.sativum mRNA for SAMS-1
Seq. No.
                   1534
Contig ID
                   819 13.R1040
                   sat701011172.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                   q3819098
BLAST score
                   205
                   1.0e-111
E value
                   1266
Match length
                   81
% identity
                  Cicer arietinum mRNA for copper containing amine oxidase
NCBI Description
                   (DAO)
Seq. No.
                   1535
                   819 14.R1040
Contig ID
5'-most EST
                   jC-gmst02400051d01a1
Method
                  BLASTN
NCBI GI
                  g726031
BLAST score
                  196
                   1.0e-105
E value
Match length
                  1006
                   82
% identity
                  Actinidia chinensis S-adenosylmethionine synthetase mRNA,
NCBI Description
                  partial cds
Seq. No.
                  1536
                   819 15.R1040
Contig ID
5'-most EST
                  LIB3139-097-P1-N1-D5
Method
                  BLASTX
NCBI GI
                  g1125691
BLAST score
                   420
E value .
                  1.0e-40
Match length
                   424
% identity
NCBI Description (X94301) DnaJ protein [Solanum tuberosum]
Seq. No.
                  1537
                  819 16.R1040
Contig ID
                  LIB3139-013-P1-N1-G4
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1724103
BLAST score
                  204
E value
                   1.0e-110
Match length
                   904
% identity
                  83
NCBI Description
                  Mesembryanthemum crystallinum methionine
                  adenosyltransferase mRNA, complete cds
Seq. No.
                  1538
                  819 17.R1040
Contig ID
```

zhf700962044.h1

Contig ID

```
Method
                   BLASTN
NCBI GI
                   g609222
BLAST score
                   266
                   1.0e-147
E value
                   848
Match length
                   86
% identity
NCBI Description
                  P.sativum mRNA for SAMS-1
Seq. No.
                   1539
                   822 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy217d08b1
Method
                   BLASTX
NCBI GI
                   q2462827
BLAST score
                   412
                   3.0e-40
E value
                   143
Match length
                   59
% identity
NCBI Description
                   (AF000657) probable thiamin biosynthetic enzyme
                   [Arabidopsis thaliana]
Seq. No.
                   1540
                   824 1.R1040
Contig ID
5'-most EST
                   seb700651176.hl
Method
                   BLASTX
NCBI GI
                   q833835
BLAST score
                   1395
                   1.0e-155
E value
Match length
                   486
% identity
                   55
                   (U26025) amygdalin hydrolase isoform AH I precursor [Prunus
NCBI Description
                   serotina]
Seq. No.
                   1541
Contig ID
                   824 2.R1040
                   zsg701122505.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1155255 ·
BLAST score
                   140
E value
                   1.0e-08
                   68
Match length
% identity
                   (U39228) beta-glucosidase [Prunus avium]
NCBI Description
                   1542
Seq. No.
Contig ID
                   824 4.R1040
                   zsg701127573.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1311386
BLAST score
                   207
E value
                   2.0e-23
Match length
                  73
% identity
                  Cyanogenic Beta-Glucosidase Mol_id: 1; Molecule: Cyanogenic
NCBI Description
                  Beta-Glucosidase; Chain: Null; Ec: 3.2.1.21
Seq. No.
                  1543
```

825\_1.R1040

```
5'-most EST
                   epx701108418.hl
                   1544
Seq. No.
                   827 1.R1040
Contig ID
5'-most EST
                   uC-gmropic028d02b1
Seq. No.
                   1545
                   827 2.R1040
Contig ID
5'-most EST
                   zhf700958170.h1
                   1546
Seq. No.
                   828 1.R1040
Contig ID
                   jex700908654.h1
5'-most EST
                   BLASTX
Method
                   g4309736
NCBI GI
BLAST score
                   244
                   3.0e-20
E value
Match length
                   61
% identity
                   (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1547
                   830 1.R1040
Contig ID
5'-most EST
                   2DA-01-Q1-B1-D4
Method
                  BLASTX
NCBI GI
                   g2642158
BLAST score
                   457
                   2.0e-45
E value
Match length
                  115
                   72
% identity
NCBI Description
                 (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  1548
                  830 2.R1040
Contig ID
                  LIB3106-006-Q1-K2-C1
5'-most EST
                  BLASTX
Method
                  g2642158
NCBI GI
BLAST score
                  295
E value
                   1.0e-26
                  80
Match length
% identity
                   (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  1549
Seq. No.
Contig ID
                  832 1.R1040
5'-most EST
                  LIB3040-003-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                  g417360
BLAST score
                  369
E value
                  5.0e-35
Match length
                  133
% identity
                  53
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                  >gi_2131280_pir__S67767 high mobility group-like protein
                  NHP2 - yeast (Saccharomyces cerevisiae)
                  >gi_666101_emb_CAA40885_ (X57714) high mobility group-like
```

nuclear protein 2 [Saccharomyces cerevisiae]

```
>gi 1431346_emb_CAA98786 (Z74256) ORF YDL208w
                  [Saccharomyces cerevisiae]
                  1550
Seq. No.
                  832 3.R1040
Contig ID
                  ncj700980996.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q417360
BLAST score
                  281
                  5.0e-25
E value
Match length
                  80
% identity
                  64
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                  >gi_2131280_pir__S67767 high mobility group-like protein
                  NHP2 - yeast (Saccharomyces cerevisiae)
                  >gi 666101 emb_CAA40885_ (X57714) high mobility group-like
                  nuclear protein 2 [Saccharomyces cerevisiae]
                  >gi 1429348 emb CAA67483 (X99000) high-mobility-group-like
                  protein [Saccharomyces cerevisiae]
                  >gi 1431346 emb CAA98786 (Z74256) ORF YDL208w
                  [Saccharomyces cerevisiae]
Seq. No.
                  1551
                  832 4.R1040
Contig ID
5'-most EST
                  LIB3072-017-Q1-E1-C5
Method
                  BLASTX
NCBI GI
                  g417360
BLAST score
                  241
                  2.0e-20
E value
                  76
Match length
                  59
% identity
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                  >gi_2131280_pir__S67767 high mobility group-like protein
                  NHP2 - yeast (Saccharomyces cerevisiae)
                  >qi 666101 emb CAA40885 (X57714) high mobility group-like
                  nuclear protein 2 [Saccharomyces cerevisiae]
                  >gi 1429348 emb CAA67483 (X99000) high-mobility-group-like
                  protein [Saccharomyces cerevisiae]
                  >gi_1431346 emb CAA98786 (Z74256) ORF YDL208w ,
                  [Saccharomyces cerevisiae]
Seq. No.
                  1552
Contig ID
                  833 1.R1040
5'-most EST
                  2DA-01-Q1-B1-D7
Method
                  BLASTX
NCBI GI
                  q3386604
BLAST score
                  207
E value
                  2.0e-16
Match length
                  129
% identity
                  (AC004665) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  1553
Contig ID
                  834 1.R1040
                  bth700845265.h1
5'-most EST
```

>gi 1429348 emb CAA67483 (X99000) high-mobility-group-like

protein [Saccharomyces cerevisiae]

Contig ID

```
Method
                    BLASTX
  NCBI GI
                    q3912919
  BLAST score
                     456
  E value
                     1.0e-45
 Match length
                    116
  % identity
                     80
 NCBI Description
                     (AF001308) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    1554
  Contig ID
                    835 1.R1040
                    LIB3138-079-P1-N1-E2
  5'-most EST
 Method
                    BLASTN
  NCBI GI
                    g14311
  BLAST score
                    850
  E value
                    0.0e + 00
 Match length
                    943
                    98
  % identity
                    G.max chloroplast gene rps19 and flanking regions
 NCBI Description
Seq. No.
                    1555
 Contig ID
                    835 2.R1040
  5'-most EST
                    jC-gmle01810070a03a1
 Method
                    BLASTN
 NCBI GI
                    g343648
 BLAST score
                    299
                    1.0e-167
 E value
 Match length
                     661
                    91
  % identity
                    Vigna unguiculata chloroplast ribosomal protein (L16 and
 NCBI Description
                    L14) genes, 3' and 5' end respectively
                    1556
  Seq. No.
                    835 3.R1040
 Contig ID
  5'-most EST
                    LIB3139-038-P1-N1-H6
 Method
                    BLASTN
 NCBI GI
                    q11748
 BLAST score
                    524
                    0.0e + 00
 E value
                    730
 Match length
  % identity
                    94
                    Nicotiana debneyi chloroplast DNA for tRNA-Ile and
 NCBI Description
                    ribosomal protein L2
                    1557
 Seq. No.
 Contig ID
                    835 4.R1040
 5'-most EST
                    ujr700646647.h1
 Method
                    BLASTN
 NCBI GI
                    g12212
 BLAST score
                    337
                    0.0e+00
 E value
                    505
 Match length
                    93
 % identity
                    S.alba chloroplast rp123 and rp12 genes for ribosomal
 NCBI Description
                    proteins L23 and L2
 Seq. No.
                    1558
```

835 9.R1040

Contig ID

5'-most EST

```
5'-most EST
                   LIB3107-071-Q1-K1-H2
Method
                   BLASTN
NCBI GI
                   g12212
BLAST score
                   141
                   2.0e-73
E value
Match length
                   185
% identity
                   94
                   S.alba chloroplast rp123 and rp12 genes for ribosomal
NCBI Description
                   proteins L23 and L2
                   1559
Seq. No.
                   835 10.R1040
Contig ID
                   LIB3138-042-Q1-N1-H5
5'-most EST
Method
                   BLASTN
                   g11748
NCBI GI
                   289
BLAST score
                   1.0e-161
E value
Match length
                   397
                   95
% identity
NCBI Description
                   Nicotiana debneyi chloroplast DNA for tRNA-Ile and
                   ribosomal protein L2
                   1560
Seq. No.
Contig ID
                   835 13.R1040
5'-most EST
                   jC-qmle01810032d10d1
                   BLASTX
Method
                   g133939
NCBI GI
BLAST score
                   314
E value
                   9.0e-29
                   80
Match length
% identity
                   72
NCBI Description
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70865 pir R3NT3
                   ribosomal protein S3 - common tobacco chloroplast
                   >gi_11865_emb_CAA77381 (Z00044) ribosomal protein S3
[Nicotiana tabacum] >gi_225235_prf__1211235BT ribosomal
                   protein S3 [Nicotiana tabacum]
                   1561
Seq. No.
Contig ID
                   836 1.R1040
                   hyd700730304.h1
5'-most EST
                   1562
Seq. No.
                   837 1.R1040
Contig ID
5'-most EST
                   uC-gmropic018e03b1
Method
                   BLASTX
NCBI GI
                   g2244898
BLAST score
                   186
E value
                   2.0e-13
Match length
                   96
% identity
NCBI Description
                   (Z97338) strong similarity to protein phosphatase 2A
                   regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.
                   1563
```

837 3.R1040

zzp700831795.hl

E value

. . .

```
1564
Seq. No.
Contig ID
                   838 1.R1040
5'-most EST
                   ssr700561089.hl
Method
                   BLASTN
NCBI GI
                   g12139
BLAST score
                   639
E value
                   0.0e + 00
Match length
                   3513
% identity
                   90
NCBI Description
                   Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and
                   trnG coding for ribosomal protein S2, one CF(1) and three
                   CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly
                   1565
Seq. No.
Contig ID
                   838 2.R1040
5'-most EST
                   fC-qmle700553639a4
Method
                   BLASTN
NCBI GI
                   g12139
BLAST score
                   145
E value
                   1.0e-75
Match length
                   414
                   91
% identity
NCBI Description
                   Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and
                   trnG coding for ribosomal protein S2, one CF(1) and three
                   CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly
Seq. No.
                   1566
Contig ID
                   838 4.R1040
5'-most EST
                   zsg701130050.hl
Method
                   BLASTN
NCBI GI
                   g12249
BLAST score
                   38
E value
                   5.0e-12
Match length
                   54
% identity
                   93
NCBI Description
                   Spinach plastid genes atpI-H-F for ATP synthase CF(O)
                   subunits IV, III and I
Seq. No.
                   1567<sup>-</sup>
Contig ID
                   838 11.R1040
5'-most EST
                   jC-qmle01810075f04a1
Method
                   BLASTN
NCBI GI
                   g12144
BLAST score
                   41
E value
                   1.0e-13
Match length
                   82
% identity
                   94
                   Pea chloroplast genes for F(O)-ATP synthase subunits a and
NCBI Description
                   c (partial)
Seq. No.
                   1568
Contig ID
                   841 1.R1040
5'-most EST
                   2DA-01-Q1-B1-E4
Method
                   BLASTX
NCBI GI
                   g2853087
BLAST score
                   199
```

3.0e-15

NCBI GI

```
Match length
                  122
                  26
% identity
                  (AL021768) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  1569
                  842 1.R1040
Contig ID
5'-most EST
                  wvk700685058.h1
Method
                  BLASTX
NCBI GI
                  g3212854
BLAST score
                  410
                  2.0e-39
E value
Match length
                  297
                  35
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  842 2.R1040
Contig ID
5'-most EST
                  LIB3107-004-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3212854
BLAST score
                  149
E value
                  2.0e-09
Match length
                  57
                  49
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                  1571
Seq. No.
                  842 3.R1040
Contig ID
5'-most EST
                  zzp700835324.h1
                  1572
Seq. No.
                  843 1.R1040
Contig ID
                  2DA-01-Q1-B1-E6
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3641870
BLAST score
                  218
                  1.0e-17
E value
Match length
                  136
% identity
                  41
                   (AJ011013) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                  844 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy083e10b1
Method
                  BLASTX
NCBI GI
                  g2598579
BLAST score
                  1461
                  1.0e-162
E value
Match length
                  364
% identity
                  (Y15295) L-ascorbate oxidase [Medicago truncatula]
NCBI Description
                  1574
Seq. No.
Contig ID
                  844 2.R1040
5'-most EST
                  hyd700725411.h1
Method
                  BLASTN
```

g2598578

```
BLAST score
                   238
                   1.0e-131
E value
Match length
                   690
                   84
% identity
                   Medicago truncatula mRNA for L-ascorbate oxidase
NCBI Description
Seq. No.
                   1575
Contig ID
                   844 4.R1040
5'-most EST
                   g4287777
Method
                   BLASTX
NCBI GI
                   g2598579
BLAST score
                   161
E value
                   3.0e-11
Match length
                   49
% identity
                   67
                   (Y15295) L-ascorbate oxidase [Medicago truncatula]
NCBI Description
Seq. No.
Contig ID
                   846 1.R1040
                   jex700908385.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2462762
BLAST score
                   961
E value
                   1.0e-104
Match length
                   338
% identity
                   58
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   846 2.R1040
Contig ID
5'-most EST
                   LIB3109-009-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   q2462762
BLAST score
                   371
E value
                   3.0e-35
Match length
                   141
                   57
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   846 4.R1040
Contig ID
5'-most EST
                   LIB3170-068-Q1-J1-D4
Seq. No.
                   1579
                   846 9.R1040
Contig ID
5'-most EST
                   qsv701053511.h1
Method
                   BLASTX
NCBI GI
                   q2462762
BLAST score
                   113
E value
                   7.0e-14
                   78
Match length
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
```

(aldo/keto reductase family) [Arabidopsis thaliana]

% identity

49

```
1580
Seq. No.
Contig ID
                  848 1.R1040
5'-most EST
                  LIB3106-033-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  g4220631
BLAST score
                  97
E value
                  7.0e-47
Match length
                  225
% identity
                  86
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5J14, complete sequence [Arabidopsis thaliana]
                  1581
Seq. No.
Contig ID
                  848 2.R1040
5'-most EST
                  LIB3056-010-Q1-N1-D9
Method
                  BLASTN
NCBI GI
                  g4220631
BLAST score
                  93
E value
                  1.0e-44
Match length
                  225
% identity
                  85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5J14, complete sequence [Arabidopsis thaliana]
Seq. No.
                  1582
                  848 3.R1040
Contig ID
5'-most EST
                  LIB3049-025-Q1-E1-G4
Method
                  BLASTN
NCBI GI
                  g4220631
BLAST score
                  89
                  2.0e-42
E value
                  225
Match length
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5J14, complete sequence [Arabidopsis thaliana]
                  1583
Seq. No.
                  848 6.R1040
Contig ID
                  pmv700888989.h1
5'-most EST
                  BLASTN
Method
                  g4220631
NCBI GI
BLAST score
                  65
                  3.0e-28
E value
                  181
Match length
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5J14, complete sequence [Arabidopsis thaliana]
                  1584
Seq. No.
                  849 1.R1040
Contig ID
                  2DA-01-Q1-B1-F11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3461848
BLAST score
                  179
E value
                  8.0e-13
Match length
                  102
```

```
(AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
                   1585
Seq. No.
                   850 1.R1040
Contig ID
5'-most EST
                   uC-gmropic026d05b1
Method
                   BLASTX
NCBI GI
                   g3688162
BLAST score
                   654
E value
                   3.0e-68
Match length
                   168
                   79
% identity
                   (AJ009672) centrin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1586
                   850 2.R1040
Contig ID
                   ssr700555006.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3386622
BLAST score
                   227
                   2.0e-18
E value
Match length
                   129
% identity
                   65
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   1587
                   850 3.R1040
Contig ID
                   2DA-01-Q1-B1-F12
5'-most EST
Method
                   BLASTX
                   g3688162
NCBI GI
BLAST score
                   491
E value
                   2.0e-49
Match length
                   135
                   52
% identity
NCBI Description
                  (AJ009672) centrin [Arabidopsis thaliana]
Seq. No.
                   1588
                   852 1.R1040
Contig ID
                   LIB3138-005-Q1-N1-F7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2315451
BLAST score
                   259
                   8.0e-22
E value
Match length
                   142
                   30
% identity
NCBI Description
                   (AF016448) No definition line found [Caenorhabditis
                   elegans]
                   1589
Seq. No.
                   853 1.R1040
Contig ID
5'-most EST
                   2DA-01-Q1-B1-F4
                   1590
Seq. No.
                   854 1.R1040
Contig ID
5'-most EST
                  LIB3092-017-Q1-K1-D4
Method
                  BLASTX
                   g2708532
NCBI GI
BLAST score
                   1184
```

NCBI Description

```
1.0e-130
E value
Match length
                  344
                  67
% identity
                   (AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
Seq. No.
Contig ID
                  854 2.R1040
                  g4397165
5'-most EST
Seq. No.
                  1592
Contig ID
                  855 1.R1040
5'-most EST
                  LIB3109-030-Q1-K1-B11
Seq. No.
                  856 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy040a11b1
Seq. No.
                  857 1.R1040
Contig ID
                  bth700845764.h1
5'-most EST
Seq. No.
                  1595
                  858 1.R1040
Contig ID
5'-most EST
                  uC-gmropic078g11b1
Method
                  BLASTX
NCBI GI
                  q629692
BLAST score
                  1174
E value
                  1.0e-129
Match length
                  533
                  48
% identity
NCBI Description
                  hypothetical protein - common tobacco
                  >gi_506471_emb_CAA56189_ (X79794) unnamed protein product
                  [Nicotiana tabacum]
                  1596
Seq. No.
Contig ID
                  858 2.R1040
                  zhf700955944.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g629692
BLAST score
                  846
E value
                  5.0e-91
Match length
                  184
                  88
% identity
NCBI Description
                  hypothetical protein - common tobacco
                  >gi 506471 emb CAA56189 (X79794) unnamed protein product
                  [Nicotiana tabacum]
Seq. No.
                  1597
Contig ID
                  861 1.R1040
5'-most EST
                  dpv701100030.h2
                  BLASTX
Method
NCBI GI
                  q1737492
BLAST score
                  1936
E value
                  0.0e + 00
Match length
                  624
% identity
                  (U81318) poly(A)-binding protein [Triticum aestivum]
```

NCBI GI

```
Seq. No.
                   1598
Contig ID
                   861 2.R1040
5'-most EST
                   LIB3051-006-Q1-E1-A7
                   1599
Seq. No.
Contig ID
                   861 4.R1040
5'-most EST
                   uC-gmronoir007h06b1
Method
                   BLASTX
NCBI GI
                   g1171978
BLAST score
                   156
                   2.0e-10
E value
                   48
Match length
                   67
% identity
                   POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                   1600
                   863 1.R1040
Contig ID
5'-most EST
                   2DA-02-Q1-B1-D6
Method
                   BLASTX
NCBI GI
                   g1279224
BLAST score
                   400
E value
                   2.0e-38
                   216
Match length
                   31
% identity
                   (X97454) specific tissue protein 1 [Cicer arietinum]
NCBI Description
Seq. No.
                   1601
                   863 2.R1040
Contig ID
5'-most EST
                   LIB3107-034-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g3393062
BLAST score
                   627
E value
                   4.0e-65
Match length
                   208
% identity
                   57
                   (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                   1602
Seq. No.
Contig ID
                  863 4.R1040
5'-most EST
                   uC-gmropic070d05b1
                   BLASTX
Method
NCBI GI
                   q1279224
BLAST score
                   324
E value
                   7.0e-30
Match length
                   186
% identity
                   32
                   (X97454) specific tissue protein 1 [Cicer arietinum]
NCBI Description
                   1603
Seq. No.
Contig ID
                   864 1.R1040
5'-most EST
                   g5752500
Method
                  BLASTX
```

q3328240

5'-most EST

```
BLAST score
                   966
E value
                   1.0e-105
Match length
                   289
% identity
                   66
                   (AF064775) early nodule-specific protein [Medicago
NCBI Description
                   truncatula]
Seq. No.
                   1604
                   865 1.R1040
Contig ID
                   zhf700952383.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4210330
BLAST score
                  2927
                  0.0e+00
E value
Match length
                   643
                   83
% identity
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  1605
                  865 3.R1040
Contig ID
5'-most EST
                  zzp700832947.h1
                  1606
Seq. No.
                  866 1.R1040
Contig ID
5'-most EST
                  2DA-01-Q1-B1-G6
Seq. No.
                  1607
                  868 1.R1040
Contig ID
5'-most EST
                  2DA-01-Q1-B1-G8
Method
                  BLASTX
NCBI GI
                  g1402878
BLAST score
                  711
E value
                   4.0e-75
Match length
                  185
% identity
                  72
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                  1608
Seq. No.
                  869 1.R1040
Contig ID
5'-most EST
                  LIB3170-064-Q1-K1-A3
Seq. No.
                  1609
Contig ID
                  869 2.R1040
                  bth700845877.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3879119
BLAST score
                  345
E value
                  4.0e-32
Match length
                  168
% identity
NCBI Description
                   (270310) similar to Glutathione S-transferases.
                  [Caenorhabditis elegans]
Seq. No.
                  1610
Contig ID
                  871 1.R1040
```

2DA-01-Q1-B1-H10

5'-most EST Method

```
Method
                   BLASTX
NCBI GI
                   g4512703
BLAST score
                   146
E value
                   7.0e-14
Match length
                   117
                   38
% identity
                   (AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1611
                   871 2.R1040
Contig ID
5'-most EST
                   LIB3050-001-Q1-E1-D12
Seq. No.
                   1612
Contig ID
                   871 3.R1040
5'-most EST
                   LIB3051-069-Q1-K1-A10
Seq. No.
                   1613
Contig ID
                   872 1.R1040
5'-most EST
                   LIB3093-050-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   g3047104
BLAST score
                   1379
E value
                   1.0e-163
Match length
                   469
% identity
                   64
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   872 2.R1040
Contig ID
5'-most EST
                   fC-gmf1700905215y1
Method
                   BLASTX
NCBI GI
                   g3047104
BLAST score
                   419
E value
                   1.0e-40
Match length
                   202
% identity
                   61
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1615
                   873 2.R1040
Contig ID
5'-most EST
                   LIB3138-023-Q1-N1-C5
Method
                   BLASTX
NCBI GI
                   g4510383
BLAST score
                   214
E value
                   4.0e-17
                   67
Match length
% identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   873 3.R1040
Contig ID
5'-most EST
                   2DA-01-Q1-B1-H4
Seq. No.
                   1617
Contig ID
                   873 4.R1040
```

LIB3139-059-P1-N1-E8

BLASTX

Method

BLASTX

```
NCBI GI
                   g4510383
BLAST score
                   188
E value
                   4.0e-14
Match length
                   63
                   62
% identity
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   874 1.R1040
                   pxt700945347.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539292
BLAST score
                   465
                   4.0e-46
E value
                   96
Match length
                   89
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   1619
                   878 1.R1040
Contig ID
5'-most EST
                   vwf700677625.h1 🗸
                   BLASTX
Method
NCBI GI
                   g2980806
BLAST score
                   338
                   8.0e-42
E value
Match length
                   207
                   35
% identity
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
                   1620
Seq. No.
Contig ID
                   878 3.R1040
5'-most EST
                   sat701013749.hl
                   1621
Seq. No.
Contig ID
                   878 4.R1040
5'-most EST
                   xpa700792783.h1
Seq. No.
                   1622
Contig ID
                   880 1.R1040
5'-most EST
                   2DA-01-Q1-B1-H9
Seq. No.
                   1623
Contig ID
                   881 1.R1040
5'-most EST
                   zsg701120314.h1
                   BLASTX
Method
NCBI GI
                   q4454032
BLAST score
                   712
E value
                   5.0e-75
                   243
Match length
% identity
                   (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   883 1.R1040
5'-most EST
                   asj700967313.hl
```

Contig ID

```
NCBI GI
                   q3953471
BLAST score
                   261
                   2.0e-22
E value
Match length
                   100
                   55
% identity
NCBI Description
                   (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
Contig ID
                  883 2.R1040
5'-most EST
                   fde700873705.hl
Seq. No.
Contig ID
                  885 1.R1040
5'-most EST
                  wvk700682626.h2
                   1627
Seq. No.
Contig ID
                  886 1.R1040
5'-most EST
                   q5688325
Method
                  BLASTX
NCBI GI
                  q1172584
BLAST score
                  1389
E value
                   1.0e-154
Match length
                   428
% identity
                   63
                  POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)
NCBI Description
                  >gi_1076478_pir__S52984 catechol oxidase (EC 1.10.3.1)
                  precursor - apple tree >gi_507280 (L29450) polyphenol
                  oxidase [Malus domestica]
Seq. No.
                  1628
                  886 2.R1040
Contig ID
                  LIB3106-111-Q1-K1-G4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1172584
BLAST score
                  509
E value
                  2.0e-51
Match length
                  207
                   49
% identity
                  POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)
NCBI Description
                  >gi_1076478_pir__S52984 catechol oxidase (EC 1.10.3.1)
                  precursor - apple tree >gi_507280 (L29450) polyphenol
                  oxidase [Malus domestica]
                  1629
Seq. No.
Contig ID
                  887 1.R1040
5'-most EST
                  taw700660372.h1
Method
                  BLASTX
NCBI GI
                  g728827
BLAST score
                  612
E value
                  4.0e-63
                  322
Match length
                  40
% identity
                  ALLANTOINASE PRECURSOR >gi_458126 (U03471) allantoinase
NCBI Description
                  [Rana catesbeiana]
Seq. No.
                  1630
```

887\_2.R1040

BLAST score

260

```
smc700744903.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g728827
BLAST score
                  185
                   1.0e-13
E value
Match length
                  93
                   43
% identity
NCBI Description
                  ALLANTOINASE PRECURSOR >gi 458126 (U03471) allantoinase
                   [Rana catesbeiana]
Seq. No.
                  1631
                  887 3.R1040
Contig ID
                  hrw701061511.hl
5'-most EST
                  1632
Seq. No.
                  889 1.R1040
Contig ID
                  LIB3107-056-Q1-K1-C3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1652704
BLAST score
                  186
E value
                  2.0e-13
Match length
                  95
% identity
                  43
                  (D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  1633
                  890 1.R1040
Contig ID
5'-most EST
                  gsv701054306.hl
Method
                  BLASTX
NCBI GI
                  g4337195
BLAST score
                  1386
E value
                  1.0e-154
Match length
                  377
% identity
                  78
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  1634
Contig ID
                  890 2.R1040
5'-most EST
                  zsg701125396.hl
                  BLASTX
Method
NCBI GI
                  g4337195
BLAST score
                  537
E value
                  8.0e-55
Match length
                  120
% identity
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  890 3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy225b07b1
Seq. No.
                  1636
                  890_5.R1040
Contig ID
5'-most EST
                  gsv701055170.h1
Method
                  BLASTX
NCBI GI
                  q4337195
```

```
2.0e-22
E value
Match length
                   60
% identity
NCBI Description
                   (AC006403) putative protein kinase [Arabidopsis thaliana]
                  1637
Seq. No.
Contig ID
                  893 1.R1040
5'-most EST
                  LIB3039-043-Q1-E1-C8
                  BLASTN
Method
NCBI GI
                  g1902893
BLAST score
                  231
E value
                  1.0e-126
Match length
                   603
                  85
% identity
                  Solanum melongena mRNA for QM family protein, complete cds
NCBI Description
Seq. No.
                  1638
                  893 2.R1040
Contig ID
5'-most EST
                  wvk700686407.h1
Method
                  BLASTX
NCBI GI
                  g1169494
BLAST score
                  1343
                  0.0e+00
E value
                  479
Match length
                  87
% identity
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                  >gi_2119915_pir__S60659 EF-Tu protein precursor - soybean
                  >gi_949873_emb_CAA61444_ (X89058) EF-Tu protein [Glycine
                  max]
Seq. No.
                  1639
Contig ID
                  893 3.R1040
5'-most EST
                  LIB3106-106-Q1-K1-A5
Method
                  BLASTN
NCBI GI
                  g18775
BLAST score
                  652
E value
                  0.0e + 00
Match length
                  986
% identity
                  93
NCBI Description
                  G.max tufA gene for chloroplast translation elongation
                  factor EF-Tu
Seq. No.
                  1640
                  893 4.R1040
Contig ID
5'-most EST
                  LIB3170-014-Q1-K1-F12
Method
                  BLASTX
                  q2500354
NCBI GI
BLAST score
                  619
E value
                  1.0e-111
Match length
                  224
% identity
                  91
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                  (AB001891) QM family protein [Solanum melongena]
Seq. No.
                  1641
```

893 5.R1040

hrw701059127.h1

Contig ID

5'-most EST

```
Method
                   BLASTX
NCBI GI
                   g121631
BLAST score
                   308
E value
                   3.0e-28
Match length
                   74
                   77
% identity
                   GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
NCBI Description
                   >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco
                   >gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana
                   sylvestris]
Seq. No.
                   1642
                   893 6.R1040
Contig ID
5'-most EST
                   fde700870636.hl
Method
                   BLASTN
                   g18775
NCBI GI
BLAST score
                   218
                   1.0e-119
E value
Match length
                   420
                   97
% identity
                   G.max tufA gene for chloroplast translation elongation
NCBI Description
                   factor EF-Tu
                   1643
Seq. No.
                   893 7.R1040
Contig ID
5'-most EST
                   LIB3039-016-Q1-E1-H9
Method
                   BLASTX
NCBI GI
                   g2500354
BLAST score
                   550
                   2.0e-56
E value
                   109
Match length
                   94
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   893 8.R1040
Contig ID
                   LIB3028-019-Q1-B1-F4
5'-most EST
Seq. No.
                   1645
                   893 9.R1040
Contig ID
5'-most EST
                   LIB3106-013-Q1-K1-F4
                   BLASTX
Method
NCBI GI
                   g2500354
BLAST score
                   213
                   4.0e-17
E value
Match length
                   46
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   893 12.R1040
Contig ID
5'-most EST
                  LIB3106-037-Q1-K1-D3
Method
                   BLASTX
```

g2500354

635

NCBI GI BLAST score

Match length

446

```
E value
                   2.0e-66
Match length
                   126
% identity
                   93
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   1647
Seq. No.
                   893 19.R1040
Contig ID
5'-most EST
                   dpv701103675.h1
Method
                   BLASTX
                   g2500354
NCBI GI
BLAST score
                   348
                   3.0e - 33
E value
Match length
                   63
                   98
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894 dbj_BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
-Seq. No.
                   1648
                   893 21.R1040
Contig ID
5'-most EST
                   rlr700902438.h1
Method
                   BLASTX
                   g2500354
NCBI GI
BLAST score
                   245
E value
                   3.0e-21
Match length
                   48
                   90
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   1649
Seq. No.
                   894 1.R1040
Contig ID
5'-most EST
                   LIB3040-038-Q1-E1-G5
                   BLASTX
Method
NCBI GI
                   g3868758
                   844
BLAST score
                   1.0e-90
E value
Match length
                   212
% identity
                   (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
Seq. No.
                   895 2.R1040
Contig ID
5'-most EST
                   uC-gmropic019f08b1
Seq. No.
                   896 1.R1040
Contig ID
5'-most EST
                   kl1\overline{7}01210028.h1
Seq. No.
                   1652
                   898 2.R1040
Contig ID
5'-most EST
                   LIB3039-021-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   g2191136
BLAST score
                   985
E value
                   1.0e-134
```

Contig ID

5'-most EST

```
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   1653
Seq. No.
Contig ID
                   898 3.R1040
                   sat701012837.hl
5'-most EST
Method .
                  BLASTX
NCBI GI
                  g2191136
BLAST score
                   511
                   1.0e-87
E value
                   442
Match length
                   32
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   1654
Seq. No.
                   898 4.R1040
Contig ID
                  LIB3040-018-Q1-E1-D4
5'-most EST
                  BLASTN
Method
NCBI GI
                  q1638836
BLAST score
                   324
                   0.0e+00
E value
                  1302
Match length
                   82
% identity
NCBI Description
                  H.vulgare mRNA for alpha-tubulin
Seq. No.
                   1655
                  898 5.R1040
Contig ID
5'-most EST
                  LIB3139-028-P1-N1-D1
Method
                  BLASTN
NCBI GI
                  g20412
BLAST score
                   507
                  0.0e + 00
E value
Match length
                  1307
                  86
% identity
                  P.amygdalus mRNA for alpha-tubulin
NCBI Description
Seq. No.
                  1656
Contig ID
                  898 6.R1040
5'-most EST
                  g5606046
Method
                  BLASTN
NCBI GI
                  g4098271
BLAST score
                  275
E value
                  1.0e-152
Match length
                  1244
% identity
                  83
                  Triticum aestivum alpha-tubulin mRNA, complete cds
NCBI Description
Seq. No.
```

899 1.R1040

2DA-02-Q1-B1-B7

E value

```
Seq. No.
                   1658
Contig ID
                   900 3.R1040
5'-most EST
                   uxk700672265.h1
Method
                   BLASTN
NCBI GI
                   g473216
BLAST score
                   118
E value
                   1.0e-59
Match length
                   354
% identity
                   83
NCBI Description
                   P.sativum (little marvel) HSC71.0 mRNA
Seq. No.
Contig ID
                   900 4.R1040
5'-most EST
                   uC-gmrominsoy170b02b1
Method
                   BLASTX
NCBI GI
                   g1076746
BLAST score
                   1030
E value
                   0.0e + 00
Match length
                   502
% identity
                   86
                   heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi 763160 emb CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   1660
                   900 5.R1040
Contig ID
                   jC-gmst02400010c01a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g629641
BLAST score
                   1143
                   0.0e + 00
E value
                   440
Match length
                   87
% identity
                   PsHSC71.0 protein - garden pea >gi_1076530_pir__S53500
NCBI Description
                   HSC71.0 protein - garden pea >gi_473217_emb_CAA83548_
                   (Z32537) PsHSC71.0 [Pisum sativum]
Seq. No.
                   1661
                   900 6.R1040
Contig ID
5'-most EST
                   wvk700683741.hl
                  BLASTX
Method
NCBI GI
                   g629641
BLAST score
                   1158
E value
                   0.0e+00
Match length
                   433
% identity
                  PsHSC71.0 protein - garden pea >gi_1076530_pir__S53500
NCBI Description
                   HSC71.0 protein - garden pea >gi_473217_emb_CAA83548
                   (Z32537) PsHSC71.0 [Pisum sativum]
                   1662
Seq. No.
Contig ID
                   900 7.R1040
                   leu701146433.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g473216
BLAST score
                   447
```

0.0e + 00

Contig ID

```
1860
Match length
% identity
                   87
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
Seq. No.
                   1663
                   901 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir033b09b1
Method
                  BLASTX
NCBI GI
                   g2702277
                   397
BLAST score
E value
                   2.0e-38
Match length
                   109
% identity
                   71
                   (AC003033) putative cyclin g-associated kinase [Arabidopsis
NCBI Description
                   thaliana] >gi_2914689 (AC003974) putative cyclin
                   g-associated kinase [Arabidopsis thaliana]
Seq. No.
                   1664
                   901 3.R1040
Contig ID
                   fua701040662.hl
5'-most EST
                   1665
Seq. No.
Contig ID
                   902 1.R1040
5'-most EST
                   2DA-02-Q1-B1-C1
                   1666
Seq. No.
                   905 1.R1040
Contig ID
5'-most EST
                   2DA-02-Q1-B1-C12
                   1667
Seq. No.
Contig ID
                   906 1.R1040
5'-most EST
                   2DA-02-Q1-B1-C2
Seq. No.
                   1668
Contig ID
                   908 1.R1040
5'-most EST.
                  uC-gmrominsoy040a12b1
Method
                  BLASTX
NCBI GI
                   g2979555
BLAST score
                   340
E value
                   8.0e-32
Match length
                   150
% identity
NCBI Description
                   (AC003680) unknown protein [Arabidopsis thaliana]
                   1669
Seq. No.
                   912 1.R1040
Contig ID
5'-most EST
                   txt700736440.h1
Method
                  BLASTX
NCBI GI
                  g1350983
BLAST score
                   1082
                   1.0e-118
E value
Match length
                  234
                  87
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
Seq. No.
```

912 5.R1040

5'-most EST

Method

```
5'-most EST
                   LIB3050-020-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   q1856971
BLAST score
                   272
E value
                   4.0e-24
Match length
                   57
% identity
NCBI Description
                   (D26058) This gene is specifically expressed at the S phase
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
Seq. No.
Contig ID
                   913 1.R1040
5'-most EST
                   seb700653717.hl
Method
                   BLASTX
NCBI GI
                   g3834307
BLAST score
                   739
E value
                   3.0e-78 .
Match length
                   226
% identity
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
NCBI Description
                   putative protein from Arabidopsis thaliana BAC gb AL021712.
                   ESTs gb_N65887 and gb_N65627 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  1672
                   913 2.R1040
Contig ID
                   zzp700835039.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3834307
BLAST score
                   941
                   1.0e-102
E value
                   223
Match length
% identity
NCBI Description
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
                   putative protein from Arabidopsis thaliana BAC gb AL021712.
                   ESTs qb N65887 and qb N65627 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   1673
Contig ID
                   913 3.R1040
5'-most EST
                   LIB3106-099-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g3834307
BLAST score
                   326
E value
                   3.0e-30
                   79
Match length
% identity
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
NCBI Description
                   putative protein from Arabidopsis thaliana BAC gb AL021712.
                   ESTs gb_N65887 and gb N65627 come from this gene.
                   [Arabidopsis thaliana]
                   1674
Seq. No.
                   913 4.R1040
Contig ID
```

zsg701118614.h1

BLASTN

Contig ID

```
g3766106
NCBI GI
BLAST score
                   58
E value
                   1.0e-23
Match length
                   158
% identity
                   84
                   Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   1675
                   913 5.R1040.
Contig ID
                   leu701147327.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3834307
BLAST score
                   253
E value
                   5.0e-22
Match length
                   52
% identity
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
NCBI Description
                   putative protein from Arabidopsis thaliana BAC gb AL021712.
                   ESTs gb_N65887 and gb_N65627 come from this gene.
                   [Arabidopsis thaliana]
                   1676
Seq. No.
                   914 1.R1040
Contig ID
5'-most EST
                   dpv701102672.h1
Method
                  BLASTX
                   g2213592
NCBI GI
BLAST score
                   822
                   9.0e-88
E value
Match length
                   287
                   37
% identity
                   (AC000348) T7N9.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1677
                   914 2.R1040
Contig ID
                   sat701015380.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2213592
BLAST score
                   829
E value
                   1.0e-88
Match length
                   298
                   35
% identity
                  (ACO00348) T7N9.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1678
Contig ID
                   914 3.R1040
5'-most EST
                  LIB3092-053-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g2213592
BLAST score
                  291
E value
                   3.0e-26
Match length
                  85
% identity
                   (AC000348) T7N9.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1679
```

915 1.R1040

Seq. No.

```
fde700871332.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3600047
BLAST score
                   476
E value
                   1.0e-47
Match length
                   160
% identity
                   61
NCBI Description
                   (AF080120) similar to elongation factor EF-Ts [Arabidopsis
                  thaliana]
Seq. No.
                  1680
                   917 1.R1040
Contig ID
                   zsq701119187.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1871577
BLAST score
                  732
                   2.0e-77
E value
Match length
                  168
% identity
                  82
                   (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
Seq. No.
                  1681
                  917 2.R1040
Contig ID
                  uC-gmrominsoy256c09b1
5'-most EST
Method
                  BLASTX
                  g1871577
NCBI GI
BLAST score
                  656
                  1.0e-68
E value
                  194
Match length
% identity
                   68
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                  1682
Seq. No.
                  917 3.R1040
Contig ID
5'-most EST
                  LIB3139-102-P1-N1-G2
Method
                  BLASTX
                  g1871577
NCBI GI
BLAST score
                  580
                  8.0e-64
E value
Match length
                  181
% identity
                   69
                   (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                  1683
Seq. No.
Contig ID
                  919 1.R1040
5'-most EST
                  leu701151275.hl
Method
                  BLASTX
NCBI GI
                  g3914136
BLAST score
                  306
E value
                  1.0e-27
Match length
                  116
                  54
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                  >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein
                  [Cicer arietinum]
```

Match length

```
919 3.R1040
Contig ID
5'-most EST
                  LIB3040-061-Q1-E11-F5
Method
                  BLASTX
NCBI GI
                  g3914136
BLAST score
                  127
E value
                  1.0e-12
Match length
                  92
% identity
                  43
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                  >gi 2632171 emb CAA05771 (AJ002958) lipid transfer protein
                  [Cicer arietinum]
Seq. No.
                  1685
                  920 1.R1040
Contig ID
                  sat701013038.hl
5'-most EST
Method
                  BLASTX
                  g548770
NCBI GI
BLAST score
                  1759
E value
                  0.0e + 00
Match length
                  385
                  83
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir _S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  1686
                  920 2.R1040
Contig ID
5'-most EST
                  zsg701120409.h1
                  BLASTX
Method
                  g132944
NCBI GI
BLAST score
                  296
                  9.0e-27
E value
Match length
                  61
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi 806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  1687
Contig ID
                  920 3.R1040
                  seb700649013.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2315210
BLAST score
                  113
E value
                  2.0e-56
Match length
                  325
% identity
NCBI Description
                  Lycopersicon esculentum mRNA for proteasome, alpha subunit
Seq. No.
                  1688
Contig ID
                  922 1.R1040
5'-most EST
                  jC-gmst02400058e10a1
Method
                  BLASTN
NCBI GI
                  q2924734
BLAST score
                  112
E value
                  8.0e-56
```

```
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXE10, complete sequence [Arabidopsis thaliana]
                   1689
Seq. No.
                   922 2.R1040
Contig ID
5'-most EST
                   crh700852414.h1
Method
                   BLASTX
NCBI GI
                   g728880
BLAST score
                   183
E value
                   2.0e-13
Match length
                   55
                   62
% identity
                   N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
NCBI Description
                   >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl
                   transferase related protein [Homo sapiens]
Seq. No.
                   1690
                   923 1.R1040
Contig ID
5'-most EST
                   rlr700899522.h1
Method
                   BLASTX
NCBI GI
                   g2494113
BLAST score
                   778
                   6.0e-83
E value
Match length
                   192
                   75
% identity
                   (AC002376) Strong similarity to Musa pectate lyase
NCBI Description
                   (gb X92943). ESTs gb AA042458, gb ATTS4502, gb_N38552 come
                   from this gene. [Arabidopsis thaliana]
                   1691
Seq. No.
                   924 2.R1040
Contig ID
5'-most EST
                   k11701207620.h1
                   1692
Seq. No.
                   925 1.R1040
Contig ID
5'-most EST
                   LIB3051-106-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   q136057
BLAST score
                   980
E value
                   1.0e-106
Match length
                   253
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi 99499 pir A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi 556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
Seq. No.
                   1693
                   925 2.R1040
Contig ID
5'-most EST
                   LIB3109-003-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   g1351279
BLAST score
                   359
                   2.0e-44
E value
```

113

Match length

```
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi 602590 emb CAA58230 (X83227) triosephosphate isomerase
                   [Petunia x hybrida]
                  1694
Seq. No.
Contig ID
                   925 3.R1040
5'-most EST
                   fC-gmle700743237f1
                  BLASTX
Method
NCBI GI
                  g136063
BLAST score
                  181
                  2.0e-13
E value
Match length
                   68
                   48
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 68426 pir__ISZMT triose-phosphate isomerase (EC
                  5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
                  isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009 (D00012)
                  triosephosphate isomerase [Zea mays]
Seq. No.
                  1695
                  925 4.R1040
Contig ID
5'-most EST
                  LIB3051-108-Q1-K1-C11
Method
                  BLASTX
                  g136057
NCBI GI
                  423
BLAST score
E value
                  1.0e-41
Match length
                  112
                  72
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi 556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
                  1696
Seq. No.
Contig ID
                  926 1.R1040
5'-most EST
                  epx701105477.h1
                  BLASTX
Method
NCBI GI
                  q4127456
BLAST score
                  914
E value
                  1.0e-98
Match length
                  232
% identity
NCBI Description
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
                  1697
Seq. No.
                  926 2.R1040
Contig ID
5'-most EST
                  LIB3040-003-Q1-E1-D3
Method
                  BLASTX
                  g4127456
NCBI GI
BLAST score
                  343
E value
                  3.0e - 32
                  96
Match length
% identity
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
```

ATTENDED TO

1698

· 6.

Seq. No.

```
926 3.R1040
Contig ID
5'-most EST
                   LIB3138-052-Q1-N1-C12
Method
                   BLASTX
                   g3057150
NCBI GI
                   151
BLAST score
                   6.0e-10
E value
Match length
                   47
% identity
                   41
                   (AF059037) chaperonin 10 [Arabidopsis thaliana]
NCBI Description
                   1699
Seq. No.
                   928 1.R1040
Contig ID
5'-most EST
                   2DA-02-Q1-B1-E4
Method
                   BLASTN
NCBI GI
                   g2351069
BLAST score
                   57
                   3.0e-23
E value
Match length
                   227
% identity
                   81
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSH12, complete sequence [Arabidopsis thaliana]
                   1700
Seq. No.
                   929 1.R1040
Contig ID
                   gsv701055259.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2935523
BLAST score
                   173
E value
                   4.0e-12
Match length
                   135
% identity
NCBI Description
                   (AF049066) 21 kD protein precursor [Pinus radiata]
Seq. No.
                   929 2.R1040
Contig ID
5'-most EST
                   uC-gmropic059d02b1
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   1.0e-10
E value
Match length
                   44
                   65
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   1702
                   931 1.R1040
Contig ID
                   vzy700751374.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4559358
BLAST score
                   271
E value
                   2.0e-23
Match length
                   97
% identity
NCBI Description
                   (AC006585) putative steroid binding protein [Arabidopsis
                   thaliana]
```

1703

Seq. No.

NCBI GI

```
931 2.R1040
Contig ID
5'-most EST
                   eep700868348.hl
Method
                  BLASTX
NCBI GI
                  g4200044
BLAST score
                   471
                   4.0e-47
E value
Match length
                  165
% identity
                   55
                   (AB022732) cytochrome P450 [Glycyrrhiza echinata]
NCBI Description
                  1704
Seq. No.
                   931 4.R1040
Contig ID
                  rlr700900741.h1
5'-most EST
Method
                  BLASTX
                  g4559358
NCBI GI
                   205
BLAST score
                   6.0e-16
E value
Match length
                  72
% identity
                   53
NCBI Description
                   (AC006585) putative steroid binding protein [Arabidopsis
                  thaliana]
                  1705
Seq. No.
                  932 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910036a06d1
Method
                  BLASTX
NCBI GI
                  g629602
BLAST score
                  3123
E value
                  0.0e+00
                  750
Match length
                  77
% identity
                  probable imbibition protein - wild cabbage
NCBI Description
                  >gi_488787_emb_CAA55893_ (X79330) putative imbibition
                  protein [Brassica oleracea]
                  1706
Seq. No.
                  932 2.R1040
Contig ID
5'-most EST
                  g5606124
Method
                  BLASTX
NCBI GI
                  g629602
BLAST score
                  587
                  3.0e-60
E value
                  142
Match length
% identity
                  76
NCBI Description
                  probable imbibition protein - wild cabbage
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
Seq. No.
                  1707
Contig ID
                  932 3.R1040
5'-most EST
                  LIB3170-050-Q1-K1-D8
Seq. No.
                  1708
Contig ID
                  933 1.R1040
5'-most EST
                  2DA-02-Q1-B1-E9
Method
                  BLASTX
```

q3367569

5'-most EST

Method

.

NCBI GI BLAST score

```
BLAST score
E value
                   4.0e-12
Match length
                   173
% identity
                   31
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
                   1709
Seq. No.
                   934 1.R1040
Contig ID
5'-most EST
                   leu701144440.h1
                   BLASTX
Method
NCBI GI
                   q2832617
BLAST score
                   256
E value
                   4.0e-22
Match length
                   71
% identity
                   66
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                   936 1.R1040
Contig ID
5'-most EST
                   hrw701057246.hl
                   1711
Seq. No.
Contig ID
                   938 1.R1040
5'-most EST
                   2DA-02-Q1-B1-F2
Method
                   BLASTX
NCBI GI
                   q3077640
BLAST score
                   304
E value
                   9.0e-28
Match length
                   116
% identity
                   55
NCBI Description (AJ223151) O-methyltransferase [Prunus dulcis]
Seq. No.
                   1712
Contig ID
                   941 1.R1040
5'-most EST
                  LIB3170-085-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                   g2447107
BLAST score
                   328
E value
                   3.0e-30
Match length
                  172
                   42
% identity
                   (U42580) A638R [Paramecium bursaria Chlorella virus 1]
NCBI Description
Seq. No.
Contig ID
                   942 1.R1040
5'-most EST
                   2DA-02-Q1-B1-F6
Seq. No.
                   1714
                   942 2.R1040
Contig ID
5'-most EST
                  rlr700899163.h1
Seq. No.
                  1715
                   943 1.R1040
Contig ID
```

395

 $LIB\overline{3}039-005-Q1-E1-G3$ 

BLASTX g125722

Seq. No.

Contig ID

```
1.0e-34
E value
Match length
                   228
% identity
                   44
                  KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR
NCBI Description
                   >gi_81814_pir__JQ1091 trypsin inhibitor KTi1 (Kunitz) -
                   soybean >gi 256635 bbs 115028 (S45035) Kunitz trypsin
                  inhibitor KTil [soybeans, Peptide, 203 aa] [Glycine max]
Seq. No.
                  1716
Contig ID
                   944 1.R1040
5'-most EST
                  pmv700888263.h1
Method
                  BLASTX
NCBI GI
                  q3522939
BLAST score
                   411
                   6.0e-55
E value
Match length
                  252
                   52
% identity
                   (AC004411) putative squamosa-promoter binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  1717
                  945 1.R1040
Contig ID
5'-most EST
                  LIB3093-036-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q2982297
BLAST score
                  1108
                  1.0e-121
E value
Match length
                  232
% identity
                  93
                  (AF051233) KIAA0107-like protein [Picea mariana]
NCBI Description
Seq. No.
                  1718
                  945 2.R1040
Contig ID
5'-most EST
                  wrg700787648.h2
                  BLASTX
Method
NCBI GI
                  g2494625
BLAST score
                  187
                  5.0e-14 ~
E value
Match length
                  109
% identity
                  40
NCBI Description
                  HYPOTHETICAL PROTEIN KIAA0107 >gi_285951_dbj_BAA03497_
                   (D14663) KIAA0107 [Homo sapiens]
Seq. No.
                  1719
Contig ID
                  947 2.R1040
5'-most EST
                  jC-gmro02910059e07a1
Method
                  BLASTX
NCBI GI
                  g3851636
BLAST score
                  471
E value
                  3.0e-47
Match length
                  108
% identity
                  83
NCBI Description
                   (AF098519) unknown [Avicennia marina] >qi 4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
```

947 3.R1040

5'-most EST

```
5'-most EST
                   q5126873
Method
                   BLASTX
NCBI GI
                   q4426565
BLAST score
                   145
E value
                   7.0e-09
Match length
                   66
% identity
                   39
NCBI Description
                   (AF031483) unknown [Rattus norvegicus]
                   1721.
Seq. No.
                   947 4.R1040
Contig ID
5'-most EST
                  LIB3093-014-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                   q4426565
BLAST score
                   175
E value
                   8.0e-12
Match length
                   238
% identity
                   34
NCBI Description
                  (AF031483) unknown [Rattus norvegicus]
Seq. No.
                   1722
Contig ID
                   947 5.R1040
5'-most EST
                  LIB3074-003-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g126085
BLAST score
                  242
                   5.0e-26
E value
Match length
                  236
% identity
                  28
                  SEED LECTIN SUBUNITS I AND II PRECURSOR
NCBI Description
                  >gi 81750 pir A29572 lectin precursor - horse gram
                  >gi 167564 (J02721) lectin subunit I precursor [Dolichos
                  biflorus]
Seq. No.
                  1723
                  947 6.R1040
Contig ID
                  ncj700986678.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3851636
BLAST score
                  255
                  9.0e-22
E value
                  58
Match length
                  83
% identity
NCBI Description
                   (AF098519) unknown [Avicennia marina] >gi_4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                  1724
Seq. No.
Contig ID
                  948 1.R1040
5'-most EST
                  jC-gmst02400054d09a1
Seq. No.
                  1725
                  948 2.R1040
Contig ID
5'-most EST
                  asn701132457.h1
Seq. No.
                  1726
                  950 1.R1040
Contig ID
```

LIB3050-005-Q1-K1-C10

```
Method
                   BLASTX
NCBI GI
                   g4325282
BLAST score
                   584
                   7.0e-60
E value
Match length
                   158
                   70
% identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi 4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   1727
Seq. No.
                   950 2.R1040
Contig ID
5'-most EST
                   jC-qmle01810020d08a1
                   BLASTX
Method
NCBI GI
                   g4218535
                   591
BLAST score
                   7.0e-61
E value
Match length
                   167
% identity
                   63
                  (AJ010829) GRAB1 protein [Triticum sp.]
NCBI Description
                   1728
Seq. No.
                   950 3.R1040
Contig ID
                   zzp700834856.hl
5'-most EST
                   BLASTX
Method
                   g2058282
NCBI GI
BLAST score
                   716
E value
                   2.0e-75
                   177
Match length
                   78
% identity
NCBI Description (X97377) atranbpla [Arabidopsis thaliana]
                   1729
Seq. No.
Contig ID
                   950 4.R1040
                   leu701152450.hl
5'-most EST
Seq. No.
                   1730
Contig ID
                   950 5.R1040
                  LIB3030-006-Q1-B1-A1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4218535
BLAST score
                   525
E value
                   3.0e-53
Match length ·
                   144
% identity
                  (AJ010829) GRAB1 protein [Triticum sp.]
NCBI Description
                   1731
Seq. No.
Contig ID
                   950 6.R1040
5'-most EST
                  pcp700992258.h1
Method
                  BLASTX
NCBI GI
                   q2443890
BLAST score
                   221
E value
                   1.0e-17
Match length
                   66
% identity
```

NCBI Description (AC002294) similar to NAM (gp X92205 1321924) and CUC2

NCBI Description

```
(qp AB002560 1944132) proteins [Arabidopsis thaliana]
Seq. No.
                   1732
                   950 9.R1040
Contig ID
5'-most EST
                   LIB3092-043-Q1-K1-E1
Method
                   BLASTX
                   g4218535
NCBI GI
BLAST score
                   374
E value
                   6.0e-36
Match length
                   93
                   70
% identity
                   (AJ010829) GRAB1 protein [Triticum sp.]
NCBI Description
Seq. No.
                   1733
                   950 10.R1040
Contig ID
5'-most EST
                   jC-gmst02400071g08d1
Seq. No.
Contig ID
                   950 11.R1040
5'-most EST
                   uC-gmflminsoy049c06b1
Seq. No.
                   950 12.R1040
Contig ID
5'-most EST
                   LIB3074-028-Q1-K1-C3
Seq. No.
                   1736
                   950 14:R1040 -
Contig ID
                   zsq701127580.hl
5'-most EST
Seq. No.
                   1737
                   950 15.R1040
Contig ID
5'-most EST
                   LIB3039-012-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   g1732511
BLAST score
                   511
E value
                   6.0e-52
Match length
                   121
                   79
% identity
                   (U62742) Ran binding protein 1 homolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   1738
Contig ID
                   950 16.R1040
5'-most EST
                   LIB3073-009-Q1-K1-C4
Seq. No.
                   1739
                   950 19.R1040
Contiq ID
5'-most EST
                   LIB3106-112-Q1-K1-A7
Method
                   BLASTN
NCBI GI
                   g1336081
BLAST score
                   45
E value
                   4.0e-16
Match length
                   77
% identity
```

mRNA, complete cds

Glycine max var. Century ascorbate peroxidase 2 (APx2)

5'-most EST Method

BLAST score

NCBI GI

E value

```
1740
Seq. No.
                   950 24.R1040
Contig ID
5'-most EST
                  LIB3106-061-Q1-K1-G2
Seq. No.
                   1741
                   950 25.R1040
Contig ID
5'-most EST
                  hyd700726095.h1
Seq. No.
                  1742
Contig ID
                   951 1.R1040
5'-most EST
                  LIB3039-026-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  q1173209
BLAST score
                  681
E value
                   1.0e-71
Match length
                  140
% identity
                   94
                   40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
NCBI Description
                  protein S16 protein - upland cotton
                  >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
Seq. No.
                  1743
Contig ID
                  951 2.R1040
5'-most EST
                  dpv701100901.hl
Method
                  BLASTX
NCBI GI
                  q1173209
BLAST score
                  683
                  8.0e-72
E value
Match length
                  140
                  95
% identity
                  40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
NCBI Description
                  protein S16 protein - upland cotton
                  >gi_439654 emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
Seq. No.
                  1744
Contig ID
                  951 3.R1040
5'-most EST
                  jC-qmst02400009b06a1
Method
                  BLASTX
NCBI GI
                  g1173209
BLAST score
                  592
                  2.0e-61
E value
                  125
Match length
% identity
                  93
NCBI Description
                  40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
                  protein S16 protein - upland cotton
                  >gi 439654 emb CAA53567 (X75954) RS16 protein, 40S subunit
                  [Gossypium hirsutum]
Seq. No.
                  1745
Contig ID
                  954 1.R1040
```

sat701007156.h1

BLASTX

963

g1486472

1.0e-107

Match length 240 % identity 84 NCBI Description (X9)

أحوا ويصعفون

NCBI Description (X99853) oxoglutarate malate translocator [Solanum

tuberosum]

Seq. No. 1746

Contig ID 954\_2.R1040 5'-most EST gsv701045595.h1

Seq. No. 1747

Contig ID 954 3.R1040

5'-most EST LIB3107-070-Q1-K1-G12

Method BLASTX
NCBI GI g1486472
BLAST score 625
E value 4.0e-65
Match length 135
% identity 90

NCBI Description (X99853) oxoglutarate malate translocator [Solanum

tuberosum]

Seq. No. 1748

Contig ID 954\_4.R1040

5'-most EST uC-gmropic109e10b1

Method BLASTX
NCBI GI g2244847
BLAST score 1400
E value 1.0e-155
Match length 529

Match length 529 % identity 56

NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

[Arabidopsis thaliana]

Seq. No. 1749

Contig ID 954 5.R1040

5'-most EST LIB3109-052-Q1-K1-D9

Seq. No. 1750

Contig ID 954 6.R1040

5'-most EST jC-qmle01810016e03a1

Seq. No. 1751

Contig ID 955 1.R1040

5'-most EST LIB3065-024-Q1-N1-B5

Seq. No. 1752

Contig ID 956 1.R1040

5'-most EST LIB3138-047-Q1-N1-D3

Method BLASTX
NCBI GI g3513736
BLAST score 311
E value 2.0e-28
Match length 141
% identity 49

NCBI Description (AF080118) No definition line found [Arabidopsis thaliana]

>gi\_4539367\_emb\_CAB40061.1\_ (AL049525) putative protein

[Arabidopsis thaliana]

tale medical pro-

```
1753
Seq. No.
Contig ID
                   957 1.R1040
5'-most EST
                  LIB3109-028-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                   g606942
BLAST score
                   577
E value
                   3.0e-59
Match length
                  190
% identity
NCBI Description
                   (U13760) unknown [Gossypium hirsutum]
                   1754
Seq. No.
Contig ID
                   958 1.R1040
5'-most EST
                  LIB3093-033-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g120658
BLAST score
                  1645
E value
                   0.0e + 00
Match length
                   403
                  82
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_66025_pir__DEPMNA
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  garden pea >gi 12159 emb CAA36396 (X52148) GAPA [Pisum
                  sativum]
Seq. No.
                  1755
Contig ID
                  958 2.R1040
                  taw700658860.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g20728
BLAST score
                  37
E value
                  1.0e-11
Match length
                  68
% identity
                  91
                  Pea chloroplast GAPA mRNA encoding
NCBI Description
                  qlyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
                  1756
Seq. No.
                  960 1.R1040
Contig ID
5'-most EST
                  LIB3170-079-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g585749
                  718
BLAST score
                  8.0e-76
E value
                  177
Match length
                  79
% identity
                  PHYTOENE SYNTHASE PRECURSOR >gi 433994 emb CAA48155
NCBI Description
                   (X68017) phytoene synthase [Capsicum annuum]
Seq. No.
                  1757
                  960 2.R1040
Contig ID
```

vzy700755950.h1

BLASTX

5'-most EST Method

Contig ID

5'-most EST

10.22

```
NCBI GI
                   g585749
BLAST score
                   259
E value
                   5.0e-23
Match length
                   105
% identity
                   61
                   PHYTOENE SYNTHASE PRECURSOR >gi 433994 emb_CAA48155_
NCBI Description
                   (X68017) phytoene synthase [Capsicum annuum]
Seq. No.
                   1758
                   961 1.R1040
Contig ID
5'-most EST
                  LIB3170-087-Q1-K1-C2
                   1759
Seq. No.
                   961 2.R1040
Contig ID
5'-most EST
                   LIB3170-084-Q1-J1-B1
                   1760
Seq. No.
                   962 1.R1040
Contig ID
                  LIB3109-010-Q1-K1-E9
5'-most EST
Method
                  BLASTX
                   q1871199
NCBI GI
BLAST score
                   189
E value
                   4.0e-14
Match length
                   103
% identity
NCBI Description
                   (U91318) pM5 (3' partial) [Homo sapiens]
Seq. No.
                   963 1.R1040
Contig ID
5'-most EST
                  LIB3040-004-Q1-E1-C8
Method
                   BLASTX
NCBI GI
                   g2501356
BLAST score
                   3168
E value
                   0.0e + 00
Match length
                   738
% identity
                   TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
NCBI Description
                   >gi 1658322_emb_CAA90427_ (Z50099) transketolase precursor
                   [Solanum tuberosum]
Seq. No.
                   1762
                   963 2.R1040
Contig ID
5'-most EST
                   g5606060
Method
                  BLASTX
NCBI GI
                   g2501353
BLAST score
                   608
E value
                   5.0e-63
Match length
                   140
                   86
% identity
                  TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300
NCBI Description
                  transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum
                   (fragment) >gi 664901 emb CAA86607 (Z46646) transketolase
                   [Craterostigma plantagineum]
                  1763
Seq. No.
```

963 3.R1040

LIB3109-035-Q1-K1-G8

E value

```
Method
                   BLASTX
NCBI GI
                  g2501356
                   165
BLAST score
E value
                   3.0e-11
                   97
Match length
                   37
% identity
NCBI Description
                  TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
                  >gi 1658322_emb_CAA90427_ (Z50099) transketolase precursor
                   [Solanum tuberosum]
                  1764
Seq. No.
                   964 1.R1040
Contig ID
                  sat701014744.hl
5'-most EST
Method
                  BLASTX
                  g3341688
NCBI GI
BLAST score
                  1023
E value
                   1.0e-111
Match length
                  259
% identity
                  74
NCBI Description
                   (AC003672) putative casein kinase II beta subunit
                   [Arabidopsis thaliana]
                  1765
Seq. No.
Contig ID
                  964 2.R1040
5'-most EST
                  LIB3093-018-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g729880
BLAST score
                  235
E value
                  2.0e-19
Match length
                  124
                  46
% identity
                  CASEIN KINASE II BETA CHAIN (CK II) >gi 1076299 pir S47967
NCBI Description
                  casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis
                  thaliana >gi 468264 (L22563) casein kinase II beta subunit
                  CKB1 [Arabidopsis thaliana]
                  1766
Seq. No.
                  964 3.R1040
Contig ID
5'-most EST
                  LIB\overline{3}092-047-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g729880
BLAST score
                  168
E value
                  1.0e-11
Match length
                  113
% identity
                  41
                  CASEIN KINASE II BETA CHAIN (CK II) >gi 1076299 pir _S47967
NCBI Description
                  casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis
                  thaliana >gi 468264 (L22563) casein kinase II beta subunit
                  CKB1 [Arabidopsis thaliana]
                  1767
Seq. No.
Contig ID
                  964 4.R1040
                  jex700908130.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                  q468263
BLAST score
                  50
```

5.0e-19

NCBI GI

```
122
Match length
                   85
% identity
                   Arabidopsis thaliana casein kinase II beta subunit CKB1
NCBI Description
                   mRNA, complete cds
                   1768
Seq. No.
                   967 1.R1040
Contig ID
5'-most EST
                   g5677191
Seq. No.
                   1769
                   968 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400015g09d1
Seq. No.
                   970 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810044a05d1
Method
                   BLASTX
NCBI GI
                   g4006868
BLAST score
                   382
E value
                   9.0e-37
                   110
Match length
% identity
                   65
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1771
                   974 1.R1040
Contig ID
5'-most EST
                   hyd700727370.h1
                   1772
Seq. No.
                   975 1.R1040
Contig ID
                   jC-gmro02910008f01a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g687844
                   982
BLAST score
E value
                   1.0e-106
Match length
                   629
                   19
% identity
                   (U21320) contains TPR domain-like repeats [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   1773
                   975 2.R1040
Contig ID
5'-most EST
                   LIB3106-034-Q1-K1-D4
Seq. No.
                   1774
                   975 3.R1040
Contig ID
5'-most EST
                   pmv700888650.h1
                   1775
Seq. No.
                   975_4.R1040
Contig ID
5'-most EST
                   LIB3170-043-Q1-K1-A4
                   1776
Seq. No.
                   975 5.R1040
Contig ID
5'-most EST
                   LIB\overline{3}106-074-Q1-K1-G9
Method
                   BLASTX
```

g2266994

% identity

91

```
205
BLAST score
                   6.0e-16
E value
Match length
                   133
% identity
                   34
                   (U77413) O-linked GlcNAc transferase [Homo sapiens]
NCBI Description
                   >gi_4505499_ref_NP_003596.1_pOGT_ O-GlcNAc transferase
                   (uridine diphospho-N-acetylglucosamine:polypeptide
                   beta-N-acetylglucosaminyl transferase)
Seq. No.
                   977 1.R1040
Contig ID
5'-most EST
                   ASG32442DA-01-Q1-E1-A8
Method
                   BLASTX
NCBI GI
                   q4538945
BLAST score
                   361
                   3.0e-34
E value
Match length
                   82
                   78
% identity
NCBI Description
                   (AL049483) putative thioredoxin [Arabidopsis thaliana]
                   1778
Seq. No.
Contig ID
                   984 1.R1040
5'-most EST
                  LIB3170-052-Q1-J1-E12
Seq. No.
                   1779
                   984 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy133h03b1
Seq. No.
                   1780
Contig ID
                   985 1.R1040
5'-most EST
                  LIB3138-123-Q1-N1-D12
Seq. No.
                   1781
                   986 1.R1040
Contig ID
5'-most EST
                  q5606936
                   1782
Seq. No.
Contig ID
                   988 1.R1040
5'-most EST
                  LIB3051-046-Q1-K1-B6
                   1783
Seq. No.
                   989 1.R1040
Contig ID
5'-most EST
                  ASG32442DA-01-Q1-E1-C1
Seq. No.
                   1784
                   992 1.R1040
Contig ID
5'-most EST
                  g5509751
Seq. No.
                  1785
Contig ID
                   995 1.R1040
5'-most EST
                   jC-qmst02400016d12d1
                  BLASTN
Method
NCBI GI
                  g3168616
BLAST score
                  75
E value
                  5.0e-34
Match length
                  119
```

\*\*\* \*\*\* \*. .

% identity

NCBI Description

```
Drosophila melanogaster DNA sequence (P1 DS07982 (D185)),
NCBI Description
                   complete sequence [Drosophila melanogaster]
                   1786
Seq. No.
                   997 1.R1040
Contig ID
5'-most EST
                  ASG32442DA-01-Q1-E1-C7
Seq. No.
                   1787
                   1004 1.R1040
Contig ID
                  LIB3028-017-Q1-B1-F12
5'-most EST
                  1788
Seq. No.
Contig ID
                   1005 1.R1040
                  LIB3053-012-Q1-N1-A6
5'-most EST
                   1789
Seq. No.
                   1010 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810088b06d1
Method
                   BLASTN
NCBI GI
                   g12139
BLAST score
                   387
E value
                   0.0e + 00
                   499
Match length
                   94
% identity
                  Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and
NCBI Description
                   trnG coding for ribosomal protein S2, one CF(1) and three
                  CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly
Seq. No.
                  1790
                   1015 1.R1040
Contig ID
5'-most EST
                  ASG32442DA-01-Q1-E1-E6
Seq. No.
                  1791
                  1019 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910031e05d1
                  BLASTN
Method
                  g2598578
NCBI GI
BLAST score
                  95
E value
                  5.0e-46
Match length
                  171
                  89
% identity
                  Medicago truncatula mRNA for L-ascorbate oxidase
NCBI Description
Seq. No.
Contig ID
                  1025 1.R1040
5'-most EST
                  ASG32442DA-01-Q1-E1-F4
Seq. No.
                  1793
Contig ID
                  1032 1.R1040
5'-most EST
                  LIB3170-087-Q1-J1-B2
Method
                  BLASTX
NCBI GI
                  g4512703
BLAST score
                  442
E value
                  2.0e-43
Match length
                  211
```

(AC006569) unknown protein [Arabidopsis thaliana]

NCBI Description

```
1794
Seq. No.
                   1035 1.R1040
Contig ID
5'-most EST
                   ASG32442DA-01-Q1-E1-G4
Method
                   BLASTX
NCBI GI
                   g2129854
BLAST score
                   418
E value
                   4.0e-41
Match length
                   105
                   72
% identity
                   early nodulin 8 precursor - alfalfa >gi 304037 (L18899)
NCBI Description
                   early nodulin [Medicago sativa]
Seq. No.
Contig ID
                   1046 1.R1040
5'-most EST
                   g4299082
Method
                   BLASTX
NCBI GI
                   q4510383
BLAST score
                   762
E value
                   9.0e-81
Match length
                   303
                   78
% identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1796
                   1046 2.R1040
Contig ID
5'-most EST
                   q4305468
Method
                   BLASTX
NCBI GI
                   g4510383
BLAST score
                   271
E value
                   1.0e-23
                   82
Match length
                   67
% identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1050 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910007g06d1
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   1320
                   1.0e-146
E value
Match length
                   311
                   79
% identity
NCBI Description
                   (AC002328) F2202.16 [Arabidopsis thaliana]
                   1798
Seq. No.
                   1050 2.R1040
Contig ID
5'-most EST
                   LIB3170-029-Q1-J1-A7
Method
                  BLASTX
NCBI GI
                   q3953471
BLAST score
                   249
E value
                   3.0e-21
Match length
                   58
                   76
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
```

% identity

```
1799
Seq. No.
                   1050 3.R1040
Contig ID
                   LIB3030-003-Q1-B1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   624
                   7.0e-65
E value
Match length
                   231
% identity
                   59
NCBI Description
                   (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                   1800
                   1050 4.R1040
Contig ID
5'-most EST
                   ASG32442DA-02-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   229
E value
                   6.0e-19
Match length
                   50
% identity
                   80
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1801
                   1051 1.R1040
Contig ID
5'-most EST
                   g4285505
                   1802
Seq. No.
                   1057 1.R1040
Contig ID
                   ASG32442DA-02-Q1-E1-A7
5'-most EST
Method
                   BLASTX
                   g1652704
NCBI GI
                   198
BLAST score
                   4.0e-15
E value
Match length
                   95
% identity
                   41
                   (D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                   1803
Seq. No.
                   1060 1.R1040
Contig ID
                   ASG32442DA-02-Q1-E1-B1
5'-most EST
                   BLASTX
Method
                   g1076288
NCBI GI
                   241
BLAST score
                   3.0e-20
E value
Match length
                   89
% identity
                   amino acid permease AAP3 - Arabidopsis thaliana
NCBI Description
                   1804
Seq. No.
Contig ID
                   1064 1.R1040
5'-most EST
                   jC-gmle01810031g05d1
Method
                   BLASTX
NCBI GI
                   g3868758
BLAST score
                   1566
E value
                   1.0e-175
Match length
                   414
```

Match length

```
(D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
Seq. No.
                   1805
                   1064 2.R1040
Contig ID
                   g5126554
5'-most EST
Method
                   BLASTX
                   g3868758
NCBI GI
BLAST score
                   518
E value
                   1.0e-52
Match length
                   144
% identity
                   68
                   (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
Seq. No.
                   1806
                   1064_4.R1040
Contig ID
                   LIB3139-055-P1-N1-C4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3868758 🕆
BLAST score
                   420
E value
                   2.0e-41
                   104
Match length
% identity
                   75
                   (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
Seq. No.
                   1807
                   1064 5.R1040
Contig ID
5'-most EST
                   LIB3170-036-Q1-K2-D11
                   BLASTX
Method
NCBI GI
                   g2160158
                   212
BLAST score
E value
                   4.0e-17
                   43
Match length
% identity
                   93
                   (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb\_EF1G\_XENLA). ESTs gb\_T20564, gb\_T45940, gb\_T04527 come
                   from this gene. [Arabidopsis thaliana]
                   1808
Seq. No.
                   1064 6.R1040
Contig ID
5'-most EST
                   sat7\overline{0}1004617.h1
                   BLASTN
Method
                   g3868757
NCBI GI
BLAST score
                   73
E value
                   5.0e-33
Match length
                   209
% identity
                   84
                   Oryza sativa mRNA for elongation factor 1B gamma, complete
NCBI Description
                   cds
Seq. No.
                   1809
                   1065 1.R1040
Contig ID
                   ASG32442DA-02-Q1-E1-B3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4454482
BLAST score
                   410
                   5.0e-40
E value
```

Match length

```
% identity
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  1071 1.R1040
Contig ID
                  LIB3093-026-Q1-K1-H10
5'-most EST
Seq. No.
                  1811
                  1074 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810087f04d1
Seq. No.
                  1074 2.R1040
Contig ID
5'-most EST
                  jC-qmle01810046b09d1
Seq. No.
                  1092 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400008f02a1
Seq. No.
                  1092 2.R1040
Contig ID
5'-most EST
                  ASG32442DA-02-Q1-E1-D8
Seq. No.
                  1093 1.R1040
Contig ID
5'-most EST
                  LIB3051-013-Q1-E1-A4
Seq. No.
                  1816
                  1094 1.R1040
Contig ID
5'-most EST
                  ASG32442DA-02-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                  g3063453
BLAST score
                  167
E value
                  2.0e-11
Match length
                  147
% identity
                  36
                 (AC003981) F22013.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  1817
                  1098 1.R1040
Contig ID
5'-most EST
                  ASG32442DA-02-Q1-E1-E3
Method
                  BLASTX
                  g4567210
NCBI GI
BLAST score
                  548
E value
                  1.0e-55
Match length
                  110
                  93
% identity
                  (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  1818
Seq. No.
                  1098 2.R1040
Contig ID
5'-most EST
                  jC-gmst02400058b05d1
                  BLASTX
Method
NCBI GI
                  g4567210
BLAST score
                  191
E value
                  3.0e-14
```

Method

NCBI GI

BLASTX

q4160280

```
% identity
                   (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1100 1.R1040
Contig ID
                   jC-gmf102220114f08d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4176531
BLAST score
                   150
                   2.0e-09
E value
Match length
                   92
                   37
% identity
NCBI Description
                   (AL035263) weak similarity to chick phosphatidylcholine-ste
                   rol acetyltransferase [Schizosaccharomyces pombe]
Seq. No.
                   1820
                   1101 1.R1040
Contig ID
                   ASG32442DA-02-Q1-E1-E5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2098709
BLAST score
                   473
E value
                   8.0e-59
Match length
                   191
% identity
                   58
NCBI Description
                   (U82975) pectinesterase [Citrus sinensis]
Seq. No.
                   1821
Contig ID
                   1103 1.R1040
5'-most EST
                   LIB3093-001-Q1-K1-G8
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   1.0e-10.
E value
Match length
                   60
                   56
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   1822
Seq. No.
Contig ID
                   1103 3.R1040
5'-most EST
                   jC-gmf102220133h03d1
                   1823
Seq. No.
Contig ID
                   1112 1.R1040
5'-most EST
                   jC-gmst02400009a05d1
Method
                   BLASTX
NCBI GI
                   g2447107
BLAST score
                   302
                   4.0e-27
E value
Match length
                   125
% identity
                   (U42580) A638R [Paramecium bursaria Chlorella virus 1]
NCBI Description
Seq. No.
                   1824
Contig ID
                   1114 1.R1040
5'-most EST
                   g5509228
```

E value

```
BLAST score
                  1489
                   1.0e-166
E value
Match length
                   430
                   62
% identity
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
NCBI Description
                  1825
Seq. No.
                  1114 2.R1040
Contig ID
                  jC-gmle01810014f06d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4160280
BLAST score
                  290
E value
                   6.0e-26
Match length
                  76
                   67
% identity
                   (AJ006224) purple acid phosphatase [Ipomoea batatas]
NCBI Description
Seq. No.
                  1826
                  1114 5.R1040
Contig ID
5'-most EST
                  LIB3106-010-Q1-K1-F9
                  BLASTX
Method
NCBI GI
                  q4160280
BLAST score
                  280
E value
                  6.0e-25
                  90
Match length
                  59
% identity
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
Seq. No.
                  1827
                  1114 7.R1040
Contig ID
5'-most EST
                  LIB3107-003-Q1-K1-D6
                  BLASTX
Method
                  g4160280
NCBI GI
BLAST score
                  251
                  2.0e-21
E value
                  88
Match length
% identity
NCBI Description
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
                  1828
Seq. No.
                  1116 1.R1040
Contig ID
5'-most EST
                  pxt700941482.h1
Method .
                  BLASTX
NCBI GI
                  q3522938
                  887
BLAST score
                  2.0e-95
E value
                  330
Match length
% identity
NCBI Description
                  (AC004411) unknown protein [Arabidopsis thaliana]
                  1829
Seq. No.
                  1130 1.R1040
Contig ID
5'-most EST
                  ASG32442DA-02-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  g1346882
BLAST score
                  868
```

2.0e-93

```
192
Match length
                   87
% identity
                   PHYTOENE SYNTHASE PRECURSOR (MEL5) >gi_2129505_pir__S56668
NCBI Description
                   geranylgeranyl-diphosphate geranylgeranyltransferase (EC
                   2.5.1.32) precursor - muskmelon >gi_870985_emb_CAA85775_
                   (Z37543) phytoene synthase [Cucumis melo]
Seq. No.
                   1830
Contig ID
                   1130 2.R1040
5'-most EST
                   fC-qmle700682749f1
Method
                   BLASTN
NCBI GI
                   q433993
BLAST score
                   51
                   9.0e-20
E value
Match length
                   95
                   88
% identity
                   C.annuum psyl mRNA for phytoene synthase
NCBI Description
Seq. No.
                   1831
Contig ID
                   1133 1.R1040
                   ncj7\overline{0}0987183.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3913008
BLAST score
                   1634
E value
                   0.0e + 00
Match length
                   358
% identity
NCBI Description
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
                   >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic
                   fructose-1,6-bisphosphate aldolase [Cicer arietinum]
Seq. No.
                   1832
                   1133 2.R1040
Contig ID
5'-most EST
                   g4300477
Method
                   BLASTN
NCBI GI
                   q3021337
BLAST score
                   120
E value
                   1.0e-60
                   342
Match length
                   85
% identity
NCBI Description
                   Cicer arietinum mRNA for cytosolic
                   fructose-1,6-bisphosphate aldolase
Seq. No.
                   1833
                   1133 3.R1040
Contig ID
                   jex700908902.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3021337
BLAST score
                   119
E value
                   4.0e-60
Match length
                   267
                   87
% identity
NCBI Description
                   Cicer arietinum mRNA for cytosolic
                   fructose-1,6-bisphosphate aldolase
Seq. No.
                   1834
```

1133 6.R1040

Contig ID

```
5'-most EST
                  LIB3167-050-P1-K1-A7
                   1835
Seq. No.
Contig ID
                   1135 1.R1040
5'-most EST
                  LIB3170-087-Q1-K1-A3
                  BLASTX
Method
NCBI GI
                   g3036810
BLAST score
                   381
E value
                   2.0e-36
Match length
                   133
% identity
                   61
NCBI Description
                   (AL022373) putative Myc-type transcription factor
                   [Arabidopsis thaliana]
Seq. No.
                   1836
                   1142 1.R1040
Contig ID
5'-most EST
                  LIB3109-047-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q1351838
BLAST score
                  2125
E value
                   0.0e + 00
Match length
                   432
% identity
                   94
                  ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
NCBI Description
                  BETA >gi 984309 (U26948) beta-carboxyltransferase subunit
                   [Glycine max]
Seq. No.
                  1837
                  1142 2.R1040
Contig ID
5'-most EST
                  LIB3092-060-Q1-K1-G6
Method
                  BLASTN
                  g984307
NCBI GI
BLAST score
                  1556
E value
                  0.0e + 00
Match length
                  1664
% identity
                  98
                  Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                  cds, beta-carboxyltransferase (accD), photosystem I
                  component (psaI), ORF 202 protein (ORF 203), ORF 151
                  protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                  precurso
                  1838
Seq. No.
                  1142 3.R1040
Contig ID
5'-most EST
                  jC-gmle01810034g10a2
Method
                  BLASTN
                  g984307
NCBI GI
BLAST score
                  324
                  0.0e + 00
E value
Match length
                  383
                  95
% identity
                  Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                  cds, beta-carboxyltransferase (accD), photosystem I
                  component (psaI), ORF 202 protein (ORF 203), ORF 151
```

unapposite.

precurso

protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

Method

NCBI GI

.

BLASTN

q4115332

```
Seq. No.
                   1839
                   1142 7.R1040
Contig ID
5'-most EST
                   LIB3093-024-Q1-K1-C1
                   BLASTN
Method
                   q984307
NCBI GI
                   230
BLAST score
                   1.0e-126
E value
Match length
                   348
                   93
% identity
                   Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                   cds, beta-carboxyltransferase (accD), photosystem I
                   component (psaI), ORF 202 protein (ORF 203), ORF 151
                   protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                  precurso
Seq. No.
                   1840
                   1144 1.R1040
Contig ID
                   LIB3139-067-P1-N1-E5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3402716
BLAST score
                   299
E value
                   1.0e-26
                   233
Match length
% identity
                   34
                   (AC004261) unknown protein [Arabidopsis thaliana]
NCBI Description
                   1841
Seq. No.
                   1149 1.R1040
Contig ID
                  LIB3139-008-P1-N1-C9
5'-most EST
                   BLASTN
Method
NCBI GI
                   g19500
BLAST score
                   164
                   1.0e-86
E value
Match length
                   433
                   88
% identity
NCBI Description
                  L.polyphyllus mRNA for pPLZ12 protein
Seq. No.
                   1149 2.R1040
Contig ID
5'-most EST
                  LIB3074-031-Q1-K1-B9
                   1843
Seq. No.
Contig ID
                   1155 1.R1040
5'-most EST
                   gsv701046559.hl
Method
                  BLASTN
NCBI GI
                   q396818
BLAST score
                   222
E value
                   1.0e-121
Match length
                  734
% identity
                  83
NCBI Description P.sativum pspor1 mRNA encoding porin
Seq. No.
                   1844
Contig ID
                  1157 1.R1040
5'-most EST
                  uC-gmrominsoy256g12b1
```

```
BLAST score
                   444
                  0.0e + 00
E value
Match length
                  879
% identity
                  21
NCBI Description Pisum sativum (Alaska) ubiquitin (PUB1) gene, complete cds
Seq. No.
                  1845
                  1157 2.R1040
Contig ID
5'-most EST
                  LIB3093-033-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g170352
BLAST score
                  1835
E value
                  0.0e + 00
Match length
                  368
% identity
                   (M74101) hexameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                  >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana]
                  >gi 4115333 (L81139) ubiquitin [Pisum sativum] >gi 4115335
                   (L81140) ubiquitin [Pisum sativum]
Seq. No.
                  1846
Contig ID
                  1157 3.R1040
                  LIB3050-011-Q1-E1-D11
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4115334
BLAST score
                  340
E value
                  0.0e+00
Match length
                  620
                  20
% identity
                  Pisum sativum (Alaska) ubiquitin (PUB2) gene, complete cds
NCBI Description
Seq. No.
                  1157 4.R1040
Contig ID
5'-most EST
                  LIB3138-025-Q1-N1-A2
Method
                  BLASTN
NCBI GI
                  g4115338
                  206
BLAST score
E value
                  1.0e-112
                  337
Match length
                  22
% identity
NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds
                  1848
Seq. No.
                  1158 1.R1040
Contig ID
5'-most EST
                  LIB3107-062-Q1-K1-A5
Method
                  BLASTN
NCBI GI
                  g12178
BLAST score
                  511
                  0.0e + 00
E value
                  745
Match length
% identity
                  92
                  Pea chloroplast rpl36 (partial), rps11, rpoA, and petD
NCBI Description
                  (partial) genes for ribosomal proteins L36 and S11, RNA
                  polymerase alpha subunit, and cytochrome bf complex subunit
                  IV
```

1849

Seq. No.

% identity

```
1158 3.R1040
Contig ID
5'-most EST
                   wvk700686173.h1
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   151
E value
                   1.0e-79
Match length
                   203
% identity
                   94
NCBI Description
                   Tobacco chloroplast genome DNA
Seq. No.
                   1850
Contig ID
                   1162 1.R1040
5'-most EST
                   LIB3040-050-Q1-E1-C5
Method
                   BLASTN
NCBI GI
                   q2264309
BLAST score
                   53
E value
                   2.0e-20
Match length
                   472
                   82
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   1851
                   1164 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220096q11a1
Method
                   BLASTX
NCBI GI
                   q461812
BLAST score
                   342
E value
                   5.0e-32
Match length
                   162
% identity
                   40
                   CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
NCBI Description
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                   Cytochrome P-450 protein [Catharanthus roseus]
                   >qi 445604 prf 1909351A cytochrome P450 [Catharanthus
                   roseus]
Seq. No.
                   1852
                   1167 1.R1040
Contig ID
5'-most EST
                   uC-gmropic032h12b1
Method
                   BLASTN
NCBI GI
                   g470126
                   220
BLAST score
E value
                   1.0e-120
Match length
                   536
% identity
                   85
                   N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
NCBI Description
Seq. No.
                   1853
                   1167 2.R1040
Contig ID
5'-most EST
                   LIB3106-051-Q1-K1-H5
Method
                   BLASTN
NCBI GI
                   g470126
                   170
BLAST score
E value
                   3.0e-90
Match length
                   566
```

```
NCBI Description N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
                   1854
Seq. No.
                   1167 3.R1040
Contig ID
5'-most EST
                   uC-gmropic010a09b1
                   BLASTN
Method
NCBI GI
                   g470126
BLAST score
                   105
E value
                   1.0e-51
Match length
                   333
% identity
                   83
                  N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
NCBI Description
Seq. No.
                   1167 4.R1040
Contig ID
                   jsh7\overline{0}1064147.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3377797
BLAST score
                   417
E value
                   4.0e-79
Match length
                   174
% identity
                   89
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  1856
                  1167 5.R1040
Contig ID
                  g5688162
5'-most EST
Method
                  BLASTN
                  g169928
NCBI GI
BLAST score
                  81
E value
                  2.0e-37
Match length
                  89
                   98
% identity
                  Glycine max alpha'-type beta conglycinin storage protein
NCBI Description
                  gene, complete cds, clone ch4A
                  1857
Seq. No.
                  1167 6.R1040
Contig ID
5'-most EST
                  LIB3170-035-Q1-K1-G2
                  BLASTN
Method
NCBI GI
                  g470126
BLAST score
                  94
                  2.0e-45
E value
                  242
Match length
                  85
% identity
NCBI Description
                  N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
                  1858
Seq. No.
                  1167 7.R1040
Contig ID
5'-most EST
                  LIB3\overline{0}50-011-Q1-E1-F12
Method
                  BLASTN
```

g470126

90

NCBI GI BLAST score

Match length

```
E value
                   5.0e-43
Match length
                   238
% identity
                   84
                   N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
NCBI Description
Seq. No.
                   1175 1.R1040
Contig ID
5'-most EST
                   LIB3107-038-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   q3378650
BLAST score
                   1274
E value
                   1.0e-141
Match length
                   313
% identity
                   76
                   (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
Seq. No.
                   1860
                   1175 2.R1040
Contig ID
5'-most EST
                   rca7\overline{0}1000823.h1
Method
                   BLASTX
NCBI GI
                   q3378650
BLAST score
                   490
E value
                   3.0e-49
Match length
                   113
% identity
                   80
                   (X97606) abscisic acid activated [Medicago sativa]
NCBI Description
Seq. No.
                   1175 3.R1040
Contig ID
                   LIB3\overline{0}93-009-Q1-K1-G11
5'-most EST
                   BLASTN
Method
                   g3378649
NCBI GI
BLAST score
                   150
                   1.0e-78
E value
Match length
                   314
                   87
% identity
                   M.sativa mRNA translated from abscisic activated gene
NCBI Description
                   1862
Seq. No.
Contig ID
                   1175 4.R1040
5'-most EST
                   uC-gmronoir023c03b1
Method
                   BLASTN
NCBI GI
                   g3378649
BLAST score
                   155
E value
                   1.0e-81
Match length
                   311
                   87
% identity
                   M.sativa mRNA translated from abscisic activated gene
NCBI Description
Seq. No.
                   1863
                   1175 5.R1040
Contig ID
5'-most EST
                   zsg701120171.h1
Method
                   BLASTX
NCBI GI
                   g3378650
BLAST score
                   378
E value
                   2.0e-45
```

5'-most EST

```
76
% identity
NCBI Description
                   (X97606) abscisic acid activated [Medicago sativa]
Seq. No.
                   1175 6.R1040
Contig ID
5'-most EST
                   LIB3092-022-Q1-K1-G11
Method
                   BLASTN
NCBI GI
                   q3378649
BLAST score
                   103
E value
                   1.0e-50
Match length
                   278
% identity
                   84
NCBI Description M.sativa mRNA translated from abscisic activated gene
Seq. No.
                   1865
Contig ID
                   1179 1.R1040
5'-most EST
                   LIB3072-053-Q1-E1-F3
Method
                   BLASTX
NCBI GI
                   q2119749
BLAST score
                   249
E value
                   7.0e-21
Match length
                   78
% identity
                   60
NCBI Description
                   oleosin - almond
Seq. No.
                   1866
                   1181 1.R1040
Contiq ID
5'-most EST
                   uC-qmrominsoy313h12b1
Seq. No.
                   1182 1.R1040
Contig ID
5'-most EST
                   LIB3027-010-Q1-B1-F2
Seq. No.
                   1868
                   1184 1.R1040
Contig ID
                   LIB3\overline{0}27-010-Q1-B1-F4
5'-most EST
                   1869
Seq. No.
                   1187 1.R1040
Contig ID
5'-most EST
                   LIB3139-081-P1-N1-C1
                   BLASTX
Method
                   g2245004
NCBI GI
BLAST score
                   345
E value
                   2.0e-32
Match length
                   106
% identity
                   59
                   (Z97341) similarity to membrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   1870
Seq. No.
                   1188 1.R1040
Contig ID
5'-most EST
                   seb700653874.h1
Seq. No.
                   1871
Contig ID
                   1188 2.R1040
```

jC-gmst02400072b08a1

```
1872
Seq. No.
Contig ID
                   1189 1.R1040
5'-most EST
                   jC-gmle01810012e01a1
Method
                   BLASTX
NCBI GI
                   g3928760
BLAST score
                   966
E value
                   1.0e-104
Match length
                   265
% identity
                   75
NCBI Description
                   (AB011797) homolog to plastid-lipid-associated protein
                   [Citrus unshiu]
                   1873
Seq. No.
                   1189 2.R1040
Contig ID
5'-most EST
                   LIB3170-056-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                   g3928760
BLAST score
                   356
E value
                   1.0e-33
Match length
                   113
% identity
NCBI Description
                   (AB011797) homolog to plastid-lipid-associated protein
                   [Citrus unshiu]
Seq. No.
                   1874
                   1189 3.R1040
Contig ID
                   LIB3106-085-Q1-K1-D3
5'-most EST
                   1875
Seq. No.
Contig ID
                   1189 4.R1040
                   V4R - \overline{0}2 - Q1 - B1 - H1
5'-most EST
                   1876
Seq. No.
                   1195 1.R1040
Contig ID
                   fua701041821.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3355658
BLAST score
                   192
E value
                   1.0e-14
Match length
                   124
% identity
                   38
                   (AJ009691) SMC2orf [Podocoryne carnea]
NCBI Description
                   1877
Seq. No.
                   1199 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400023e02a1
Method
                   BLASTX
NCBI GI
                   g1705574
                   176
BLAST score
E value
                   3.0e-12
Match length
                   172
                   33
% identity
                   CALPAIN (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP)
NCBI Description
                   >gi 562289 emb CAA55298_ (X78555) calpain [Drosophila
                   melanogaster]
```

Seq. No.

```
Contig ID
                   1202 1.R1040
                   zpv700758807.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g633890
BLAST score
                   455
                   2.0e-45
E value
                   143
Match length
% identity
                   61
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
                   1879
Seq. No.
                   1203 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220061g03a1
Method
                   BLASTX
NCBI GI
                   g4139266
BLAST score
                   937
E value
                   1.0e-101
Match length
                   325
% identity
                   60
                   (AF112444) L-asparaginase [Lupinus.luteus]
NCBI Description
                   -1880
Seq. No.
                   1203 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy129c01b1
                   BLASTX
Method
NCBI GI
                   g2462826
BLAST score
                   219
                   2.0e-17
E value
Match length
                   137
                   40
% identity
                   (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1203 3.R1040
Contig ID
5'-most EST
                   LIB3049-001-Q1-E1-C8
                   1882
Seq. No.
                   1203 4.R1040
Contig ID
5'-most EST
                   jC-gmro02910005f01a1
Method
                   BLASTX
NCBI GI
                   g2462826
                   173
BLAST score
                   3.0e-12
E value
Match length
                   81
% identity
                   (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
                   1883
Seq. No.
                   1203 6.R1040
Contig ID
5'-most EST
                   jC-qmf102220061g03d1
                   1884
Seq. No.
                   1203 7.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy044h10b1
Method
                   BLASTX
```

g1703446

NCBI GI

```
BLAST score
                   235
                   1.0e-19
E value
Match length
                   83
                   61
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi 1076292_pir__S53127 asparaginase - Arabidopsis thaliana
                  >gi 735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis
                   thaliana]
                   1885
Seq. No.
                   1203 11.R1040
Contig ID
5'-most EST
                   zhf700961256.h1
Method
                  BLASTX
                  q1703446
NCBI GI
BLAST score
                   186
E value
                   3.0e-14
                   65
Match length
                   63
% identity
NCBI Description
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                  >gi 1076292 pir S53127 asparaginase - Arabidopsis thaliana
                      735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis
                  thaliana]
                  1886
Seq. No.
                  1204 1.R1040
Contig ID
                  awf700839244.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4204308
BLAST score
                  237
                  7.0e-20
E value
Match length
                   43
                   91
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  1887
Seq. No.
                  1206 1.R1040
Contig ID
5'-most EST
                  LIB3027-010-Q1-B1-C9
Seq. No.
                  1888
                  1210 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy005a10b1
Method.
                  BLASTX
NCBI GI
                  g2623309
BLAST score
                  702
                  2.0e-73
E value
Match length
                  435
% identity
                   (AC002409) similar to tgacg-specific DNA-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  1889
Seq. No.
Contig ID
                  1212 1.R1040
5'-most EST
                  LIB3029-006-Q1-B1-H7
Method
                  BLASTX
                  q1710077
NCBI GI
BLAST score
                  558
```

5'-most EST Method

BLASTX

```
E value
                     2.0e-74
Match length
                     190
% identity
                     71 ·
                     PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)
NCBI Description
                    >gi_2130029_pir__S60285 B15C protein - barley
>gi_471321_emb_CAA54066_ (X76605) HvB15C [Hordeum vulgare]
>gi_1694833_emb_CAA65387_ (X96551) peroxiredoxin [Hordeum
                     vulgare]
Seq. No.
                     1890
                     1215 1.R1040
Contig ID
                    LIB3040-022-Q1-E1-D9
5'-most EST
Method
                    BLASTX
NCBI GI
                     g3759184
BLAST score
                     805
                     4.0e-86
E value
                     225
Match length
% identity
                     68
                     (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                     1891
Seq. No.
Contig ID
                    1219 1.R1040
                    LIB3051-097-Q1-K1-G7
5'-most EST
Method
                    BLASTN
NCBI GI
                    g22075
BLAST score
                     167
                     9.0e-89
E value
                    247
Match length
                     92
% identity
                    Vigna unguiculata cDNA for stored cotyledon mRNA
NCBI Description
Seq. No.
                    1223 1.R1040
Contig ID
5'-most EST
                     jC-gmle01810030e08a2
Method
                    BLASTX
NCBI GI
                    g1173555
BLAST score
                    1661
                    0.0e + 00
E value
Match length
                    350
% identity
                     90
                     (U31544) UDP-galactose-4-epimerase [Pisum sativum]
NCBI Description
                    1893
Seq. No.
                    1223 2.R1040
Contig ID
5'-most EST
                    jex700910050.hl
Method
                    BLASTX
NCBI GI
                    q1173555
BLAST score
                    180
                    1.0e-13
E value
Match length
                    43
% identity
                    (U31544) UDP-galactose-4-epimerase [Pisum sativum]
NCBI Description
                    1894
Seq. No.
Contig ID
                    1223 3.R1040
                    wrg700787631.h2
```

NCBI GI

```
NCBI GI
                   q1173555
BLAST score
                   232
E value
                   1.0e-19
Match length
                   71
                   69
% identity
                   (U31544) UDP-galactose-4-epimerase [Pisum sativum]
NCBI Description
Seq. No.
                   1225 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy101e03b1
                   BLASTX
Method
NCBI GI
                   g2244814
BLAST score
                   722
E value
                   2.0e-76
Match length
                   189
                   75
% identity
NCBI Description
                   (Z97336) protein kinase [Arabidopsis thaliana]
Seq. No.
                   1896
                   1228 1.R1040
Contig ID
5'-most EST
                   LIB3109-054-Q1-K1-H11
Method
                   BLASTX
NCBI GI
                   g4510348
BLAST score
                   774
E value
                   2.0e-82
Match length
                   213
                   64
% identity
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1230 1.R1040
Contig ID
5'-most EST
                   LIB3027-009-Q1-B1-E6
Method
                   BLASTX
NCBI GI
                   g3892055
BLAST score
                   325
                   3.0e-30
E value
Match length
                   121
                   55
% identity
                   (AC002330) putative transport protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   1898
                   1243 1.R1040
Contig ID
5'-most EST
                   LIB3049-039-Q1-E1-A2
Method
                   BLASTX
NCBI GI
                   g3650033
                   959
BLAST score
E value
                   1.0e-104
Match length
                   302
% identity
                   (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1899
Contig ID
                   1243 2.R1040
5'-most EST
                   uC-gmropic036g10b1
Method
                   BLASTX
```

q3650033

```
328
BLAST score
                   2.0e-30
E value
                   85
Match length
% identity
                   78
                   (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                   1900
Seq. No.
                   1244 1.R1040
Contig ID
5'-most EST
                   LIB3027-009-Q1-B1-B12
Seq. No.
                   1901
                   1246 1.R1040
Contig ID
5'-most EST
                   LIB3029-007-Q1-B1-A2
                   BLASTN
Method
NCBI GI
                   g256634
BLAST score
                   810
E value
                   0.0e + 00
Match length
                   872
                   45
% identity
                   KTil=Kunitz trypsin inhibitor KTil, KTi2=Kunitz trypsin
NCBI Description
                   inhibitor KTi2 [soybeans, Genomic, 3269 nt]
Seq. No.
                   1902
                   1246 3.R1040
Contig ID
5'-most EST
                   vwf700673594.hl
Method .
                   BLASTN
NCBI GI
                   g256634
BLAST score
                   185
E value
                   1.0e-100
Match length
                   250
% identity
                   50
                   KTil=Kunitz trypsin inhibitor KTil, KTi2=Kunitz trypsin
NCBI Description
                   inhibitor KTi2 [soybeans, Genomic, 3269 nt]
Seq. No.
                   1903
                   1247 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy042f10b1
Method
                   BLASTN
                   q2970653
NCBI GI
BLAST score
                   458
                   0.0e+00
E value
                   738
Match length
                   92
% identity
                   Vigna unquiculata ferritin subunit cowpea2 precursor, mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
                   1904
Seq. No.
                   1247 2.R1040
Contig ID
                   LIB3049-045-Q1-E1-C6
5'-most EST
                   BLASTN
Method
                   g2970653
NCBI GI
BLAST score
                   198
                   1.0e-107
E value
                   346
Match length
% identity
                   92
NCBI Description
                   Vigna unquiculata ferritin subunit cowpea2 precursor, mRNA,
```

nuclear gene encoding chloroplast protein, complete cds

5'-most EST

q4305784

```
1905
Seq. No.
                   1248 1.R1040
Contig ID
                  LIB3139-026-P1-N1-C10
5'-most EST
                  BLASTX
Method
                   g3023832
NCBI GI
BLAST score
                   1513
E value
                   1.0e-169
Match length
                   320
                   52
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1
NCBI Description
                  >gi 1835161 emb CAB06618 (Z84820) G protein beta subunit
                   [Nicotiana tabacum]
                  1906
Seq. No.
                  1248 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy167g11b1
Method
                  BLASTX
NCBI GI
                  g3023832
BLAST score
                   663
E value
                  1.0e-69
Match length
                  142
                  88
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1
NCBI Description
                  >gi 1835161 emb CAB06618 (Z84820) G protein beta subunit
                   [Nicotiana tabacum]
Seq. No.
                  1907
                  1248 3.R1040
Contig ID
5'-most EST
                  LIB3109-021-Q1-K2-H8
Method
                  BLASTX
NCBI GI
                  g3023841
BLAST score
                  304
E value
                  1.0e-27
Match length
                  68
                  87
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
NCBI Description
                  >gi 1695179 emb CAA70704 (Y09513) G protein beta subunit
                  [Nicotiana plumbaginifolia]
                  1908
Seq. No.
Contig ID
                  1248 4.R1040
5'-most EST
                  zpv700762067.h1
Method
                  BLASTX
                  g3023841
NCBI GI
                  254
BLAST score
E value
                  4.0e-22
Match length
                  70
% identity
                  69
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
NCBI Description
                  >gi 1695179 emb CAA70704 (Y09513) G protein beta subunit
                  [Nicotiana plumbaginifolia]
Seq. No.
                  1909
Contig ID
                  1250 1.R1040
```

```
1910
Seq. No.
Contig ID
                   1253 1.R1040
5'-most EST
                   qsv7\overline{0}1046538.h1
Method
                   BLASTX
NCBI GI
                   g2506470
BLAST score
                   2270
E value
                   0.0e + 00
Match length
                   541
% identity
                   82
NCBI Description
                   ALPHA-1,4 GLUCAN PHOSPHORYLASE, L ISOFORM PRECURSOR (STARCH
                   PHOSPHORYLASE L) >gi_1616637_emb_CAA85354_ (Z36880)
                   alpha-1,4 Glucan Phosphorylase, L isoform precursor [Vicia
                   fabal
Seq. No.
                   1911
                   1253 2.R1040
Contig ID
5'-most EST
                   jC-qmst02400070b12a1
Method
                   BLASTN
NCBI GI
                   q534971
BLAST score
                   122
E value
                   6.0e-62
Match length
                   178
% identity
                   92
                   V.faba (var. minor) mRNA for alpha 1,4-glucan phosphorylase
NCBI Description
                   L isoform
Seq. No.
                   1912
                   1253 3.R1040
Contig ID
5'-most EST
                   LIB3074-036-Q1-K1-C4
Method
                   BLASTN
NCBI GI
                   g11576
BLAST score
                   583
E value
                   0.0e + 00
Match length
                   1120
% identity
                   99
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                   NADH dehydrogenase and ORF
                   1913
Seq. No.
                   1253 8.R1040
Contig ID
5'-most EST
                   LIB3093-053-Q1-K1-E4
Method
                   BLASTN
                   g11576
NCBI GI
BLAST score
                   116
E value
                   2.0e-58
Match length
                   413
                   93
% identity
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                   NADH dehydrogenase and ORF
Seq. No.
                   1914
                   1253 9.R1040
Contig ID
                   leu7\overline{0}1144377.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g11576
BLAST score
```

1.0e-55

E value

```
Match length
                   170
                   93
% identity
NCBI Description
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
                   NADH dehydrogenase and ORF
Seq. No.
                   1915
                   1267 1.R1040
Contig ID
5'-most EST
                   awf7\overline{0}0842486.h1
                   BLASTN
Method
NCBI GI
                   g3046856
BLAST score
                   35
E value
                   1.0e-09
Match length
                   301
% identity
                   84
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXI22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   1272 1.R1040
Contig ID
                   q5688109
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170005
BLAST score
                   1008
E value
                   0.0e + 00
Match length
                   1022
% identity
                   100
                   Soybean lectin (Le1) gene, complete cds
NCBI Description
                   1917
Seq. No.
                   1272 2.R1040
Contig ID
5'-most EST
                   LIB3092-053-Q1-K1-D3
Seq. No.
                   1918
                   1273 1.R1040
Contig ID
5'-most EST
                   LIB3107-061-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   q4115934
BLAST score
                   593
                   3.0e-61
E value
Match length
                   128
% identity
                   79
                   (AF118223) contains similarity to Methanobacterium
NCBI Description
                   thermoautotrophicum transcriptional regulator (GB:AE000850)
                   [Arabidopsis thaliana]
Seq. No.
                   1919
                   1273 2.R1040
Contig ID
5'-most EST
                   LIB3107-016-Q1-K1-D1
Method
                   BLASTX
NCBI GI
                   g4115939
BLAST score
                   237
                   7.0e-20
E value
Match length
                   57
% identity
NCBI Description
                   (AF118223) contains similarity to Methanobacterium
                   thermoautotrophicum transcriptional regulator (GB:AE000850)
```

[Arabidopsis thaliana]

```
1920
Seq. No.
                   1274 1.R1040
Contig ID
                   LIB3109-001-Q1-K2-B7
5'-most EST
                   BLASTX
Method
                   g401188
NCBI GI
BLAST score
                   383
E value
                   4.0e-48
Match length
                   305
% identity
                   22
                  NUCLEOLYSIN TIA-1 >gi 107354 pir A39293 cytotoxic
NCBI Description
                   granule-associated RNA-binding protein TIA1 precursor,
                   leukocyte - human
                   1921
Seq. No.
                   1274 2.R1040
Contig ID
5'-most EST
                   LIB3051-001-Q1-E1-D4
Seq. No.
                   1922
                   1274 3.R1040
Contig ID
5'-most EST
                   LIB3170-042-Q1-K1-C2
                   1923
Seq. No.
                   1276 1.R1040
Contig ID
                  LIB3107-075-Q1-K1-E5
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3193298
BLAST score
                   190
E value
                   6.0e-14
                   108
Match length
                   35
% identity
NCBI Description
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
                   1924
Seq. No.
                  1279 1.R1040
Contig ID
5'-most EST
                  LIB3106-070-P1-K1-F1
Method
                  BLASTN
NCBI GI
                   g3603398
BLAST score
                   336
                   0.0e+00
E value
                   1019
Match length
                   87
% identity
                  Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad2)
NCBI Description
                  mRNA, complete cds
                  1925
Seq. No.
                  1279 2.R1040
Contig ID
5'-most EST
                  pmv700890767.h1
Method
                  BLASTN
NCBI GI
                  q19594
BLAST score
                  143
                  2.0e-74
E value
                  338
Match length
% identity
                  88
NCBI Description
                  M.sativa encoding cinnamyl alcohol dehydrogenase
```

Seq. No.

```
1279 3.R1040
Contiq ID
                   LIB3138-062-Q1-N1-E10
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3603398
BLAST score
                   140
                   2.0e-72
E value
                   387
Match length
% identity
                   89
NCBI Description
                   Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad2)
                   mRNA, complete cds
                   1927
Seq. No.
                   1279 5.R1040
Contig ID
                   sat7\overline{0}1009719.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3603398
BLAST score
                   129
                   3.0e-66
E value
Match length
                   284
% identity
                   86
                   Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad2)
NCBI Description
                   mRNA, complete cds
                   1928
Seq. No.
                   1281 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800043h04a1
Method
                   BLASTX
NCBI GI
                   g2865175
BLAST score
                   412
E value
                   3.0e-40
Match length
                   132
                   61
% identity
                  (AB010945) AtRerlA [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1929
                   1281 2.R1040
Contig ID
                   pxt700941249.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2642434
BLAST score
                   229
E value
                   5.0e-19
Match length
                   102
                   46
% identity
NCBI Description
                   (ACO02391) putative Rerl protein [Arabidopsis thaliana]
Seq. No.
                   1930
                   1282 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1152518.h1
Method
                   BLASTN
NCBI GI
                   g343480
BLAST score
                   877
                   0.0e+00
E value
Match length
                   1323
                   92
% identity
NCBI Description
                   tobacco chloroplast atpase gene (b and e subunits) and
```

flanks

Match length

279

```
1931
Seq. No.
                   1282 6.R1040
Contig ID
                   fde700872028.h1
5'-most EST
Method
                   BLASTN
                   g3929530
NCBI GI
BLAST score
                   168
                   1.0e-89
E value
Match length
                   244
% identity
                   96
NCBI Description
                   Anisoptera marginata ATP synthase beta subunit (atpB) gene,
                   chloroplast gene encoding chloroplast protein, partial cds
                   1932
Seq. No.
                   1283 1.R1040
Contig ID
                   sat7\overline{0}1003615.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3043427
BLAST score
                   278
E value
                   1.0e-155
Match length
                   594
                   87
% identity
NCBI Description
                  Cicer arietinum mRNA for 40S ribosomal protein S5
                   1933
Seq. No.
                   1283 2.R1040
Contig ID
                   rca700999874.h1
5'-most EST
                   1934
Seq. No.
                   1283_3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy068d03b1
                   BLASTN
Method
NCBI GI
                   g3043427
                   248
BLAST score
E value
                   1.0e-137
                   592
Match length
                   85
% identity
NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S5
Seq. No.
                   1935
Contig ID
                   1283 4.R1040
5'-most EST
                   LIB3170-014-Q1-K1-E1
                   BLASTN
Method
NCBI GI
                   g3043427
BLAST score
                   183
E value
                   4.0e-98
Match length
                   567
% identity
                   86
NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S5
Seq. No.
                   1936
                   1283 6.R1040
Contig ID
5'-most EST
                   LIB3051-015-Q1-E1-C1
                   BLASTN
Method
NCBI GI
                   g3043427
BLAST score
                   117
                   4.0e-59
E value
```

5'-most EST

Method

....

```
% identity
                  Cicer arietinum mRNA for 40S ribosomal protein S5
NCBI Description
                  1937
Seq. No.
                  1285 1.R1040
Contig ID
                  LIB3049-048-Q1-E1-A5
5'-most EST
                  BLASTN
Method
NCBI GI
                  g20657
BLAST score
                  362
                  0.0e+00
E value
                  753
Match length
                  89
% identity
NCBI Description P.sativum Cab II gene for chlorophyll a/b-binding protein
                  1938
Seq. No.
                  1285 2.R1040
Contig ID
5'-most EST
                  LIB3170-023-Q1-J1-B4
Method
                  BLASTX
NCBI GI
                  g3560529
BLAST score
                  194
E value
                  7.0e-15
Match length
                  49
                  80
% identity
NCBI Description
                   (AF039598) light harvesting chlorophyll A/B binding protein
                   [Prunus persica]
                  1939
Seq. No.
                  1285 3.R1040
Contig ID
                  hyd700727351.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g20657
BLAST score
                  229
E value
                  1.0e-126
Match length
                  450
% identity
                  91
                  P.sativum Cab II gene for chlorophyll a/b-binding protein
NCBI Description
                  1940
Seq. No.
Contig ID
                  1287 1.R1040
5'-most EST
                  LIB3106-019-Q1-K1-H2
                  BLASTX
Method
NCBI GI
                  g3183247
BLAST score
                  1178
E value
                  1.0e-129
Match length
                  391
                  58
% identity
NCBI Description
                  PUTATIVE GTP-BINDING PROTEIN W08E3.3
                  >gi 3880615 emb CAB07131 (292773) predicted using
                  Genefinder; Similarity to Yeast hypothetical 44.2 KD
                  protein, putative GTP-binding protein (SW:P38219); cDNA EST
                  EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777
                  comes from this gene; cDNA EST EMB
Seq. No.
                  1941
Contig ID
                  1290 1.R1040
```

kmv700739112.h1

BLASTX

```
q4056479
NCBI GI
BLAST score
                   291
E value
                   4.0e-26
Match length
                   82
                   73
% identity
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
                   1942
Seq. No.
Contig ID
                   1291 1.R1040
5'-most EST
                  LIB3027-008-Q1-B1-A3
                   1943
Seq. No.
Contig ID
                   1292 1.R1040
5'-most EST
                  LIB3029-012-Q1-B1-B1
Method
                  BLASTX
NCBI GI
                   g1839188
BLAST score
                   539
E value
                   7.0e-55
Match length
                   157
% identity
NCBI Description
                   (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                   1944
Contig ID
                   1293 1.R1040
5'-most EST
                  leu701153506.h1
Seq. No.
                   1945
                  1294 1.R1040
Contig ID
5'-most EST
                  g5687992
Method
                  BLASTX
NCBI GI
                  g729470
BLAST score
                  1608
E value
                   1.0e-180
Match length
                   356
% identity
                  83
NCBI Description
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi 297798 emb CAA79702
                   (Z21493) mitochondrial formate dehydrogenase precursor
                   [Solanum tuberosum]
                  1946
Seq. No. ..
                  1294 2.R1040
Contig ID
5'-most EST
                  k117\overline{0}1213327.h1
Method
                  BLASTX
NCBI GI
                  q729470
BLAST score
                  518
E value
                  1.0e-52
Match length
                  115
% identity
                  85
NCBI Description
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798 emb CAA79702
                   (Z21493) mitochondrial formate dehydrogenase precursor
```

[Solanum tuberosum]

NCBI GI

```
1947
Seq. No.
                   1294 4.R1040
Contig ID
                   hrw701059575.hl
5'-most EST
Method
                   BLASTX
                   g729470
NCBI GI
BLAST score
                   536
E value
                   7.0e-55
Match length
                   139
% identity
                   77
                   MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                    (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                   >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                    (Z21493) mitochondrial formate dehydrogenase precursor
                    [Solanum tuberosum]
Seq. No.
                   1948
                   1294 5.R1040
Contig ID
5'-most EST
                   LIB3072-059-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   q729470
BLAST score
                   293
E value
                   2.0e-26
Match length
                   71
                   75
% identity
                   MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                   >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                   precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                   (Z21493) mitochondrial formate dehydrogenase precursor
                   [Solanum tuberosum]
Seq. No.
                   1949
                   1294 7.R1040
Contig ID
5'-most EST
                   LIB3072-017-Q1-E1-H12
                                                              . -
                   1950
Seq. No.
Contig ID
                   1294 8.R1040
5'-most EST
                   rca701002059.h1
Seq. No.
                   1951
                   1294 9.R1040
Contig ID
5'-most EST
                   jC-gmf102220063f11d1
Method
                   BLASTX
NCBI GI
                   q4062934
BLAST score
                   444
E value
                   4.0e-44
Match length
                   85
% identity
NCBI Description (D88272) formate dehydrogenase [Hordeum vulgare]
Seq. No.
                   1952
Contig ID
                   1294 11.R1040
5'-most EST
                   kmv700742307.h1
Method
                   BLASTX
```

q3821730

E value

```
BLAST score
                  142
                   3.0e-09
E value
                  55
Match length
% identity
                  51
NCBI Description (299991) formate dehydrogenase [Solanum tuberosum]
                  1953
Seq. No.
                  1295 1.R1040
Contig ID
5'-most EST
                  LIB3109-029-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2245086
BLAST score
                  540
                   4.0e-55
E value
Match length
                  158
% identity
                  72
NCBI Description
                  (297343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  1954
                  1295_2.R1040
Contig ID
                  jC-gmst02400016b09d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2245086 ·
BLAST score
                  329
E value
                  2.0e-30
Match length
                  89
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  1955
Contig ID
                  1296 1.R1040
5'-most EST
                  ssr700555601.h1
Method
                  BLASTX
NCBI GI
                  g231660
BLAST score
                  1146
E value
                  1.0e-125
Match length
                  636
% identity
                  44
                  HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
NCBI Description
Seq. No.
                  1956
                  1296 2.R1040
Contig ID
                  LIB3138-059-Q1-N1-C5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g82200
BLAST score
                  734
E value
                  2.0e-77
Match length
                  404
% identity
                  46
                  hypothetical protein 1244 - common tobacco chloroplast
NCBI Description
                  1957
Seq. No.
                  1296 9.R1040
Contig ID
5'-most EST
                  uC-gmropic097d09b1
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  55
```

4.0e-22

Seq. No.

Contig ID

1963

1298 5.R1040

```
203
Match length
                   82
% identity
                   Tobacco chloroplast genome DNA
NCBI Description
                   1958
Seq. No.
                   1296 10.R1040
Contig ID
5'-most EST
                   leu701148723.hl
Seq. No.
                   1959
Contig ID
                   1298 1.R1040
                   rlr700896228.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g19701
BLAST score
                   206
E value
                   1.0e-111
Match length
                   470
% identity
                   86
                   N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2)
NCBI Description
Seq. No.
                   1298 2.R1040
Contig ID
5'-most EST
                   asn701132523.h1
Method
                   BLASTN
NCBI GI
                   q3986749
BLAST score
                   382
                                                                                1. Telepine
E value
                   0.0e + 00
Match length
                   977
% identity
                   86
                   Hevea brasiliensis serine/threonine protein phosphatase
NCBI Description
                   type 2A (PP2A) mRNA, complete cds
Seq. No.
                   1961
                   1298 3.R1040
Contig ID
5'-most EST
                   LIB3170-083-Q1-J1-F9
Method
                   BLASTX
NCBI GI
                   g3859548
BLAST score
                   368
                   4.0e-35
E value
Match length
                   66
                   100
% identity
                   (AF097182) protein phosphatase 2A catalytic subunit [Oryza
NCBI Description
                   sativa]
                   1962
Seq. No.
                   1298 4.R1040
Contig ID
                   LIB3170-083-Q1-K1-F10
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3986749
BLAST score
                   119
E value
                   4.0e-60
                   270
Match length
                   87
% identity
                   Hevea brasiliensis serine/threonine protein phosphatase
NCBI Description
                   type 2A (PP2A) mRNA, complete cds
```

```
jC-gmle01810089f02a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q19600
BLAST score
                  174
E value
                   9.0e-93
Match length
                   470
% identity
                  85
NCBI Description
                  M.sativa mRNA for eIF-4D
Seq. No.
                  1298 6.R1040
Contig ID
5'-most EST
                  LIB3049-054-Q1-E1-D11
Method
                  BLASTN
NCBI GI
                  q19701
BLAST score
                  149
E value .
                  4.0e-78
Match length
                  401
% identity
                  84
NCBI Description
                  N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2)
Seq. No.
                  1965
                  1298 7,R1040
Contig ID
5'-most EST
                  LIB3051-107-Q1-K1-C3
Method
                  BLASTN
NCBI GI
                  q3986749
BLAST score
                  96
                  2.0e-46
E value
Match length
                  243
                  86
% identity
                  Hevea brasiliensis serine/threonine protein phosphatase
NCBI Description
                  type 2A (PP2A) mRNA, complete cds
Seq. No.
                  1966
                  1298 11.R1040
Contig ID
                  jex700904182.hl
5'-most EST
Method
                  BLASTN
                  q3986749
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
Match length
                  66
                  88
% identity
                  Hevea brasiliensis serine/threonine protein phosphatase
NCBI Description
                  type 2A (PP2A) mRNA, complete cds
Seq. No.
                  1967
                  1298 12.R1040
Contig ID
                  xpa700793188.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2225884
BLAST score
                  123
                  1.0e-62
E value
                  339
Match length
                  84
% identity
                  Solanum tuberosum mRNA for eukaryotic initiation factor
NCBI Description
                  5A5, complete cds
```

Seq. No.

NCBI Description

```
1299 1.R1040
Contig ID
                   djj700606009.h2
5'-most EST
Method
                   BLASTX
                   g2194139
NCBI GI
                   237
BLAST score
                   6.0e-20
E value
Match length
                   66
% identity
                   65
                   (AC002062) EST gb ATTS0887 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   1969
Seq. No.
                   1303 1.R1040
Contig ID
                   LIB3138-128-Q1-N1-B10
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2664210
BLAST score
                   536
E value
                   5.0e-55
Match length
                   123
                   80
% identity
                   (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   1970
Seq. No.
                   1303 2.R1040
Contig ID
                   LIB3138-022-Q1-N1-F2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g210811
                   127
BLAST score
                   1.0e-64
E value
Match length
                   634
                   88
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   1971
Seq. No.
                   1304 1.R1040
Contig ID
5'-most EST
                   LIB3029-006-Q1-B1-G2
Method
                   BLASTX
NCBI GI
                   g691752
BLAST score
                   1150
                   1.0e-126
E value
                   424
Match length
% identity
                  (D29803) preproMP27-MP32 [Cucurbita sp.]
NCBI Description
                   1972
Seq. No.
                   1306 1.R1040
Contig ID
5'-most EST
                   vwf700676455.hl
Method
                   BLASTX
NCBI GI
                   g872116
BLAST score
                   1674
                   0.0e+00
E value
Match length
                   580
% identity
```

(X79770) sti (stress inducible protein) [Glycine max]

```
1973
Seq. No.
                   1306 2.R1040
Contig ID
5'-most EST
                   txt700732045.hl
Method
                  BLASTX
NCBI GI
                   g4115918
BLAST score
                  502
E value
                   2.0e-50
Match length
                   154
% identity
                   69
NCBI Description
                   (AF118222) similar to nascent polypeptide associated
                   complex alpha chain [Arabidopsis thaliana]
Seq. No.
                   1974
                   1306_3.R1040
Contig ID
5'-most EST
                   dpv701101850.hl
Method
                  BLASTN
NCBI GI
                   g872115
BLAST score
                   93
E value
                   2.0e-44
Match length
                   277
% identity
                   83
NCBI Description
                  G.max gmsti mRNA
                   1975
Seq. No.
Contig ID
                   1306 4.R1040
5'-most EST
                   jC-gmro02910039g01d1
Method
                  BLASTX
NCBI GI
                   q4115918
                   207
BLAST score
E value
                   2.0e-16
                   70
Match length
% identity
                   (AF118222) similar to nascent polypeptide associated
NCBI Description
                   complex alpha chain [Arabidopsis thaliana]
Seq. No.
                   1976
                   1306 5.R1040
Contig ID
                   asj7\overline{0}0967426.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4115918
BLAST score
                   325
E value
                   4.0e-30
                   77
Match length
% identity
                   (AF118222) similar to nascent polypeptide associated
NCBI Description
                   complex alpha chain [Arabidopsis thaliana]
                   1977
Seq. No.
                   1307 1.R1040
Contig ID
                   awf700840576.hl
5'-most EST
Method
                   BLASTX
                   g2275196
NCBI GI
                   475
BLAST score
                   8.0e-49
E value
                  132
Match length
% identity
                   81
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
```

à,

## [Arabidopsis thaliana] Seq. No. 1978

1309 1.R1040 Contig ID

uC-gmflminsoy045g04b1 5'-most EST

Method BLASTX g3063713 NCBI GI BLAST score 193 E value 2.0e-14 Match length 122 % identity 46

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

1313 1.R1040 Contiq ID

5'-most EST uC-gmrominsoy060b07b1

Seq. No.

Contig ID 1313 2.R1040

5'-most EST jC-qmf102220108a04d1

Seq. No.

1313 3.R1040 Contig ID

5'-most EST LIB3106-006-Q1-K1-B4

Method BLASTN NCBI GI q4038468 BLAST score 157 1.0e-82 E value Match length 409 % identity 86

NCBI Description Porteresia coarctata histone H3 mRNA, complete cds

Seq. No. 1982

1313 4.R1040 Contig ID

5'-most EST jC-gmf102220052g08d1

Method BLASTX g1200205

NCBI GI BLAST score 725 E value 3.0e-76

Match length 217 % identity 65

NCBI Description (X95753) DAG [Antirrhinum majus]

Seq. No. 1983

Contig ID 1313 5.R1040

5'-most EST jC-gmle01810001g08d1

Method BLASTN NCBI GI q4038468 BLAST score 161 E value 6.0e-85 409 Match length 86 % identity

Porteresia coarctata histone H3 mRNA, complete cds NCBI Description

Seq. No. 1984

Contig ID 1314 1.R1040 5'-most EST crh700852056.h1

```
Method
                   BLASTN
NCBI GI
                   q170023
BLAST score
                   112
E value
                   6.0e-56
Match length
                   112
                   100
% identity
                  Glycine max maturation-associated protein (MAT9) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   1985
                   1318 1.R1040
Contig ID
                  LIB3170-046-Q1-J1-E6
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2501578
BLAST score
                   1322
E value
                   1.0e-146
Match length
                   308
                   85
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  1986
Seq. No.
                  1318 3.R1040
Contig ID
                  kl1701209129.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2501578
BLAST score
                   409
E value
                   4.0e-40
Match length
                  88
% identity
NCBI Description
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  1987
Seq. No.
                  1319 1.R1040
Contig ID
5'-most EST
                  k117\overline{0}1214022.h1
                  1988
Seq. No.
                  1319 2.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy119b03b1
Seq. No.
                  1989
Contig ID
                  1321 1.R1040
5'-most EST
                  LIB3051-016-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  q2131352
BLAST score
                  289
                  1.0e-25
È value
Match length
                  136
                  39
% identity
NCBI Description
                  hypothetical protein YDL166c - yeast (Saccharomyces
```

protein [Saccharomyces cerevisiae]

cerevisiae) >gi\_1061273\_emb\_CAA91580\_ (Z67750) putative

## >gi\_1431264\_emb\_CAA98740\_ (Z74214) ORF YDL166c [Saccharomyces cerevisiae]

. ...

Seq. No.1990Contig ID1322\_1.R10405'-most ESTLIB3027-007-Q1-B1-A5Seq. No.1991Contig ID1323\_1.R10405'-most ESTLIB3106-098-Q1-K1-A6

 Seq. No.
 1992

 Contig ID
 1331\_1.R1040

 5'-most EST
 zpv700759728.h1

 Method
 BLASTX

 NCBI GI
 g2129842

BLAST score 157
E value 5.0e-10
Match length 58
% identity 50

NCBI Description SE60 protein - soybean >gi\_509769\_emb\_CAA79164\_ (Z18359) seed-specific low molecular weight sulfur-rich protein

[Glycine max]

Seq. No. 1993

Contig ID 1331\_2.R1040 5'-most EST ssr700560357.h1

Method BLASTX
NCBI GI g1667373
BLAST score 1785
E value 0.0e+00
Match length 371
% identity 90

NCBI Description (X82270) protein kinase [Medicago sativa]

Seq. No. 1994

Contig ID 1331 3.R1040

5'-most EST LIB3051-054-Q1-K2-F4

Seq. No. 1995

Contig ID 1331\_5.R1040

5'-most EST LIB3072-027-Q1-E1-C8

Method BLASTX
NCBI GI g2129842
BLAST score 157
E value 3.0e-10
Match length 58
% identity 50

NCBI Description SE60 protein - soybean >gi\_509769\_emb\_CAA79164\_ (Z18359)

seed-specific low molecular weight sulfur-rich protein

[Glycine max]

Seq. No. 1996

Contig ID 1331\_7.R1040

5'-most EST LIB3051-031-Q1-K1-C10

Method BLASTN NCBI GI g1667372

```
105
BLAST score
                   1.0e-51
E value
Match length
                   240
% identity
                   86
                  M.sativa MMK4 mRNA for protein kinase
NCBI Description
                   1997
Seq. No.
                   1331 8.R1040
Contig ID
5'-most EST
                   LIB3170-061-Q1-J1-F1
Seq. No.
                   1998
Contig ID
                   1331 9.R1040
5'-most EST
                   LIB3051-031-Q1-K1-C11
Method
                   BLASTN
                   g1667372
NCBI GI
BLAST score
                   75
E value
                   8.0e-34
Match length
                   91
% identity
                   96
NCBI Description
                  M.sativa MMK4 mRNA for protein kinase
                   1999
Seq. No.
Contig ID
                   1331 11.R1040
5'-most EST
                   jC-qmro02910024c08a1
Method
                  BLASTN
NCBI GI
                   q1667372
BLAST score
                   133
E value
                   2.0e-68
                  293
Match length
% identity
                  86
NCBI Description M.sativa MMK4 mRNA for protein kinase
                   2000
Seq. No.
                   1331 12.R1040
Contig ID
5'-most EST
                  LIB3051-064-Q1-K1-F1
                   2001
Seq. No.
                   1331 14.R1040
Contig ID
5'-most EST
                   jC-gmst02400060f10d1
                   2002
Seq. No.
                   1331 15.R1040
Contig ID
5'-most EST
                   uC-gmropic063f01b1
Method
                  BLASTN
NCBI GI
                  g1667372
                  95
BLAST score
E value
                   7.0e-46
Match length
                  250
                  83
% identity
NCBI Description
                  M.sativa MMK4 mRNA for protein kinase
                   2003
Seq. No.
                   1331 17.R1040
Contig ID
5'-most EST
                  LIB3170-051-Q1-J1-B10
```

Seq. No. 2004

Contig ID 1331\_22.R1040

```
5'-most EST
                   fua701042265.h1
                   2005
Seq. No.
                   1331 23.R1040
Contig ID
                  LIB3051-012-Q1-E1-C2
5'-most EST
Seq. No.
                  2006
                   1331 24.R1040
Contig ID
                  LIB3051-054-Q1-K2-B8
5'-most EST
                  2007
Seq. No.
                  1333 1.R1040
Contig ID
5'-most EST
                  LIB3039-018-Q1-E1-G5
                  BLASTX
Method
NCBI GI
                  g3860259
BLAST score
                  189
                   3.0e-14
E value
Match length
                  105
                   42
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  2008
Seq. No.
                  1338 1.R1040
Contig ID
                  LIB3109-034-Q1-K1-C2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3025860
BLAST score
                  35
E value
                  7.0e-10
Match length
                  111
                  92
% identity
NCBI Description Medicago truncatula Mt4 genomic sequence
                  2009
Seq. No.
Contig ID
                  1341 1.R1040
5'-most EST
                  LIB3167-078-P1-K2-B7
                  BLASTX
Method
NCBI GI
                  q3914472
BLAST score
                  526
E value
                  2.0e-53
Match length
                  129
                  78
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                  >gi_322764_pir__S32021 photosystem II 10K protein - common
                  tobacco >gi 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana
                  tabacum]
                  2010
Seq. No.
                  1341 2.R1040
Contig ID
5'-most EST
                  fde700876719.h1
                  BLASTX
Method
                  g3914472
NCBI GI
BLAST score
                  318
                  2.0e-29
E value
Match length
                  99
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
```

>gi 322764 pir S32021 photosystem II 10K protein - common

Method

BLASTX

```
Seq. No.
                   2011
                   1341 3.R1040
Contig ID
5'-most EST
                  LIB3093-012-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   q3914472
BLAST score
                   272
E value
                   6.0e-24
Match length
                   126
% identity
                   41
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                   >gi 322764 pir S32021 photosystem II 10K protein - common
                   tobacco >qi 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana
                   tabacum]
Seq. No.
                   2012
Contig ID
                   1341_5.R1040
5'-most EST
                  uC-gmropic043e05b1
Method
                  BLASTN
NCBI GI
                   q1418983
BLAST score
                   59
E value
                   2.0e-24
Match length
                  167
% identity
                  84
                  L.esculentum mRNA for photosystem II 10 kD protein
NCBI Description
Seq. No.
                   2013
Contig ID
                   1341 6.R1040
                  LIB3040-027-Q1-E1-A2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3914472
BLAST score
                  391
E value
                   1.0e-37
Match length
                  89
% identity
                  83
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                  >qi 322764 pir S32021 photosystem II 10K protein - common
                  tobacco >q1 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana
                  tabacum]
                  2014
Seq. No..
                  1343 1.R1040
Contig ID
5'-most EST
                  LIB3139-052-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  g2982303
BLAST score
                  1215
E value
                  1.0e-133
Match length
                  267
% identity
                  84
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
Seq. No.
                  1343 2.R1040
Contig ID
5'-most EST
                  jC-qmle01810024e10d1
```

tobacco > qi 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana

tabacuml

```
NCBI GI
                   q4204315
BLAST score
                   801
E value
                   0.0e + 00
                   717
Match length
                   50
% identity
                   (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2016
                   1343 4.R1040
Contig ID
                   bth700846788.h1
5'-most EST
                   BLASTX
Method
                   g4128133
NCBI GI
                   377
BLAST score
E value
                   5.0e-36
Match length
                   131
                   55
% identity
                   (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
NCBI Description
Seq. No.
                   2017
                   1343 5.R1040
Contig ID
5'-most EST
                   LIB3106-028-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   q3337435
BLAST score
                   158
                   3.0e-23
E value
Match length
                   172
                   32
% identity
NCBI Description
                   (AF060198) PsbY precursor; putative photosytem II peptide
                   [Spinacia oleracea]
Seq. No.
                   2018
Contig ID
                   1343 7.R1040
                   LIB3073-016-Q1-K1-C7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3337435
BLAST score
                   265
E value
                   4.0e-23
Match length
                   131
% identity
                   38
                   (AF060198) PsbY precursor; putative photosytem II peptide
NCBI Description
                   [Spinacia oleracea]
Seq. No.
                   2019
Contig ID
                   1343 11.R1040
                   vzy7\overline{0}0753763.h1
5'-most EST
                   2020
Seq. No.
                   1343 12.R1040
Contig ID
                   jC-gmle01810075b12a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3337435
BLAST score
                   189
E value
                   3.0e-14
Match length
                   56
% identity
                   43
NCBI Description
                   (AF060198) PsbY precursor; putative photosytem II peptide
```

[Spinacia oleracea]

```
Seq. No.
                   2021
Contig ID
                   1343 14.R1040
5'-most EST
                   taw700656383.hl
                   2022
Seq. No.
                   1343 15.R1040
Contig ID
5'-most EST
                   zhf700963687.h1
Seq. No.
                   2023
                   1343 16.R1040
Contig ID
                   hrw701057276.h1
5'-most EST
Seq. No.
                   2024
                   1344 1.R1040
Contig ID
                   LIB3051-026-Q1-K1-B3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3747050
BLAST score
                   411
E value
                   5.0e-40
Match length
                   101
% identity
                   80
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                   2025
                   1344 2.R1040
Contig ID
                   LIB3106-093-Q1-K1-H2
5'-most EST
Method
                   BLASTN
                   g3747049
NCBI GI
BLAST score
                   92
E value
                   5.0e-44
                   224
Match length
                   85
% identity
                   Zea mays ribosomal protein L26 mRNA, partial cds
NCBI Description
Seq. No.
                   2026
                   1345 1.R1040
Contig ID
                   k117\overline{0}1215182.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4337178
                   707
BLAST score
E value
                   1.0e-74
Match length
                   155
% identity
NCBI Description
                  (AC006416) T31J12.5 [Arabidopsis thaliana]
                   2027
Seq. No.
                   1345 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy265e12b1
Method
                   BLASTX
NCBI GI
                   g4337178
BLAST score
                   348
E value
                   6.0e-33
Match length
                   76
% identity
                   (AC006416) T31J12.5 [Arabidopsis thaliana]
NCBI Description
```

NCBI Description

```
Seq. No.
                   2028
                   1348 1.R1040
Contig ID
                   LIB3027-006-Q1-B1-A10
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3241920
BLAST score
                   41
                   1.0e-13
E value
Match length
                   81
% identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAE1, complete sequence [Arabidopsis thaliana]
                   2029
Seq. No.
                   1350 1.R1040
Contig ID
                   gsv701052806.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4539307
BLAST score
                   229
E value
                   1.0e-18
Match length
                   62
                   71
% identity
                   (AL049480) putative acidic ribosomal protein [Arabidopsis
NCBI Description
                   thaliana]
                   2030
Seq. No.
                   1350 2:R1040
Contig ID
5'-most EST
                   g4397512
Method
                   BLASTX
NCBI GI
                   g4539307
                   260
BLAST score
                   2.0e-22
E value
Match length
                   68
% identity
NCBI Description
                   (AL049480) putative acidic ribosomal protein [Arabidopsis
                   thaliana]
                   2031
Seq. No.
Contig ID
                   1352 1.R1040
5'-most EST
                   jsh7\overline{0}1063775.h1
                   BLASTN
Method
NCBI GI
                   g555973
BLAST score
                   269
E value
                   1.0e-149
Match length
                   692
% identity
                   85
                  Pisum sativum 14-3-3-like protein mRNA, complete cds
NCBI Description
                   2032
Seq. No.
                   1352 2.R1040
Contig ID
                  LIB3093-015-Q1-K1-C6
5'-most EST
Method
                   BLASTN
NCBI GI
                   g555973
BLAST score
                   313
E value
                   1.0e-175
Match length.
                   786
% identity
                   86
```

Pisum sativum 14-3-3-like protein mRNA, complete cds

```
2033
Seq. No.
                   1352 3.R1040
Contig ID
5'-most EST
                   LIB3167-004-P1-K1-A2
                   BLASTN
Method
NCBI GI
                   g555973
BLAST score
                   224
                   1.0e-122
E value
Match length
                   706
                   86
% identity
                  Pisum sativum 14-3-3-like protein mRNA, complete cds
NCBI Description
                   2034
Seq. No.
                   1352 4.R1040
Contig ID
                   zhf700963441.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2921511
BLAST score
                   70
E value
                   4.0e-31
Match length
                   146
% identity
                   87
                   Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds
NCBI Description
Seq. No.
Contig ID
                   1352 5.R1040
                   LIB3055-011-Q1-N1-A8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4544412
BLAST score
                   303
E value
                   2.0e-27
                   82
Match length
                   70
% identity
                   (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2036
                   1352 6.R1040
Contig ID
                   LIB3139-084-P1-N1-A1
5'-most EST
                   BLASTN
Method
                   g555973
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
                   353
Match length
                   86
% identity
NCBI Description
                  Pisum sativum 14-3-3-like protein mRNA, complete cds
Seq. No.
                   2037
                   1352 9.R1040
Contig ID
5'-most EST
                   g4396272
                   BLASTX
Method
NCBI GI
                   q4544412
BLAST score
                   464
                   2.0e-46
E value
Match length
                   111
% identity
NCBI Description
                   (AC006955) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.

```
Contig ID
                   1352 13.R1040
5'-most EST
                   LIB3039-012-Q1-E1-A6
Method
                   BLASTN
NCBI GI
                   g2921511
                   69
BLAST score
                   1.0e-30
E value
                   69
Match length
% identity
                   100
NCBI Description
                   Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds
                   2039
Seq. No.
                   1353 1.R1040
Contig ID
5'-most EST
                   kmv700741661.hl
Method
                   BLASTN
                   g2264310
NCBI GI
BLAST score
                   48
E value
                   1.0e-17
Match length
                   279
% identity .
                   86
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MKP11, complete sequence [Arabidopsis thaliana]
                   2040
Seq. No.
                   1355 1.R1040
Contig ID
                   LIB3109-017-Q1-K1-D12
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2267138
                   177
BLAST score
E value
                   2.0e-94
Match length
                   365
                   87
% identity
                   Prunus armeniaca ubiquitin-conjugating enzyme mRNA, partial
NCBI Description
                   2041
Seq. No.
                   1355 2.R1040
Contig ID
                   jex7\overline{0}0908608.h1
5'-most EST
                   BLASTN
Method
                   g2267138
NCBI GI
BLAST score
                   145
                   1.0e-75
E value
                   293
Match length
                   87
% identity
NCBI Description
                   Prunus armeniaca ubiquitin-conjugating enzyme mRNA, partial
                   2042
Seq. No.
Contig ID
                   1355 3.R1040
5'-most EST
                   LIB3\overline{0}51-048-Q1-K1-F7
Method
                   BLASTN
NCBI GI
                   g19497
BLAST score
                   105
E value
                   9.0e-52
Match length
                   207
% identity
                   91
```

NCBI Description L.polyphyllus pPLB07 mRNA

5'-most EST

```
2043
Seq. No.
Contig ID
                   1355 4.R1040
5'-most EST
                   LIB3049-054-Q1-E1-B4
Method
                   BLASTX
NCBI GI
                   g1174162
BLAST score
                   534
E value
                   1.0e-54
Match length
                   105
% identity
                   90
NCBI Description
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis-
                   thaliana] >gi_3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1355 6.R1040
5'-most EST
                   uC-qmrominsoy050f02b1
Seq. No.
Contig ID
                   1356 1.R1040
5'-most EST
                  LIB3072-060-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                   q2832620
BLAST score
                   562
E value
                   8.0e-58
Match length
                   175
% identity
                   (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2046
Contig ID
                   1363 1.R1040
5'-most EST
                  LIB3139-068-P1-N1-D3
Method
                  BLASTX
NCBI GI
                   g4432844
BLAST score
                   394
E value
                   7.0e-38
Match length
                  207
% identity
                   41
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  1363 2.R1040
Contig ID
                  sat701010967.h1
5'-most EST
                  2048
Seq. No.
                  1364 1.R1040
Contig ID
5'-most EST
                   fde700876671.hl
Method
                  BLASTX
                  g4033838
NCBI GI
BLAST score
                  1220
E value
                  1.0e-134
                   410
Match length
% identity
                   (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                  2049
Seq. No.
                  1364 2.R1040
Contig ID
```

jC-gmf102220132ab11d1

```
Method
                   BLASTX
NCBI GI
                   q4033838
BLAST score
                   430
E value ·
                   2.0e-42
Match length
                   101
% identity
                   84
                   (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2050
                   1364 3.R1040
Contig ID
                   jC-gmro02910008c07a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4033838
BLAST score
                   317
E value
                   4.0e-29
Match length
                   185
% identity
                   45
                   (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1364 4.R1040
Contig ID
5'-most EST
                   jC-gmle01810004d04a1
Method
                   BLASTX
NCBI GI
                   g4033838
BLAST score
                   226
E value
                   2.0e-18
                   120
Match length
% identity
                   41
                   (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                   2052
Seq. No.
                   1367 1.R1040
Contig ID
                   LIB3027-005-Q1-B1-G11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2225877
BLAST score
                   211
                   1.0e-16
E value
                   76
Match length
% identity
NCBI Description
                   (AB002406) TIP49 [Rattus norvegicus] >gi 4106528 (AF100694)
                   Pontin52 [Mus musculus] >gi 4521276 dbj BAA76313.1
                   (AB001581) DNA helicase p50 [Rattus norvegicus]
                   2053
Seq. No.
                   1368 1.R1040
Contig ID
5'-most EST
                   wvk700680956.h1
                   BLASTX
Method
NCBI GI
                   g2191191
                   513
BLAST score
E value
                   7.0e-52
Match length
                   166
% identity
                   (AF007271) A TM021B04.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   2054
```

1372 1.R1040

Contig ID

NCBI Description

```
zsq701123846.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3250679
BLAST score
                   447
                   4.0e-44
E value
Match length
                   236
                   44
% identity
NCBI Description
                   (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1375 1.R1040
5'-most EST
                   hyd700730420.h1
Method
                   BLASTX
NCBI GI
                   q3334299
BLAST score
                   1049
E value
                   1.0e-114
Match length
                   219
                   94
% identity
NCBI Description
                   PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                   COMPLEX ALPHA SUBUNIT) >gi 2315211_emb_CAA74725_ (Y14339)
                   proteasome alpha subunit [Lycopersicon esculentum]
                   2056
Seq. No.
                   1376 1.R1040
Contig ID
5'-most EST
                   kl1701213854.hl
Method
                   BLASTX
NCBI GI
                   q3176874
BLAST score
                   753
E value
                   1.0e-132
Match length
                   478
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   2057
                   1377 1.R1040
Contig ID
                   rca7\overline{0}1002041.h1
5'-most EST
                   BLASTX
Method
                   g3193314
NCBI GI
BLAST score
                   906
E value
                   1.0e-97
                   328
Match length
                   55
% identity
                   (AF069299) contains similarity to Arabidopsis scarecrow
NCBI Description
                   (GB:U62798) [Arabidopsis thaliana]
                   2058
Seq. No.
                   1379 1.R1040
Contig ID
                   awf700843166.hl
5'-most EST
                   BLASTX
Method
                   q2270990
NCBI GI
BLAST score
                   200
E value
                   3.0e-15
Match length
                   116
                   44
% identity
```

۶.-

(AF004807) dehydrin [Glycine max]

NCBI GI

```
2059
Seq. No.
                     1385 1.R1040
Contig ID
5'-most EST
                     LIB3050-002-Q1-E1-H4
                     2060
Seq. No.
                     1386 1.R1040
Contig ID
                     rca701000271.h1
5'-most EST
Method
                     BLASTN
NCBI GI
                     q1498327
BLAST score
                     272
E value
                     1.0e-151
Match length
                     276
% identity
                     100
NCBI Description
                    Glycine max actin (Soy70) gene, partial cds
Seq. No.
                     1386 2.R1040
Contig ID
5'-most EST
                     trc700562963.h1
Method
                     BLASTX
NCBI GI
                     g1531672
BLAST score
                     1602
E value
                     0.0e+00
Match length
                     377
% identity
                     93
NCBI Description
                     (U68461) actin [Striga asiatica]
                     2062
Seq. No.
                     1386 3.R1040
Contig ID
                     hyd700730194.hl
5'-most EST
Method
                     BLASTX
NCBI GI
                     g4139264
BLAST score
                     1157
E value
                     0.0e + 00
Match length
                     376
% identity
                     96
NCBI Description
                     (AF111812) actin [Brassica napus]
                                                                     .
                     2063
Seq. No.
                     1386 4.R1040
Contig ID
5'-most EST
                     k11701206694.h1
Method
                     BLASTX
NCBI GI
                     g1703108
                     1856
BLAST score
E value
                     0.0e+00
Match length
                     369
% identity
                     97
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                     thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                     thaliana]
                     2064
Seq. No.
                     1386 5.R1040
Contig ID
5'-most EST
                    LIB3094-054-Q1-K1-E3
Method
                     BLASTN
```

g1498339

5'-most EST

Method

```
498
BLAST score
                   0.0e + 00
E value
                   1018
Match length
% identity
                   95
                   Glycine max actin (Soy118) gene, partial cds
NCBI Description
                   2065
Seq. No.
                   1386 6.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy035g05b1
                   BLASTN
Method
NCBI GI-
                   q1498333
BLAST score
                   540
E value
                   0.0e + 00
Match length
                   1020
% identity
                   96
NCBI Description
                   Glycine max actin (Soy57) gene, partial cds
Seq. No.
                   1391 1.R1040
Contig ID
5'-most EST
                   sat701008458.hl
Method
                   BLASTX
NCBI GI
                   q3337356
BLAST score
                   2273
E value
                   0.0e + 00
Match length
                   476
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
Seq. No.
                   2067
                   1391 2.R1040
Contig ID
                   asn7\overline{0}1140282.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827544
BLAST score
                   243
E value
                   3.0e-20
Match length
                   57
% identity
                   81
                   (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                   thaliana]
                   2068
Seq. No.
                   1391_3.R1040
Contig ID
                   LIB3170-053-Q1-J1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3337356
BLAST score
                   385
E value
                   5.0e-37
                   76
Match length
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   2069
Seq. No.
                   1391 4.R1040
Contig ID
```

jC-gmf102220063a06a1

BLASTX

% identity

```
NCBI GI
                   q3337356
BLAST score
                   628
E value
                   1.0e-65
Match length
                   126
% identity
                   98
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
Seq. No.
                   2070
                   1391 5.R1040
Contig ID
5'-most EST
                   jC-gmro02910040c03a1
                   BLASTN
Method
                   g3766106
NCBI GI
BLAST score
                   47
E value
                   3.0e-17
Match length
                   135
% identity
                   84
                   Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   2071
Seq. No.
                   1391 6.R1040
Contig ID
                   LIB3028-053-Q1-B1-G8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3337356
                   350
BLAST score
                   5.0e-33
E value
                   70
Match length
                   97
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
Seq. No.
                   2072
                   1391 8.R1040
Contig ID
                                                                          5'-most EST
                   uC-gmrominsoy174e10b1
                   2073
Seq. No.
                   1391 9.R1040
Contiq ID
5'-most EST
                   hyd7\overline{0}0725385.h1
Method.
                   BLASTX
NCBI GI
                   g3337356
                   210
BLAST score
E value
                   8.0e-17
Match length
                   55
% identity
                   78
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   2074
Seq. No.
Contig ID
                   1391 10.R1040
5'-most EST
                   sat701013338.hl
                   BLASTX
Method
NCBI GI
                   g2827544
BLAST score
                   213
E value
                   3.0e-17
Match length
                   50
```

Method

BLASTN

```
NCBI Description
                   (AL021635) HSP associated protein like [Arabidopsis
                   thalianal
                   2075
Seq. No.
                   1391 11.R1040
Contig ID
                   uaw700665063.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827544
BLAST score
                   241
E value
                   3.0e-20
Match length
                   54
% identity
                   87
                   (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                   thaliana]
                   2076
Seq. No.
                   1391 18.R1040
Contig ID
5'-most EST
                   dpv701098828.hl
Method
                   BLASTX
NCBI GI
                   q3834321
BLAST score
                   248
E value
                   4.0e-21
Match length
                   143
% identity
                   50
NCBI Description
                   (AC005679) Strong similarity to F13P17.9 gi 3337356
                   transport protein SEC61 alpha subunit homolog from
                   Arabidopsis thaliana BAC gb AC004481. [Arabidopsis
                   thaliana]
Seq. No.
                   2077
                   1394 1.R1040
Contig ID
                   LIB3028-031-Q1-B1-C9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3355468
BLAST score
                   536
E value
                   1.0e-54
Match length
                   123
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   2078
Seq. No.
                   1394 2.R1040
Contig. ID
5'-most EST
                   LIB3093-022-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   g4545262
BLAST score
                   172
E value
                   5.0e-12
Match length
                   42
% identity
                   (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                   hirsutum]
                   2079
Seq. No.
                   1394 3.R1040
Contig ID
                   LIB3\overline{1}07-060-Q1-K1-C9
5'-most EST
```

```
NCBI GI
                    q4545261
BLAST score
                    40
E value
                    4.0e-13
Match length
                    142
                    86
% identity
                    Gossypium hirsutum metallothionein-like protein mRNA,
NCBI Description
                    complete cds
Seq. No.
                    2080
                    1394 5.R1040
Contig ID
                    LIB3093-052-Q1-K1-F5
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3355468
BLAST score
                    186
E value
                    1.0e-13
Match length
                    50
% identity
NCBI Description
                     (AC004218) putative ribosomal protein L35 [Arabidopsis
                    thaliana]
Seq. No.
                    2081
                    1397 1.R1040
Contig ID
                    awf700836730.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g126078
BLAST score
                    380
                    2.0e-73
E value
Match length
                    248
                    51
% identity
NCBI Description
                    LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
                    >gi_81554_pir__S04046 embryonic abundant protein gD-34 - upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
                    protein [Gossypium hirsutum] >gi_167385 (M19389) storage
protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea
                    D-34 gene [Saguinus oedipus]
                    2082
Seq. No.
                    1400 1.R1040
Contig ID
5'-most EST
                    LIB3051-088-Q1-K1-E7
Method
                    BLASTX
                    g2146740
NCBI GI
BLAST score
                    435
E value
                    5.0e-43
                    133
Match length
                    64
% identity
NCBI Description
                    inner mitochondrial membrane protein - Arabidopsis thaliana
                    >qi 603056 (U18126) inner mitochondrial membrane protein
                    [Arabidopsis thaliana]
                    2083
Seq. No.
Contig ID
                    1401 1.R1040
5'-most EST
                    uC-gmflminsoy016c08b1
Method
                    BLASTX
NCBI GI
                    g4490732
BLAST score
                    2599
E value
                    0.0e + 00
Match length
                    666
```

```
% identity
                   75
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                  protein [Arabidopsis thaliana]
                   2084
Seq. No.
                   1401 2.R1040
Contig ID
                  LIB3065-027-Q1-N1-G12
5'-most EST
                  BLASTX
Method
NCBI GI
                   q2623310
BLAST score
                   571
E value
                   3.0e-58
Match length
                   248
                   49
% identity
NCBI Description
                   (AC002409) unknown protein [Arabidopsis thaliana]
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
                   2085
Seq. No.
                   1401 3.R1040
Contig ID
5'-most EST
                  LIB3051-018-Q1-E1-H5
                  BLASTX
Method
NCBI GI
                  q2623310
BLAST score
                  289
E value
                   2.0e-25
Match length
                  138
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  2086
                  1401 4.R1040
Contig ID
                  uC-gmropic023d09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2623310
BLAST score
                  516
                   3.0e-52
E value
Match length
                  184
% identity
                  58
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
                  2087
Seq. No.
                  1401 5.R1040
Contig ID
5'-most EST
                  LIB3106-087-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q2623310
                  216
BLAST score
                  3.0e-17
E value
Match length
                  61
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
```

2088

Seq. No.

·....

```
1401 6.R1040
Contig ID
5'-most EST
                    fC-gmst700665357f2
                    BLASTX
Method
                   g2623310
NCBI GI
                   295
BLAST score
                    2.0e-26
E value
Match length
                    86
% identity
                    66
                    (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3402721 (AC004261) unknown protein [Arabidopsis
                   thaliana]
                    2089
Seq. No.
                   1401 7.R1040
Contig ID
                   LIB3170-075-Q1-K2-H11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1172571
BLAST score
                   224
                    2.0e-18
E value
Match length
                    44
% identity
                    PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
NCBI Description
                   >gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase
(ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899)
                   phosphoenolpyruvate carboxykinase [Cucumis sativus]
                   2090
Seq. No.
Contig ID
                    1401 8.R1040
5'-most EST
                   jC-gmst02400036f12d2
Seq. No.
                   2091
Contig ID
                   1405 1.R1040
5'-most EST
                    jC-gmst02400077a05a1
Method
                   BLASTX
                   g3327957
NCBI GI
BLAST score
                   229
                    1.0e-18
E value
Match length
                   94
% identity
                    (AF060490) TLS-associated protein TASR-2 [Mus musculus]
NCBI Description
                   >gi 3327976 (AF067730) TLS-associated protein TASR-2 [Homo
                   sapiens]
Seq. No.
                   2092
Contig ID
                   1405 2.R1040
                   eep7\overline{0}0864535.h1
5'-most EST
Seq. No.
Contig ID
                   1405 3.R1040
                   LIB3027-004-Q1-B1-E1
5'-most EST
Seq. No.
                   1409 1.R1040
Contig ID
5'-most EST
                   sat701013306.h1
Method
                   BLASTX
                   q2980760
NCBI GI
```

BLAST score

BLAST score

```
E value
                   2.0e-19
Match length
                   93
% identity
                   53
                   (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   2095
Seq. No.
                   1409 2.R1040
Contig ID
5'-most EST
                   zsg701119142.hl
Method
                   BLASTX
NCBI GI
                   g2980760
BLAST score
                   226
E value
                   2.0e-18
Match length
                   58
% identity
                   (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   2096
Seq. No.
                   1409 3.R1040
Contig ID
5'-most EST
                   pcp700995525.h1
Method
                   BLASTX
NCBI GI
                   g421855
                                                                          المراجع المراجع
BLAST score
                   1044
E value
                   1.0e-114
Match length
                   342
% identity
                   61
                   alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana
NCBI Description
                   (fragment)
                   2097
Seq. No.
                   1409 5.R1040
Contig ID
                   LIB3092-041-Q1-K1-H8
5'-most EST
Method
                   BLASTX
                   g1673366
NCBI GI
BLAST score
                   201
E value
                   2.0e-15
Match length
                   86
% identity
                   (Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   2098
Seq. No.
                   1411 1.R1040
Contig ID
5'-most EST
                   zsg701129392.hl
                   BLASTN
Method
NCBI GI
                   g1372965
BLAST score
                   387
                   0.0e+00
E value
Match length
                   832
                   88
% identity
NCBI Description
                  Vicia faba CREB-like protein mRNA, complete cds
Seq. No.
                   1411 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir037g03b1
Method
                   BLASTN
                   g1372965
NCBI GI
```

% identity

```
E value
                   4.0e-19
Match length
                   113
% identity
                   91
                  Vicia faba CREB-like protein mRNA, complete cds
NCBI Description
Seq. No.
                   2100
                   1411 3.R1040
Contig ID
5'-most EST
                   uaw700664458.hl
Method
                   BLASTN
NCBI GI
                   g1372965
BLAST score
                   32
                   1.0e-08
E value
Match length
                   44
% identity
                   93
NCBI Description Vicia faba CREB-like protein mRNA, complete cds
                   2101
Seq. No.
                   1412 1.R1040
Contig ID
5'-most EST
                   LIB3028-032-Q1-B1-A11
Method
                   BLASTX
NCBI GI
                   g2257756
BLAST score
                   300
E value
                   1.0e-26
Match length
                   286
% identity
                   33
                   (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                   >qi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                   mays]
Seq. No.
                   2102
                   1412 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy192h04b1
                   2103
Seq. No.
                   1412 3.R1040
Contig ID
                   LIB3139-021-P1-N1-D5
5'-most EST
                   2104
Seq. No.
                   1416 1.R1040
Contig ID
                   LIB3170-017-Q1-K1-G9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1350956
                   534
BLAST score
E value
                   2.0e-54
Match length
                   116
% identity
                   91
NCBI Description
                  40S RIBOSOMAL PROTEIN S20 (S22)
                   2105
Seq. No.
Contig ID
                   1416 2.R1040
5'-most EST
                  LIB3040-026-Q1-E1-B2
                   BLASTX
Method
NCBI GI
                   g1350956
BLAST score
                   556
E value
                   5.0e-57
Match length
                  116
```

```
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
Seq. No.
                   2106
                   1416 4.R1040
Contig ID
                   pxt700941510.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1350956
BLAST score
                   303..
                   2.0e-49
E value
                   117
Match length
                   85
% identity
                   40S RIBOSOMAL PROTEIN S20 (S22)
NCBI Description
                   2107
Seq. No.
                   1416 5.R1040
Contig ID
                   kl1701215312.hl
5'-most EST
                   BLASTX
Method
                   g1350956
NCBI GI
BLAST score
                   274
E value
                   3.0e-24
Match length
                   74
                   70
% identity
                  40S RIBOSOMAL PROTEIN S20 (S22)
NCBI Description
                   2108
Seq. No.
                   1416 6.R1040
Contig ID
                   taw700655032.hl
5'-most EST
                  BLASTX
Method
                   g1350956
NCBI GI
BLAST score.
                   194
E value
                   4.0e-15
Match length
                   48
                   81
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S20 (S22)
                   2109
Seq. No.
Contig ID
                   1418 1.R1040
5'-most EST
                   g4313692
Method
                  BLASTN
NCBI GI
                  g20901
BLAST score .
                   285
E value
                   1.0e-159
Match length
                  730
% identity
                  85
NCBI Description Pisum sativum mRNA for manganese superoxide dismutase
                   2110
Seq. No.
Contig ID
                   1418 2.R1040
5'-most EST
                  bth700849612.h1
                  BLASTX
Method
NCBI GI
                  g3287977
BLAST score
                   556
E value
                   3.0e-57
Match length
                  127
% identity
                   82
NCBI Description
                  SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi 945044 (U30841)
```

manganese superoxide dismutase precursor [Pisum sativum]

Contig ID

```
Seq. No.
                   2111
Contig ID
                   1422 1.R1040
                   LIB3167-050-P1-K1-F9
5'-most EST
Method
                   BLASTX
                   q3776572
NCBI GI
BLAST score
                   449
E value
                   2.0e-44
Match length
                   171
% identity
                   59
                   (AC005388) ESTs gb R65052, gb AA712146, gb H76533,
NCBI Description
                   gb_H76282, gb_AA650771, gb_H76287, gb_AA650887, gb_N37383,
                   qb Z29721 and gb Z29722 come from this gene. [Arabidopsis
                   thalianal
                   2112
Seq. No.
                   1424 1.R1040
Contig ID
5'-most EST
                   gsv7\overline{0}1056551.h1
Method
                   BLASTX
NCBI GI
                   g3193303
BLAST score
                   342
                   1.0e-31
E value
                   99
Match length
% identity
NCBI Description
                   (AF069298) similar to several proteins containing a tandem
                   repeat region such as Plasmodium falciparum GGM tandem
                   repeat protein (GB:U27807); partial CDS (Arabidopsis
                   thaliana]
                   2113
Seq. No.
                   1425 1.R1040
Contig ID
5'-most EST
                   LIB3107-053-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g3176690
BLAST score
                   1639
                   0.0e + 00
E value
                   377
Match length
% identity
NCBI Description
                   (AC003671) Similar to ubiquitin ligase gb D63905 from S.
                   cerevisiae. EST gb R65295 comes from this gene.
                   [Arabidopsis thaliana]
                   2114
Seq. No.
Contig ID
                   1425 2.R1040
                   vwf700678792.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3176690
BLAST score
                   731
E value
                   2.0e-77
Match length
                   306
% identity
NCBI Description
                   (AC003671) Similar to ubiquitin ligase gb_D63905 from S.
                   cerevisiae. EST gb_R65295 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   2115
```

1427 1.R1040

NCBI GI

```
5'-most EST
                   LIB3072-056-Q1-K1-A9
                   2116
Seq. No.
Contig ID
                   1430 1.R1040
                   ncj7\overline{0}0985904.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3928869
BLAST score
                   219
E value
                   5.0e-17
Match length
                   306
                   27
% identity
                   (AF093420) Hsp70 binding protein HspBP1 [Homo sapiens]
NCBI Description
Seq. No.
                   1430 2.R1040
Contig ID
5'-most EST
                   LIB3027-001-Q1-B1-G7
Seq. No.
                   2118
Contig ID
                   1430 4.R1040
5'-most EST
                   jC-gmro02910070c02a1
Seq. No.
                   2119
                   1431 1.R1040
Contig ID
5'-most EST
                   LIB3109-014-Q1-K1-E7
                   2120
Seq. No.
                   1433 1.R1040
Contig ID
                   LIB3\overline{0}27-003-Q1-B1-E4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3243274
BLAST score
                   148
                   2.0e-09
E value
Match length
                   61
% identity
                   51
                   (AF072134) TCP3 [Arabidopsis thaliana]
                                                                      7.
NCBI Description
                   2121
Seq. No.
                   1433 2.R1040
Contig ID
5'-most EST
                   LIB3049-028-Q1-E1-F10
                   2122
Seq. No.
                   1434 1.R1040
Contig ID
5'-most EST
                   LIB3040-048-Q1-E1-F9
Method
                   BLASTX
NCBI GI
                   g2852449
BLAST score
                   927
E value
                   1.0e-167
Match length
                   398
                   77
% identity
                   (D88207) protein kinase [Arabidopsis thaliana] >gi 2947061
NCBI Description
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   2123
Contig ID
                   1434 2.R1040
5'-most EST
                   LIB3051-104-Q1-K1-G3
Method
                   BLASTX
```

q2852449

5'-most EST

```
BLAST score
                   887
E value
                   1.0e-95
Match length
                   246
% identity
                   73
                   (D88207) protein kinase [Arabidopsis thaliana] >gi 2947061
NCBI Description
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1434 3.R1040
5'-most EST
                   epx701106557.hl
Method
                   BLASTX
NCBI GI
                   q2852449
BLAST score
                   532
E value
                   3.0e-54
Match length
                   142
% identity
                   (D88207) protein kinase [Arabidopsis thaliana] >gi 2947061
NCBI Description
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1434 4.R1040
5'-most EST
                   zsq7\overline{0}1126118.h1
Method
                   BLASTX
NCBI GI
                   g2852447
BLAST score
                   178
                   7.0e-13
E value
                   50
Match length
% identity
                   68
                   (D88206) protein kinase [Arabidopsis thaliana]
NCBI Description
                   2126
Seq. No.
                   1437 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{0}65-027-Q1-N1-G9
Method
                   BLASTX
NCBI GI
                   g1169200
BLAST score
                  195
                  .6.0e-15
E value
                   59
Match length
% identity
                   66
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR
NCBI Description
                   >gi_421829_pir__S33706 DNA-damage resistance protein -
                  Arabidopsis thaliana >gi_166694 (M98455) [Arabidopsis
                   thaliana recombination and DNA-damage resistance protein
                   (DRT111) mRNA, complete cds.], gene product [Arabidopsis
                  thaliana]
                  2127
Seq. No.
                  1438 1.R1040
Contig ID
5'-most EST
                  zhf700963184.h1
                  2128
Seq. No.
                  1438 2.R1040
Contig ID
5'-most EST
                  LIB3107-054-Q1-K1-E1
Seq. No.
                  2129
Contig ID
                  1438 3.R1040
```

pmv700891037.h1

% identity

```
BLASTX
Method
NCBI GI
                   g2623299
BLAST score
                   480
E value
                   5.0e-48
Match length
                   143
% identity
                   64
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2130
                   1438 4.R1040
Contig ID
                                                              5'-most EST
                   LIB3093-024-Q1-K1-D1
                   2131
Seq. No.
Contig ID
                   1439 1.R1040
                   LIB3028-009-Q1-B1-A11
5'-most EST
Method
                   BLASTX
                   g3257577
NCBI GI
BLAST score
                   165
E value
                   5.0e-11
                   196
Match length
% identity
                   24
                   (AP000005) 211aa long hypothetical protein [Pyrococcus
NCBI Description
                   horikoshii]
Seq. No.
                   2132
                   1439 3.R1040
Contig ID
                   LIB3\overline{0}94-033-Q1-K1-B3
5'-most EST
Seq. No.
                   2133
                   1439 4.R1040
Contig ID
5'-most EST
                   LIB3170-075-Q1-K1-F8
                   2134
Seq. No.
                   1442 1.R1040
Contig ID
                   LIB3027-003-Q1-B1-H12
5'-most EST
Seq. No.
                   2135
                   1446 1.R1040
Contig ID
5'-most EST
                   LIB3051-038-Q1-K1-E9
                   BLASTN
Method
NCBI GI
                   g3985954
BLAST score
                   34
                   3.0e-09
E value
Match length
                   85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   2136
Contig ID
                   1451 1.R1040
                   LIB3027-003-Q1-B1-B8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539009
BLAST score
                   639
                   1.0e-66
E value
Match length
                   182
```

```
NCBI Description
                   (AL049481) putative protein [Arabidopsis thaliana]
                   2137
Seq. No.
                   1454 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800031a06a1
Method
                   BLASTX
NCBI GI
                   g3461820
BLAST score
                   414
E value
                   2.0e-40
Match length
                   97
% identity
                   (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2138
                   1456 1.R1040
Contig ID
5'-most EST
                   LIB3051-080-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g3861189
BLAST score
                   285
E value
                   5.0e-25
Match length
                   118
% identity
                   52
                   (AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia
NCBI Description
                   prowazekii]
                   2139
Seq. No.
                   1456 2.R1040
Contig ID
5'-most EST
                   LIB3027-003-Q1-B1-C8
Seq. No.
                   2140
                   1456 3.R1040
Contig ID
5'-most EST
                   jex700906734.h1
Seq. No.
                   2141
                   1457 1.R1040
Contig ID
                   uC-gmrominsoy095h04b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1008880
BLAST score
                   753
                   0.0e+00
E value
                   1479
Match length
                   89
% identity
                   Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5)
NCBI Description
                   gene, complete cds
                   2142
Seq. No.
                   1457 2.R1040
Contig ID
                   leu701149702.hl
5'-most EST
Method
                   BLASTN
                   g1008880
NCBI GI
BLAST score
                   111
E value
                   3.0e-55
Match length
                   212
% identity
NCBI Description
                   Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5)
```

gene, complete cds

BLAST score

```
2143
Seq. No.
                   1457 3.R1040
Contig ID
5'-most EST
                   LIB3170-005-Q1-K1-F5
Method
                   BLASTN
                   g1008880
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
Match length
                   120
                   87
% identity
                   Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5)
NCBI Description
                   gene, complete cds
                   2144 .
Seq. No.
                   1457 4.R1040
Contig ID
5'-most EST
                   uC-gmropic059d08b1
Method
                   BLASTN
                   g1008880
NCBI GI
BLAST score
                   60
E value
                   5.0e-25
Match length
                   120
% identity
                   88
NCBI Description
                   Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5)
                   gene, complete cds
Seq. No.
                   2145
                   1457 5.R1040
Contig ID
                   fde700870816.h1
5'-most EST
                   2146
Seq. No.
                   1457 7.R1040
Contig ID
5'-most EST
                   jC-gmst02400073d03d1
                   BLASTN
Method
                   g1008880
NCBI GI
BLAST score
                   67
E value
                   3.0e-29
Match length
                   178
                   90
% identity
                  Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5)
NCBI Description
                   gene, complete cds
                   2147
Seq. No.
                   1458 1.R1040
Contig ID
                   LIB3109-021-Q1-K1-A4
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1694621
BLAST score
                   1838
                   0.0e+00
E value
                   461
Match length
% identity
NCBI Description
                  (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
Seq. No.
                   2148
                   1461_1.R1040
Contig ID
5'-most EST
                   smc7\overline{0}0744304.h1
Method
                   BLASTX
NCBI GI
                   g2827552
```

5'-most EST

```
2.0e-15
E value
Match length
                   60
                   73
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1464 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910001d10d1
Seq. No.
                   1466 1.R1040
Contig ID
                   LIB3074-031-Q1-K2-E8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4102634
BLAST score
                   255
E value
                   1.0e-21
Match length
                   48
% identity
                   81
NCBI Description (AF014396) Snakin-1 [Solanum tuberosum]
Seq. No.
                   2151
                   1466 2.R1040
Contig ID
5'-most EST
                   sat701006340.hl
Method
                   BLASTX
NCBI GI
                   q4102634
BLAST score
                   255
E value
                   3.0e-22
Match length
                   48
% identity
                   81
NCBI Description
                  (AF014396) Snakin-1 [Solanum tuberosum]
Seq. No.
                   1469 1.R1040
Contig ID
                   awf700840524.h1
5'-most EST
Seq. No.
                   2153
                   1469 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy244g10b1
                   2154
Seq. No.
                   1469 3.R1040
Contig ID
5'-most EST
                   LIB3\overline{0}73-011-Q1-K1-G3
                   2155
Seq. No.
Contig ID
                   1470 1.R1040
                   xpa7\overline{0}0797086.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3478637
BLAST score
                   355
E value
                   2.0e-33
Match length
                   181
                   40
% identity
NCBI Description
                  (AC005546) R29425 1 [Homo sapiens]
Seq. No.
                   2156
                   1473 1.R1040
Contig ID
```

LIB3027-005-Q1-B1-F8

Seq. No.

Contig ID

2163

1480 1.R1040

```
2157
Seq. No.
                   1477 1.R1040
Contig ID
5'-most EST
                   ncj700983761.h1
Method
                   BLASTX
NCBI GI
                   g4454009
BLAST score
                   210
E value
                   2.0e-16
Match length
                   102
% identity
                   43
                   (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2158
                   1477 2.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy226a03b1
Method
                   BLASTX
NCBI GI
                   g2252829
BLAST score
                   165
E value
                   3.0e-11
                   97
Match length
% identity
                   (AF013293) A IG005I10.6 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2159
                   1477 3.R1040
Contig ID
                   k11701214748.h1
5'-most EST
                   2160
Seq. No.
                   1477 4.R1040
Contig ID
                   LIB3051-017-Q1-E1-G5
5'-most EST
                   2161
Seq. No.
                   1479 1.R1040
Contig ID
                   jC-gmle01810041h06a1
5'-most EST
Method
                   BLASTX
                   q2459448
NCBI GI
                   692
BLAST score
                   1.0e-105
E value
Match length
                   311
                   59
% identity
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   2162
Seq. No.
                   1479 2.R1040
Contig ID
5'-most EST
                   LIB3106-057-Q1-K1-B9
                   BLASTX
Method
                   g2459446
NCBI GI
BLAST score
                   322
E value
                   9.0e-30
                   145
Match length
% identity
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
```

```
5'-most EST
                  LIB3040-028-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                   q4539408
BLAST score .
                   389
E value
                   4.0e-37
Match length
                  221
% identity
NCBI Description (ALO49524) putative alpha NAC [Arabidopsis thaliana]
Seq. No.
                  1480_2.R1040
Contig ID
                  LIB3049-054-Q1-E1-F10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4539408
BLAST score
                  287
E value
                  1.0e-25
Match length
                  84
% identity
                   69
NCBI Description
                  (ALO49524) putative alpha NAC [Arabidopsis thaliana]
Seq. No.
                  2165
                  1480 3.R1040
Contig ID
                  LIB3040-014-Q1-E1-H10
5'-most EST
Seq. No.
                  2166
                  1480 4.R1040
Contig ID
                  crh700853176.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4115918
BLAST score
                  200
E value
                  2.0e-15
Match length
                  93
                  49
% identity
                   (AF118222) similar to nascent polypeptide associated
NCBI Description
                  complex alpha chain [Arabidopsis thaliana]
                  2167
Seq. No.
                  1480 7.R1040
Contig ID
5'-most EST
                  fua701039265.h1
                  2168
Seq. No.
                  1480 8.R1040
Contig ID
5'-most EST
                  kl1701212553.h1
                                        .....
Seq. No.
                  2169
Contig ID
                  1481 1.R1040
                  txt700736308.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1085622
BLAST score
                  1427
E value
                  1.0e-175
Match length
                  378
                  77
% identity
                  alcohol dehydrogenase (EC 1.1.1.1) 1F - Phaseolus
NCBI Description
                  acutifolius >gi_452769_emb_CAA80691_ (Z23170) alcohol
```

dehydrogenase-1F [Phaseolus acutifolius]

NCBI GI

```
2170
Seq. No.
                    1482 1.R1040
Contig ID
                    zsg701120954.h1
5'-most EST
                    2171
Seq. No.
                    1482 2.R1040
Contig ID
                    LIB3049-040-Q1-E1-F3
 5'-most EST
                    2172
Seq. No.
Contig ID
                    1483_1.R1040
                    LIB3\overline{0}65-011-Q1-N1-F6
 5'-most EST
Method
                    BLASTX
                    g1903034
NCBI GI
· BLAST score
                    292
E value
                    3.0e-26
Match length
                    110
                    55
 % identity
                    (X94625) amp-binding protein [Brassica napus]
NCBI Description
                    2173
Seq. No.
Contig ID
                    1488_1.R1040
                    LIB3\overline{0}49-031-Q1-E1-E3
5'-most EST
                    BLASTX
Method
NCBI GI
                    g1039355
BLAST score
                    491
E value
                    2.0e-49
                    151
Match length
                    59
 % identity
                    (X92179) alcohol dehydrogenase [Solanum tuberosum]
NCBI Description
Seq. No.
                    2174
                    1489 1.R1040
Contig ID
                    LIB3139-044-P1-N1-E3
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3264767
BLAST score
                    543
E value
                    5.0e-55
Match length
                    279
                    43
 % identity
                    (AF071893) AP2 domain containing protein [Prunus armeniaca]
NCBI Description
Seq. No.
                    2175
                    1489 2.R1040
Contig ID
 5'-most EST
                    ssr700556206.hl
Method
                    BLASTX
NCBI GI
                    g3264767
BLAST score
                    660
E value
                    7.0e-69
                    272
Match length
 % identity
                    (AF071893) AP2 domain containing protein [Prunus armeniaca]
NCBI Description
                    2176
Seq. No.
                    1489 3.R1040
Contig ID
                    gsv7\overline{0}1056072.h1
 5'-most EST
Method
                    BLASTX
```

g3264767

E value

Match length

1.0e-28

```
BLAST score
                   160
E value
                   3.0e-10
Match length
                   73
% identity
                   48
                   (AF071893) AP2 domain containing protein [Prunus armeniaca]
NCBI Description
                   2177
Seq. No.
                   1489 4.R1040
Contig ID
5'-most EST
                   LIB3093-038-Q1-K1-E4
                   2178
Seq. No.
                   1489 6.R1040
Contig ID
5'-most EST
                   jC-gmf102220068b09d1
                   2179
Seq. No.
                   1492 1.R1040
Contig ID
5'-most EST
                   LIB3040-030-Q1-E1-A10
Method
                   BLASTX
NCBI GI
                   g3367515
BLAST score
                   912
E value
                   1.0e-139
Match length
                   363
                   71
% identity
                   (AC004392) Similar to
NCBI Description
                   glucose-6-phosphate/phosphate-translocator (GPT)
                   gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
                   2180
Seq. No.
                   1493 1.R1040
Contig ID
                   LIB3027-002-Q1-B1-B8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4467147
BLAST score
                   199
E value
                   2.0e-15
Match length
                   110
% identity
                   51
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   2181
Seq. No.
                   1493 2.R1040
Contig ID
                   sat701013373.h1
5'-most EST
                   BLASTX
Method
                   g4467147
NCBI GI
BLAST score
                   307
E value
                   5.0e-34
Match length
                   159
% identity
                   53
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   2182
Seq. No.
                   1495 1.R1040
Contig ID
5'-most EST
                   crh7\overline{0}0850359.h1
Method
                   BLASTX
NCBI GI
                   g2281631
BLAST score
                   317
```

BLAST score

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```
% identity
                    (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                    [Arabidopsis thaliana]
                   2183
Seq. No.
                   1495 2.R1040
Contig ID
5'-most EST
                   awf700842114.hl
Method
                   BLASTX
NCBI GI
                   g2281631
BLAST score
                   305
E value
                   3.0e-27
Match length
                   140
                   52
% identity
                    (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   2184
                   1495 3.R1040
Contig ID
5'-most EST
                   LIB3170-067-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2281631
BLAST score
                   304
E value
                   2.0e-27
Match length
                   83
% identity
                   73
                    (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   2185
                   1497 1.R1040
Contig ID
5'-most EST
                   smc7\overline{0}0749770.h1
Seq. No.
                   2186
Contig ID
                   1498 1.R1040
5'-most EST
                   asj700967459.h1
                   2187
Seq. No.
                   1499 1.R1040
Contig ID
5'-most EST
                   uxk7\overline{0}0669903.h1
Seq. No.
                   2188
                   1500 1.R1040
Contig ID
5'-most EST
                   LIB3028-048-Q1-B1-A3
                   BLASTX
Method
NCBI GI
                   g2213538
BLAST score
                   191
                   2.0e-14
E value
                   155
Match length
% identity
                   43
NCBI Description
                   (X98740) DNA-binding protein PD2 [Pisum sativum]
                   2189
Seq. No.
                   1501 1.R1040
Contig ID
5'-most EST
                   LIB3072-028-Q1-E1-B4
Method
                   BLASTX
NCBI GI
                   g1531756
```

```
9.0e-13
E value
Match length
                   70
                   46
% identity
                   (X82413) proline-rich-like protein [Asparagus officinalis]
NCBI Description
Seq. No.
Contig ID
                   1502 1.R1040
5'-most EST
                   k117\overline{0}1204348.h2
Method
                   BLASTX
NCBI GI
                   q3128174
BLAST score
                   251
E value
                   2.0e-21
                   93
Match length
% identity
                   59
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2191
                   1503 1.R1040
Contig ID
5'-most EST
                   fua7\overline{0}1041667.h1
Method
                  BLASTX
NCBI GI
                   q3850581
BLAST score
                   648
E value
                   2.0e-70
Match length
                   185
% identity
                   (AC005278) EST gb N96383 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   2192
Seq. No.
                   1507 1.R1040
Contig ID
5'-most EST
                  LIB3028-053-Q1-B1-E2
                   2193
Seq. No.
                   1510 1.R1040
Contig ID
5'-most EST
                   LIB3049-030-Q1-E1-D6
Method
                  BLASTX
NCBI GI
                   g266743
BLAST score
                   2213
E value
                   0.0e + 00
Match length
                   477
                   87
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
NCBI Description
                   DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                   (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi 68467 pir ISAASS protein disulfide-isomerase (EC
                   5.3.4.1) precursor (clone L1) - alfalfa
                   >gi 19654 emb_CAA77575_ (Z11499) protein disulfide
                   isomerase [Medicago sativa]
Seq. No.
                   2194
                   1510 2.R1040
Contig ID
5'-most EST
                  ncj700980254.hl
                  BLASTN
Method
NCBI GI
                  g166417
BLAST score
                   97
E value
                   5.0e-47
Match length
                  141
```

```
% identity
                  92
NCBI Description Alfalfa putative endomembrane protein mRNA, complete cds
                  2195
Seq. No.
                  1513 2.R1040
Contig ID
5'-most EST
                  LIB3027-001-Q1-B1-D2
Method
                  BLASTX
                  g119640
NCBI GI
BLAST score
                  206
                  2.0e-16
E value
Match length
                  90
                  51
% identity
                  1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
NCBI Description
                  E8) >gi 82109 pir S01642 ripening protein E8 - tomato
                  >qi 19199 emb CAA31789 (X13437) E8 protein [Lycopersicon
                  esculentum]
                  2196
Seq. No.
                  1514 1.R1040
Contig ID
5'-most EST
                  pxt7\overline{0}0943448.h1
                  2197
Seq. No.
Contig ID
                  1517 1.R1040
5'-most EST
                  zhf700955891.h1
Method
                  BLASTX
NCBI GI
                  q3335374
BLAST score
                  342
E value
                  5.0e-32
Match length
                  157
% identity
                  (AC003028) glutaredoxin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  2198
Contig ID
                  1518 1.R1040
5'-most EST
                  LIB3051-068-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q3023817
BLAST score
                  566
E value
                  6.0e-58
Match length
                  152
% identity
                  72
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM
NCBI Description
                  PRECURSOR (G6PD) >gi 1480344 emb CAA67782 (X99405)
                  glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
Seq. No.
                  2199
Contig ID
                  1518 2.R1040
5'-most EST
                  uC-gmrominsoy311f07b1
Method
                  BLASTX
NCBI GI
                  q3023817
BLAST score
                  762
E value
                  3.0e-81
Match length
                  171
                  87
% identity
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM
NCBI Description
                  PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405)
```

glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

```
2200
Seq. No.
                   1519 1.R1040
Contig ID
5'-most EST
                   uC-qmropic058q03b1
                  BLASTX
Method
NCBI GI
                  q3915847
BLAST score
                  898
                   6.0e-97
E value
Match length
                  180
                   94
% identity
                  40S RIBOSOMAL PROTEIN S2 >qi 2335095 (AC002339) putative
NCBI Description
                   40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  1519 2.R1040
Contig ID
5'-most EST
                  uC-qmronoir034a10b1
Method
                  BLASTX
NCBI GI
                  q3915847
BLAST score
                  1063
E value
                  1.0e-116
                                                          .
. . . .
Match length
                  219 ·
                  92
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  2202
                  1519 3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy315d11b1
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  474
E value
                  2.0e-47
Match length
                  103
% identity
                  89
NCBI Description
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  2203
Seq. No.
                  1519 4.R1040
Contig ID
5'-most EST
                  jC-qmst02400009e05d1
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  184
                  2.0e-13
E value
Match length
                  53
% identity
                  66
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  2204
                  1519 5.R1040
Contig ID
5'-most EST
                  LIB3106-062-Q1-K1-D6
Method
                  BLASTX
                  g3915847
NCBI GI
BLAST score
                  295
                  1.0e-26
E value
```

67

Match length

```
% identity
                   84
                   40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
NCBI Description
                   40S ribosomal protein S2 [Arabidopsis thaliana]
                   2205
Seq. No.
                   1523 1.R1040
Contig ID
                   LIB3\overline{0}72-047-Q1-K1-C3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g125722
BLAST score
                   427
                   8.0e-42
E value
Match length
                   201
% identity
                   51
                   KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR
NCBI Description
                   >gi_81814_pir__JQ1091 trypsin inhibitor KTi1 (Kunitz) -
                   soybean >gi 256635 bbs 115028 (S45035) Kunitz trypsin
                   inhibitor KTil [soybeans, Peptide, 203 aa] [Glycine max]
                   2206
Seq. No.
Contig ID
                   1523 3.R1040
                   crh7\overline{0}0854192.h1
5'-most EST
                   2207
Seq. No.
                   1524 1.R1040
Contig ID
                   rca700999295.h1
5'-most EST
Method
                   BLASTX
                   a1935019
NCBI GI
BLAST score
                   835
                   2.0e-89
E value .
Match length
                   330
% identity
                   53
NCBI Description
                   (Z93774) sucrose transport protein [Vicia faba]
Seq. No.
                   1526 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220078e07a1
Method
                   BLASTX
NCBI GI
                   q4263711
BLAST score
                   323
E value
                   8.0e-30
Match length
                   119
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   2209
Contig ID
                   1528 1.R1040
                   uC-gmflminsoy081g03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3096919
BLAST score
                   550
E value
                   3.0e-56
Match length
                   125
% identity
                   81
                   (AL023094) putative serine/threonine protein kinase
NCBI Description
```

[Arabidopsis thaliana]

```
2210
Seq. No.
                   1529 1.R1040
Contig ID
                   LIB3040-041-01-E1-G7
5'-most EST
Method
                   BLASTX
                   q100200
NCBI GI
BLAST score
                   1080
                   1.0e-118
E value
Match length
                   273
% identity
                   75
NCBI Description
                  chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                   1529 2.R1040
Contig ID
5'-most EST
                   LIB3040-026-Q1-E1-E6
Method
                   BLASTX
NCBI GI
                   q100200
BLAST score
                   555
E value
                   6.0e-57
Match length
                   144
% identity
                   73
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                   2212
                   1529 3.R1040
Contig ID
5'-most EST
                  LIB3138-088-P1-N1-H4
Method
                  BLASTN
NCBI GI
                  q4538949
BLAST score
                  47
E value
                   2.0e-17
Match length
                  67
% identity
                   93
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24
NCBI Description
                   (ESSA project)
Seq. No.
                   2213
Contig ID
                   1529 4.R1040
                  leu701157323.h1
5'-most EST
                  BLASTX
Method
                  g100200
NCBI GI
BLAST score
                  398
E value
                   1.0e-38
                  118
Match length
                   66
% identity
                  chlorophyll a/b-binding protein type I precursor - tomato
NCBI Description
Seq. No.
                   2214
                  1529 9.R1040
Contig ID
5'-most EST
                  LIB3138-120-Q1-N1-F12
Method
                  BLASTX
NCBI GI
                  q4538963
                  475
BLAST score
E value
                  2.0e-47
Match length
                  145
                  73
% identity
                   (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
```

[Arabidopsis thaliana]

Match length

```
Seq. No.
                   2215
                   1529 10.R1040
Contig ID
5'-most EST
                   jC-qmst02400078b01d1
Method '
                   BLASTX
NCBI GI
                   g4538963
BLAST score
                   349
                   7.0e-33
E value
Match length
                   80
% identity
                   88
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana]
                   2216
Seq. No.
                   1529 11.R1040
Contig ID
                   ssr700556044.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1644288
BLAST score
                   60
E value
                   5.0e-25
Match length
                   120
% identity
                   88
NCBI Description
                   B.juncea mRNA for chlorophyll a/b-binding protein
Seq. No.
                                               - 15 s
                   1529 12.R1040
Contig ID
5'-most EST
                   jC-gmst02400023f02d1
Seq. No.
                   2218
                   1529 13.R1040
Contig ID
5'-most EST
                   LIB3106-093-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g100200
BLAST score
                   514
E value
                   3.0e-52
Match length
                   114
% identity
                   63
                   chlorophyll a/b-binding protein type I precursor - tomato
NCBI Description
                   2219
Seq. No.
                   1530 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810041e09a1
Method
                   BLASTX
                   g2407800
NCBI GI
BLAST score
                   506
E value
                   4.0e-51
Match length
                   110
                   92
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2220
                   1538 1.R1040
Contig ID
5'-most EST
                   LIB3073-019-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   g3935169
BLAST score
                   238
E value
                   8.0e-20
```

5'-most EST

```
% identity
                   (AC004557) F17L21.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1538 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810020g02d1
Method
                   BLASTX
NCBI GI
                   g2739382
BLAST score
                   357
E value
                   2.0e-33
                   205
Match length
% identity
                   47
                   (AC002505) myosin heavy chain-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   2222
Seq. No.
                   1538 3.R1040
Contig ID
                   bth700845402.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3228389
BLAST score
                   42
E value
                   3.0e-14
                   102
Match length
% identity
                   43
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F17L21,
                   complete sequence [Arabidopsis thaliana]
                   2223
Seq. No.
                   1541 1.R1040
Contig ID
                   LIB3106-102-Q1-K1-D12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2677830
BLAST score
                   772
E value
                   3.0e-82
Match length
                  166
% identity
                   90
                   (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                   2224
Seq. No.
                   1541 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910008a06d1
                  BLASTX
Method
NCBI GI
                   g4371282
BLAST score
                   236
E value
                   9.0e-20
Match length
                  52
% identity
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                  thaliana]
                   2225
Seq. No.
                   1543 1.R1040
Contig ID
5'-most EST
                  LIB3027-003-Q1-B1-C7
Seq. No.
                  2226
Contig ID
                  1548 1.R1040
```

LIB3T39-004-P1-N1-C7

```
BLASTX
Method
                   q729335
NCBI GI
BLAST score
                   864
E value
                   8.0e-93
Match length
                   240
                   64
% identity
                   SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN
NCBI Description
                   PRECURSOR (IP) >gi_508849 (L27705) succinate dehydrogenase
                   iron-protein subunit [Drosophila melanogaster]
Seq. No.
                   2227
                   1552 1.R1040
Contig ID
5'-most EST
                   LIB3109-020-Q1-K1-F3
Method
                   BLASTN
NCBI GI
                   q2353172
BLAST score
                   56
E value
                   2.0e-22
Match length
                   200
                   82
% identity
NCBI Description
                   Arabidopsis thaliana sigma factor 2 (SIG2) mRNA, nuclear
                   gene encoding chloroplast protein, complete cds
Seq. No.
                   2228
Contig ID
                   1554 1.R1040
5'-most EST
                   LIB3051-017-Q1-E1-C9
Method
                   BLASTX
NCBI GI
                   q417494
BLAST score
                   237
E value
                   9.0e-20
Match length
                   106
% identity
                   49
                   18 KD SEED MATURATION PROTEIN >gi 170008 (M80666)
NCBI Description
                   maturation polypeptide [Glycine max]
                   >gi_444332_prf__1906381A 18kD late embryogenesis abundant
                   protein [Glycine max]
                   2229
Seq. No.
                   1562 1.R1040
Contiq ID
5'-most EST
                   jC-qmro02910060a09a1
Method
                   BLASTN
NCBI GI
                   q4234940
BLAST score
                   316
E value
                   1.0e-177
                   950
Match length
                   83
% identity
NCBI Description
                   Populus tremula x Populus tremuloides cytosolic
                   phosphoglucomutase (pgm) mRNA, complete cds
                   2230
Seq. No.
                   1562 2.R1040
Contig ID
5'-most EST
                   smc7\overline{0}0747567.h1
Method
                   BLASTX
NCBI GI
                   g4234941
BLAST score
                   353
                   2.0e-33
E value
Match length
                   83
```

86

% identity

Contig ID

```
(AF097938) cytosolic phosphoglucomutase [Populus tremula x
NCBI Description
                   Populus tremuloides]
                   2231
Seq. No.
                   1562 3.R1040
Contig ID
5'-most EST
                   LIB3139-039-P1-N1-B9
Method
                   BLASTN
NCBI GI
                   g4234940
BLAST score
                   168
E value
                   2.0e-89
Match length
                   491
                   84
% identity
                   Populus tremula x Populus tremuloides cytosolic
NCBI Description
                   phosphoglucomutase (pgm) mRNA, complete cds
                   2232
Seq. No.
                   1563_1.R1040
Contig ID
                   sat701003565.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1353352
BLAST score
                   1572
                   1.0e-175
E value
Match length
                   462
                   64
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   2233
Seq. No.
                   1563 2.R1040
Contig ID
5'-most EST
                   fC-gmle7000743719a1
Method
                   BLASTX
NCBI GI
                   g1353352
BLAST score
                   401
                   6.0e-39
E value
Match length
                   104
                   72
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
Seq. No.
                   2234
                   1563 3.R1040
Contig ID
5'-most EST
                   LIB3073-025-Q1-K1-B2
                   2235
Seq. No.
Contig ID
                   1563 4.R1040 -
                   trc700564493.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1353352
BLAST score
                   494
E value
                   1.0e-49
Match length
                  146
% identity
                   68
NCBI Description
                   (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
Seq. No.
                   2236
```

1563 8.R1040

```
5'-most EST
                   zzp700834807.h1
                   2237
Seq. No.
Contig ID
                   1563 10.R1040
                   g4395740
5'-most EST
                   2238
Seq. No.
                   1563 11.R1040
Contig ID
5'-most EST
                   asn701138988.h1
                   BLASTN
Method
NCBI GI
                   q16472
BLAST score
                   54
                   2.0e-21
E value
Match length
                   70
% identity
                   94
NCBI Description
                   A.thaliana rRNA repeat unit, most frequent IGR type
Seq. No.
                   2239
                   1565_1.R1040
Contig ID
5'-most EST
                   jC-gmle01810049bl1a1
Method
                   BLASTN
NCBI GI
                   q1885325
BLAST score
                   378
E value
                   0.0e + 00
Match length
                   786
% identity
                   87
NCBI Description
                  P.sativum mRNA for phosphoribulokinase, partial
Seq. No.
                   2240
Contig ID
                   1565 2.R1040
5'-most EST
                   LIB3055-013-Q1-N1-F6
Method
                   BLASTN
NCBI GI
                   g1885325
BLAST score
                   348
E value
                   0.0e + 00
Match length
                   651
% identity
                   88
                   P.sativum mRNA for phosphoribulokinase, partial
NCBI Description
Seq. No.
                   2241
                   1565 3.R1040
Contig ID
5'-most EST
                   zsg701127883.hl
                   BLASTN
Method
NCBI GI
                   g1885325
BLAST score
                   113
E value
                   2.0e-56
                   277
Match length
                   85
% identity
                   P.sativum mRNA for phosphoribulokinase, partial
NCBI Description
Seq. No.
                   2242
                   1569 1.R1040
Contig ID
5'-most EST
                   LIB3170-055-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g2499497
BLAST score
                   1898
```

٠<sup>٩</sup>. .

0.0e+00

E value

Seq. No.

```
406
Match length
% identity
                   94
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 1161600 emb CAA88841 (Z48977) phosphoglycerate kinase
                   [Nicotiana tabacum]
Seq. No.
                   2243
                   1572 1.R1040
Contig ID
5'-most EST
                  LIB3039-006-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  g2431769
BLAST score
                  199
E value
                   4.0e-15
                   59
Match length
                   59
% identity
NCBI Description
                   (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                  2244
                  1572 2.R1040
Contig ID
5'-most EST
                  LIB3040-021-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  g1076627
BLAST score
                  3517
                  0.0e+00
E value
Match length
                  767
                   91
% identity
                  inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco
NCBI Description
                  >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase
                   [Nicotiana tabacum]
Seq. No.
                  2245
Contig ID
                  1572 3.R1040
5'-most EST
                   fC-gmse7000754883d1
Method
                  BLASTN
NCBI GI
                  q790478
BLAST score
                  158
E value
                  3.0e-83
Match length
                  434
% identity
                  84
                  N.tabacum mRNA for inorganic pyrophosphatase (TVP9 clone)
NCBI Description
Seq. No.
Contig ID
                  1572 4.R1040
5'-most EST
                  uC-gmflminsoy003e03b1
                  BLASTN
Method
NCBI GI
                  q951322
BLAST score
                  406
E value
                  0.0e + 00
Match length
                  689
                  90
% identity
                  Vigna radiata pyrophosphatase mRNA, complete cds
NCBI Description
                  2247
Seq. No.
Contig ID
                  1572 5.R1040
5'-most EST
                  LIB3039-008-Q1-E1-C11
```

```
1572_6.R1040
Contig ID
                   LIB3138-015-Q1-N2-D10
5'-most EST
Method
                   BLASTN
NCBI GI
                   g951322
                   90
BLAST score
                   7.0e-43
E value
                   130
Match length
% identity
                   92
NCBI Description
                   Vigna radiata pyrophosphatase mRNA, complete cds
                   2249
Seq. No.
                   1572 7.R1040
Contig ID
                   uaw700664346.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4249662
BLAST score
                   606
E value
                   4.0e-63
Match length
                   134
% identity
                   88
                   (AF089810) Altered Response to Gravity [Arabidopsis
NCBI Description
                   thaliana]
                   2250
Seq. No.
Contig ID
                   1572 8.R1040
5'-most EST
                   uC-qmronoir002d10b1
Method
                   BLASTN
NCBI GI
                   q2653445
BLAST score
                   182
E value
                   6.0e-98
Match length
                   238
% identity
                   94
                   Vigna radiata mRNA for proton pyrophosphatase, complete cds
NCBI Description
Seq. No.
Contig ID
                   1572 10.R1040
5'-most EST
                   g5057881
Method
                   BLASTN
NCBI GI
                   g2653445
BLAST score
                   206
E value
                   1.0e-112
Match length
                   510
% identity
                   89
                   Vigna radiata mRNA for proton pyrophosphatase, complete cds
NCBI Description
                   2252
Seq. No.
                   1572 12.R1040
Contig ID
5'-most EST
                   LIB3139-006-P1-N1-G12
Method
                   BLASTN
NCBI GI
                   g2653445
BLAST score
                   115
E value
                   7.0e-58
Match length
                   267
% identity
                   87
                   Vigna radiata mRNA for proton pyrophosphatase, complete cds
NCBI Description
Seq. No.
```

1572 14.R1040

Contig ID

```
5'-most EST
                   epx701105007.hl
Method
                   BLASTX
NCBI GI
                   q485742
BLAST score
                   674
E value
                   1.0e-145
Match length
                   319
% identity
                   85
NCBI Description
                   (L32791) pyrophosphatase [Beta vulgaris]
Seq. No.
                   1574 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400073d06a1
Method
                   BLASTX
NCBI GI
                   q534982
BLAST score
                   595
E value
                   3.0e-61
Match length
                   331
% identity
                   45
NCBI Description
                   (X75898) phosphoglucomutase [Spinacia oleracea]
Seq. No.
                   2255
                   1575 1.R1040
Contig ID
5'-most EST
                   LIB3049-043-Q1-E1-A1
Method
                   BLASTN
NCBI GI
                   q3184053
BLAST score
                   247
E value
                   1.0e-136
Match length
                   423
% identity
                   90
NCBI Description
                   Pisum sativum mRNA for MADS-box transcription factor
Seq. No.
                   2256
                   1575 2.R1040
Contig ID
5'-most EST
                   LIB3109-052-Q1-K1-B1
Method
                   BLASTN
NCBI GI
                   q3184053
BLAST score
                   283
                   1.0e-158
E value
Match length
                   559
                   88
% identity
NCBI Description
                   Pisum sativum mRNA for MADS-box transcription factor
Seq. No.
                   225.7
                   1575 3.R1040
Contig ID
5'-most EST
                   asj700967431.h1
Method
                   BLASTN
NCBI GI
                   g1239962
BLAST score
                   116
E value
                   1.0e-58
                   148
Match length
                   95
% identity
NCBI Description
                  A.majus mRNA for MADS-box protein (DEFH72)
Seq. No.
                   1576 1.R1040
Contig ID.
5'-most EST
                   LIB3\overline{0}49-050-Q1-E1-F6
```

BLASTX

Method

```
g4218169
NCBI GI
BLAST score
                    395
E value
                    4.0e-38
Match length
                    120
% identity
                    69
                    (AJ009724) MADs-box protein, GDEF1 [Gerbera hybrida]
NCBI Description
                    2259
Seq. No.
Contig ID
                    1576 2.R1040
                    k11701207013.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4218169
BLAST score
                    413
E value
                    1.0e-40
Match length
                    105
% identity
                    77
                    (AJ009724) MADs-box protein, GDEF1 [Gerbera hybrida]
NCBI Description
                    2260
Seq. No.
Contig ID
                    1577 1.R1040
                    LIB3170-048-Q1-J1-B7
5'-most EST
                    BLASTX
Method
NCBI GI
                    g1729860
BLAST score
                    2053
                    0.0e + 00
E value
Match length
                    423
                    95
% identity
                    26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                    PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1)
                    (LEMA-1) >gi_1362099_pir__ S56672 probable 26S proteinase chain MA-1 - tomato >gi_732815_emb_CAA52445_ (X74426)
                    Mg-dependent ATPase 1 [Lycopersicon esculentum]
                    2261
Seq. No.
                    1577 2.R1040
Contig ID
5'-most EST
                    LIB3092-062-Q1-K1-A4
Method
                    BLASTX
NCBI GI
                    q1777386
BLAST score
                    853
E.value
                    2.0e-91
Match length
                    369
% identity
NCBI Description
                    (U39301) caffeic acid O-methyltransferase [Pinus taeda]
Seq. No.
                    2262
Contig ID
                    1577 3.R1040
5'-most EST
                    cks700764831.hl
Method
                    BLASTX
NCBI GI
                    g1729860
BLAST score
                    527
E value
                    9.0e-54
Match length
                    118
% identity
                    87
                    26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                    PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1)
                    (LEMA-1) >gi_1362099_pir__S56672 probable 26S proteinase chain MA-1 - tomato >gi_732815_emb_CAA52445_ (X74426)
```



## Mg-dependent ATPase 1 [Lycopersicon esculentum]

2263 Seq. No. Contig ID 1577 4.R1040 jC-qmf102220060e09a1 5'-most EST BLASTX · Method q3024434 NCBI GI BLAST score 470 E value 8:0e-70 Match length 167 % identity 74 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 1) (TBP-1) >gi\_2564337\_dbj\_BAA22951\_ (D88663) Tat binding protein 1 [Brassica rapa] Seq. No. 1577 5.R1040 Contig ID 5'-most EST zhf700960240.h1 Seq. No. 2265 1577 7.R1040 Contig ID 5'-most EST LIB3028-031-Q1-B1-B9 Method BLASTX NCBI GI q1777386 BLAST score 171 E value 6.0e-12 Match length 52 % identity NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda] Seq. No. 2266 1577 8.R1040 Contig ID 5'-most EST  $q430\overline{5}637$ Method BLASTX NCBI GI g3024434 BLAST score 302 E value 2.0e-51 Match length 126 % identity 93 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 1) (TBP-1) >gi\_2564337\_dbj\_BAA22951\_ (D88663) Tat binding protein 1 [Brassica rapa] Seq. No. 2267 1579 3.R1040 Contig ID 5'-most EST jC-gmf102220148g09a1 Method BLASTN NCBI GI g1870205 BLAST score 265 1.0e-147 E value 576 Match length % identity

Medicago sativa (clone nmh7) MADS-box protein mRNA, NCBI Description

complete cds

2268 Seq. No.

Contig ID 1580 1.R1040

```
LIB3107-052-Q1-K1-B8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2129933
BLAST score
                    691
                    5.0e-73
E value
Match length
                   131
                    95
% identity
NCBI Description
                   myb-related transcription factor TMH27 - tomato
                   >gi_1167484_emb_CAA64614_ (X95296) transcription factor
[Lycopersicon esculentum]
                   2269
Seq. No.
                   1580 2.R1040
Contig ID
5'-most EST
                   hyd700730584.hl
Method ·
                   BLASTX
NCBI GI
                   q82308
BLAST score
                    412
E value
                   3.0e-40
Match length
                   120
% identity
                   77
NCBI Description myb protein 308 - garden snapdragon
Seq. No.
                   2270
                   1582 1.R1040
Contig ID
5'-most EST
                   leu701152088.hl
Method
                   BLASTX
NCBI GI
                   q4105772
BLAST score
                   301
E value
                   2.0e-27
Match length
                   67
% identity
                   39
                    (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
Seq. No.
Contig ID
                   1584 1.R1040
                   wrg700786265.h2
5'-most EST
Method
                   BLASTX
                   g399024
NCBI GI
BLAST score
                   1708
                   0.0e+00
E value
Match length
                   355
                   93
% identity
```

>gi\_322710\_pir\_\_S29047 fructose-bispho

FRUCTOSE-BISPHOSPHATE ALDOLASE 1, CHLOROPLAST PRECURSOR >gi 322710 pir S29047 fructose-bisphosphate aldolase (EC

4.1.2.13) precursor, chloroplast - garden pea (fragment)

>gi\_169037 (M97476) aldolase [Pisum sativum]

Seq. No. 2272

NCBI Description

Contig ID 1584\_2.R1040

5'-most EST LIB3107-016-Q1-K1-C2

Method BLASTN
NCBI GI g169036
BLAST score 189
E value 1.0e-102
Match length 369
% identity 88

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

NCBI Description

```
2273
Seq. No.
                   1584 3.R1040
Contig ID
                   fde700877186.hl
5'-most EST
Method
                   BLASTN
                   g169038
NCBI GI
                   238
BLAST score
E value
                   1.0e-131
Match length '
                   495
% identity
                   89
                  Pisum sativum L. aldolase gene, 3' end cds
NCBI Description
                   2274
Seq. No.
Contig ID
                   1584 6.R1040
5'-most EST
                   LIB3138-096-Q1-N1-B6
Method
                   BLASTN
NCBI GI
                   g169036
BLAST score
                   240
E value
                   1.0e-132
Match length
                   420
% identity
                   90
NCBI Description
                   Pisum sativum L. aldolase gene, 3' end cds
                   2275
Seq. No.
Contig ID
                   1586 1.R1040
                   LIB3106-057-Q1-K1-D2
5'-most EST
Method
                   BLASTX
NCBI GI ,
                   g4033424
BLAST score
                   889
E value
                   8.0e-96
                   208
Match length
                   82
% identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                   pyrophosphatase [Zea mays]
                   2276
Seq. No.
                   1588 1.R1040
Contig ID
                   pmv700888137.h1
5'-most EST
                   BLASTX
Method
                   g4105772
NCBI GI
                   818
BLAST score
                   2.0e-87
E value
                   183
Match length
% identity
                   54
                  (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
                   2277
Seq. No.
                   1588 2.R1040
Contig ID
5'-most EST
                   LIB3106-005-Q1-K1-H8
Method
                   BLASTX
NCBI GI
                   g4105772
BLAST score
                   818
                   2.0e-87
E value
Match length
                   193
% identity
                   41
```

- 589

(AF049917) PGP9B [Petunia x hybrida]

```
2278
Seq. No.
Contig ID
                   1590 1.R1040
                   kmv700737719.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2318116
BLAST score
                   617
E value
                   0.0e+00
Match length
                  1267
% identity
                   89
                   Pisum sativum Mg-chelatase subunit D (ChlD) mRNA, complete
NCBI Description
Seq. No.
                   2279
                   1591 1.R1040
Contig ID
                   zhf700960315.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1841474
BLAST score
                   171
E value
                   5.0e-91
Match length
                   434
% identity
                   88
NCBI Description
                  P.sativum mRNA for Myb-like protein (Myb26)
Seq. No.
                   2280
                   1591 2.R1040
Contig ID
                   zhf700960664.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1841474
BLAST score
                   227
E value
                   1.0e-124
Match length
                   363
                   91
% identity
NCBI Description
                  P.sativum mRNA for Myb-like protein (Myb26)
Seq. No.
                   2281
                   1592 1.R1040
Contig ID
                   LIB3028-039-Q1-B1-E7
5'-most EST
Method
                   BLASTN
                   g2104680
NCBI GI
BLAST score
                   227
                   1.0e-124
E value
                   894
Match length
% identity
                   83
NCBI Description V.faba mRNA for putative transciption factor (1556bp)
                   2282
Seq. No.
                   1593 1.R1040
Contig ID.
                   LIB3028-056-Q1-B1-H7
5'-most EST
                   BLASTN
Method
NCBI GI
                   g1223925
BLAST score
                   258
E value
                   1.0e-143
Match length
                   393
                   92
% identity
```

NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds

```
2283
Seq. No.
Contig ID
                   1595 1.R1040
5'-most EST
                   jC-qmf102220055h11a1
Method
                   BLASTX
NCBI GI
                   g2541876
BLAST score
                   1190
E value
                   1.0e-131
Match length
                   465
% identity
                   53
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   2284
Contig ID
                   1595 2.R1040
5'-most EST
                   jC-qmle01810023c07d1
Seq. No.
                   2285
                   1595 3.R1040
Contig ID
5'-most EST
                   hyd7\overline{0}0726241.h1
Method
                   BLASTX
NCBI GI
                   q2541876
BLAST score
                   306
E value
                   1.0e-27
Match length
                   113
% identity
                   65
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   2286
Contig ID
                   1595 4.R1040
5'-most EST
                   uC-gmflminsoy115h12b1
Seq. No.
                   2287
Contig ID
                   1596 1.R1040
5'-most EST
                   k117\overline{0}1212428.h1
Method
                   BLASTX
NCBI GI
                   g3979665
BLAST score
                   269
E value
                   3.0e-23
                   102
Match length
% identity
                   53
                   (X66482) orf [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2288
                   1596 2.R1040
Contig ID
5'-most EST
                   hyd7\overline{0}0727018.h1
                   2289
Seq. No.
                   1596 3.R1040
Contig ID
5'-most EST
                   qsv7\overline{0}1046770.h1
Seq. No.
                   2290
                   1596 5.R1040
Contig ID
5'-most EST
                   epx701104051.h1
                   2291
Seq. No.
```

1600 1.R1040

Contig ID

Method

```
LIB3028-006-Q1-B1-A7
5'-most EST
Method
                   BLASTX
                   q4099921
NCBI GI
BLAST score
                   451
                   1.0e-44
E value
                   219
Match length
                   48
% identity
NCBI Description
                   (U91982) EREBP-3 homolog [Stylosanthes hamata]
Seq. No.
                   2292
                   1600 2.R1040
Contig ID
5'-most EST
                   LIB3087-005-Q1-K1-D1
                   BLASTN
Method
NCBI GI
                   q4099920
BLAST score
                   95
E value
                   7.0e-46
Match length
                   179
% identity
NCBI Description
                   Stylosanthes hamata EREBP-3 homolog mRNA, complete cds
                   2293
Seq. No.
                   1601 1.R1040
Contig ID
5'-most EST
                   LIB3028-056-Q1-B1-G1
Method
                   BLASTX
NCBI GI
                   g2370253
BLAST score
                   300
E value
                   3.0e-27
Match length
                   143
                   51
% identity
NCBI Description
                   (Y13273) putative protein kinase [Lycopersicon esculentum]
                   2294
Seq. No.
Contig. ID
                   1602 1.R1040
5'-most EST
                   g5057999
Method
                   BLASTX
NCBI GI
                   q3860247
BLAST score
                   1871
E value
                   0.0e + 00
Match length
                   385
% identity
                   91
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
                   2295
Seq. No.
                   1602 2.R1040
Contig ID
                   trc700565474.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3860247
BLAST score
                   1863
E value
                   0.0e+00
Match length
                   383
% identity
                   91
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   2296
Seq. No.
                   1602 3.R1040
Contig ID
5'-most EST
                   uC-gmronoir011h03b1
```

BLASTX

```
g3860247
NCBI GI
                   539
BLAST score
                  .7.0e-93
E value
Match length
                   190
                   89
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   2297
Seq. No.
Contig ID
                   1602 4.R1040
5'-most EST
                   rlr700895868.h1
Method
                   BLASTX
                   q3860247
NCBI GI
BLAST score
                   513
                   4.0e-52
E value
Match length
                   114
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   2298
Seq. No.
Contig ID
                   1602 10.R1040
                   bth7\overline{0}0845653.h1
5'-most EST
Method
                   BLASTX
                   g3860247
NCBI GI
BLAST score
                   329
                   8.0e-31
E value
Match length
                   65
% identity
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1604 1.R1040
5'-most EST
                   jC-qmro02910064f06a1
Method
                   BLASTX
NCBI GI
                   q1076389
BLAST score
                   2747
E value
                   0.0e+00
Match length
                   587
% identity
                   91
                   protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                   >gi_683502_emb_CAA57528 (X82002) protein phosphatase 2A 65
kDa regulatory subunit [Arabidopsis thaliana]
                   2300
Seq. No.
                   1604 2.R1040
Contig ID
5'-most EST
                   fC-gmse700668369h1
Method
                   BLASTX
NCBI GI
                   q1076389
                   1095
BLAST score
                   1.0e-160
E value
Match length
                   325
                   19
% identity
NCBI Description
                   protein phosphatase 2A pDF1 - Arabidopsis thaliana
                   >gi 683502 emb CAA57528 (X82002) protein phosphatase 2A 65
                   kDa regulatory subunit [Arabidopsis thaliana]
                   2301
Seq. No.
```

1604 3.R1040

Contig ID

BLAST score

678

```
jC-qmle01810047f12d1
5'-most EST
                  BLASTX
Method
                  q1076389
NCBI GI
BLAST score
                  405
                  2.0e-39
E value
                  94
Match length
                  26
% identity
                  protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                  >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                  kDa regulatory subunit [Arabidopsis thaliana]
                  2302
Seq. No.
                  1604 4.R1040
Contig ID
                  LIB3170-058-Q1-K1-H1
5'-most EST
                  BLASTX
Method
                  g1568511
NCBI GI
                  299
BLAST score
E value
                  5.0e-27
Match length
                  162
                  37
% identity
                   (X97913) protein phosphatase 2A [Nicotiana tabacum]
NCBI Description
                  2303
Seq. No.
Contig ID '
                  1604 5.R1040
                  LIB3109-036-Q1-K1-E3
5'-most EST
                  BLASTX
Method
                  a1076389
NCBI GI
                  326
BLAST score
                  2.0e-30
E value
                  78
Match length
                  95
% identity
                  protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                  >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                  kDa regulatory subunit [Arabidopsis thaliana]
Seq. No.
                  2304
Contig. ID
                  1606 1.R1040
5'-most EST
                  q5509172
                  BLASTX
Method
NCBI GI
                  q1346812
BLAST score
                  1568
E value
                  1.0e-175
Match length
                   418
                  75
% identity
                  26S PROTEASE REGULATORY SUBUNIT 8 (PROTEASOME SUBUNIT P45)
NCBI Description
                   (THYROID HORMONE RECEPTOR INTERACTING PROTEIN 1) (TRIP1)
                  >gi_2136007_pir__I53510 proteasome subunit p45 - human
                      976227 dbj BAA07919 (D44467) 26S proteasome subunit
                  p45 [Homo sapiens] >gi_1096205_prf__2111282A 26S proteasome
                   [Homo sapiens]
Seq. No.
                  2305
                  1606 2.R1040
Contig ID
                   jC-gmf102220071h07a1
5'-most EST
                  BLASTX
Method
                  q3747111
NCBI GI
```

Match length

NCBI Description

% identity

94 49

```
E value
                   6.0e-71
Match length
                   237
                   57
% identity
                   (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1606 4.R1040
Contig ID
5'-most EST
                   LIB3051-112-Q1-K1-B12
Method
                   BLASTX
                   g1171978
NCBI GI
BLAST score
                   1202
                   1.0e-133
E value
Match length
                   431
                   33
% identity
                   POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                   2307
                   1606 5.R1040
Contig ID
                   LIB3167-049-P1-K1-G8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1171978
BLAST score
                   1300
E value
                   1.0e-144
Match length
                   331
                   28
% identity
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                   2308
Contig ID
                   1606 6.R1040
5'-most EST
                   LIB3170-049-Q1-J1-B1
Method
                   BLASTX
NCBI GI
                   g2213871
BLAST score
                   295
                   1.0e-26
E value
Match length
                   73
% identity
                   (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   2309
                   1606 12.R1040
Contig ID
                   qsv7\overline{0}1056823.h1
5'-most EST
Method
                   BLASTX
                   g1170767
NCBI GI
BLAST score
                   221
E value
                   7.0e-18
```

26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN)

fission yeast (Schizosaccharomyces pombe) >gi\_406051

>qi 626074 pir S45176 transcription factor SUG1 homolog -

e.





(U02280) Let1 [Schizosaccharomyces pombe] >gi\_4106689\_emb\_CAA22628\_ (AL035065) 26s protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]

2310 Seq. No.

Contig ID 1606\_13.R1040 5'-most EST ncj700977584.h1

2311 Seq. No.

1606\_14.R1040 Contig ID 5'-most EST g4397126

2312 Seq. No.

1606\_15.R1040 Contig ID 5'-most EST gsv701044733.hl

Seq. No. 2313

1606\_16.R1040 Contig ID

LIB3050-022-Q1-K1-C11 5'-most EST

Seq. No. 2314

1606\_19.R1040 Contig ID

5'-most EST jC-gmf102220084c12d1

BLASTX Method g2982331 NCBI GI 288 BLAST score E value 1.0e-25 58 Match length

% identity

NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No. 2315

1607\_1.R1040 Contig ID zpv700757870.h1 5'-most EST

BLASTX Method g2213425 NCBI GI BLAST score 1277 E value 1.0e-141 279 Match length 84 % identity

(Z97064) hypothetical protein [Citrus x paradisi] NCBI Description

Seq. No.

1607\_3.R1040 Contig ID

jC-gmro02910073h07a1 5'-most EST

BLASTN Method NCBI GI q2213424 BLAST score 145 1.0e-75 E value Match length 409 84 % identity

NCBI Description Citrus paradisi mRNA for hypothetical protein

Seq. No. 2317

1607\_4.R1040 Contig ID

5'-most EST uC-gmronoir040f06b1

```
Seq. No.
                   2318
                   1607_5.R1040
Contig ID
                   jC-gmro02910005a04d1
5'-most EST
                   BLASTX
Method
                   g2213425
NCBI GI
BLAST score
                   391
E value
                   7.0e-38
                   88
Match length
% identity
                   46
                   (Z97064) hypothetical protein [Citrus x paradisi]
NCBI Description
                   2319
Seq. No.
                   1607_6.R1040
Contig ID
                   LIB3040-059-Q1-E1-B4
5'-most EST
                   BLASTX
Method
                   g2213425
NCBI GI
BLAST score
                   376
E value
                   3.0e - 36
Match length
                   78
                   47
% identity
                   (Z97064) hypothetical protein [Citrus x paradisi]
NCBI Description
                   2320
Seq. No.
                   1607_9.R1040
Contig ID
5'-most EST
                   zhf700958949.h1
                   BLASTN
Method
                   g2213424
NCBI GI
· BLAST score
                   73
E value
                   5.0e-33
                   177
Match length
                   86
% identity
NCBI Description Citrus paradisi mRNA for hypothetical protein
Seq. No.
                   2321
                   1608_1.R1040
Contig ID
                   uaw700666018.h1
 5'-most EST
                   BLASTN
Method
                   g3449326
NCBI GI
BLAST score
                   46
                   2.0e-16
E value
                   151
Match length
                   86
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19M22, complete sequence [Arabidopsis thaliana]
                   2322
 Seq. No.
                   1608_2.R1040
Contig ID
                   gsv701049801.h1
 5'-most EST .
                   BLASTN
Method
                   g3869065
NCBI GI
BLAST score
                   51
E value
                    2.0e-19
Match length
                   155
                   86
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
```

K24M7, complete sequence [Arabidopsis thaliana]

Match length

62

```
2323
Seq. No.
Contig ID
                  1611_1.R1040
                  jC-gmro02910016b07a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3935150
                  655
BLAST score
E value
                  1.0e-68
Match length
                  194
% identity
                  45
NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]
                  2324
Seq. No.
                  1612_1.R1040
Contig ID
                  LIB3039-046-Q1-E1-H12
5'-most EST
Method
                  BLASTN
NCBI GI
                  g563328
BLAST score
                  116
E value
                  4.0e-58
Match length
                  320
                  86
% identity
NCBI Description A.officinalis mRNA for histone 2B
                  2325
Seq. No.
                  1612_2.R1040
Contig ID
                  jC-gmro02910020f12d1
5'-most EST
                  BLASTN
Method
                  g3510337
NCBI GI
BLAST score
                  34
E value
                  3.0e-09
Match length
                  188
% identity
                  84
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  2326
                  1613_1.R1040
Contig ID
5'-most EST
                  LIB3051-053-Q1-K2-D4
                  2327
Seq. No.
                  1613_3.R1040
Contig ID
                  zhf700952934.h1
5'-most EST
                  BLASTN
Method
                  g1370171
NCBI GI
BLAST score
                  37
                  1.0e-11
E value
                  70
Match length
                  89
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X
                - 2328
Seq. No.
                  1614_1.R1040
Contig ID
                  LIB3106-039-Q1-K1-A10
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2253442
BLAST score
                  268
E value
                   4.0e-23
```

```
% identity
                   66
                   (AF007784) LTCOR11 [Lavatera thuringiaca]
NCBI Description
                   2329
Seq. No.
                   1614 2.R1040
Contig ID
                   g5126588
5'-most EST
                   BLASTX
Method
                   g2253442
NCBI GI
BLAST score
                   271
E value
                   9.0e-24
Match length
                   62
% identity
                   68
NCBI Description
                   (AF007784) LTCOR11 [Lavatera thuringiaca]
                   2330
Seq. No.
                   1614 3.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1146240.h1
                   BLASTX
Method
NCBI GI
                   g2792297
BLAST score
                   175
E value
                   1.0e-12
                   48
Match length
                   60
% identity
                   (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                   2331
Seq. No.
                   1615_1.R1040
Contig ID
                   LIB3028-056-Q1-B1-E10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3510538
BLAST score
                   634
                   4.0e-66
E value
Match length
                   124
% identity
                  (U93167) expansin [Prunus armeniaca]
NCBI Description
                   2332 . -
Seq. No.
                   1615 2.R1040
Contig ID
5'-most EST
                   asn701135733.h1
                   BLASTX
Method
NCBI GI
                   g3643603
BLAST score
                   586
E value
                   2.0e-70
Match length
                   192
% identity
NCBI Description
                   (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   2333
Contig ID
                   1617 1.R1040
5'-most EST
                   qsv701055578.hl
Method
                   BLASTN
NCBI GI
                   q1262145
BLAST score
                   201
                   1.0e-109
E value
Match length
                   533
% identity
                   84
```

NCBI Description S.oleracea mRNA for proteasome 37kD subunit

% identity

39

```
2334
Seq. No.
                    1617 2.R1040
Contig ID
5'-most EST
                    zzp7\overline{0}0834205.h1
Method
                    BLASTX
                    q1709761
NCBI GI
BLAST score
                    433
                    1.0e-46
E value
Match length
                    105
                    95
% identity
                    PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                    COMPLEX 27 KD SUBUNIT) >gi_1262146_emb_CAA65660_ (X96974)
                    proteasome subunit [Spinacia oleracea]
Seq. No.
                    2335
                    1618 1.R1040
Contig ID
                    pcp700990455.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3513727
BLAST score
                    2263
                    0.0e + 00
E value
Match, length
                    525
% identity
NCBI Description
                    (AF080118) contains similarity to TPR domains (Pfam:
                    TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                    kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
                    protein [Arabidopsis thaliana]
Seq. No.
                    2336
                    1618 2.R1040
Contig ID
                    zsg7\overline{0}1130248.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3513727
BLAST score
                    385
E value
                    5.0e-37
Match length
                    148
% identity
                    (AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                    TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                    kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                    thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
                    protein [Arabidopsis thaliana]
Seq. No.
                    2337
                    1620 1.R1040
Contig ID
                    LIB3094-083-Q1-K1-C2
5'-most EST
Seq. No.
                    2338
Contig ID
                    1620 2.R1040
5'-most EST
                    leu7\overline{0}1152744.h1
Method
                    BLASTX
                    g4249376
NCBI GI
BLAST score
                    357
E value
                    3.0e-33
Match length
                    225
```

```
(AC005966) Strong similarity to gi 2829864 F316.6 zinc
 NCBI Description
                   metalloproteinase homolog from Arabidopsis thaliana BAC
                   qb AC002396. EST qb Z26412 comes from this gene.
                    [Arabidopsis thaliana]
                   2339
 Seq. No.
                   1620 3.R1040
 Contig ID
 5'-most EST
                   LIB3056-008-Q1-N1-E3
Method
                   BLASTX
NCBI GI
                   g2827777
BLAST score
                   241
                   5.0e-20
E value
                   141
Match length
 % identity
                   39
                   METALLOENDOPROTEINASE 1 PRECURSOR (SMEP1) >gi 1679656
NCBI Description
                    (U63725) metalloproteinase [Glycine max]
Seq. No.
 Contig ID
                   1620 4.R1040
                   uC-gmflminsoy059d12b1
 5'-most EST
Seq. No.
                   1620 5.R1040
 Contig ID
                   LIB3107-006-Q1-K1-G11
 5'-most EST
                   2342
Seq. No.
                   1620 6.R1040
Contig ID
                   LIB3051-010-Q1-E1-C4
 5'-most EST
Method
                   BLASTX
                   g3776080
NCBI GI
BLAST score
                   164
                   4.0e-11
E value
Match length
                   54
                   56
 % identity
NCBI Description (Y18249) MtN9 [Medicago truncatula]
                   2343
Seq. No.
                   1620 7.R1040
Contig ID
 5'-most EST
                   leu701148815.h1
Seq. No.
                   2344
                   1620 8.R1040
Contig ID
 5'-most EST
                   uaw700663327.hl
Seq. No.
                   2345
                   1620 10.R1040
Contig ID
 5'-most EST
                   uaw700662277.hl
                   2346
Seq. No.
Contig ID
                   1621 1.R1040
 5'-most EST
                   eep7\overline{0}0869770.h1
Method
                   BLASTX
NCBI GI
                   g1680686
BLAST score
                   497
E value
                   1.0e-49
```

189

53

Match length % identity

```
(U51330) rust resistance kinase Lr10 [Triticum aestivum]
NCBI Description
Seq. No.
                  2347
                  1621 2.R1040
Contig ID
                  LIB3138-008-Q1-N1-A8
5'-most EST
Method
                  BLASTX
                  q3025189
NCBI GI
BLAST score
                  799
E value
                  5.0e-85
Match length
                  458
% identity
                  39
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
NCBI Description
                  >gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                  2348
Seq. No.
                  1621 3.R1040
Contig ID
5'-most EST
                  jC-qmf102220094b06a1
Seq. No.
                  1621 8.R1040
Contig ID
5'-most EST
                  jC-qmle01810006e09a1
Method
                  BLASTX
NCBI GI
                  g3025189
BLAST score
                  192
E value
                  2.0e-14
                  79
Match length
% identity
                  43
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
NCBI Description
                  >gi 1652753_dbj_BAA17672 (D90908) ABC1-like [Synechocystis
                  sp.]
                  2350
Seq. No.
                  1622 1.R1040
Contig ID
5'-most EST
                  zhf700961260.h1
Method
                  BLASTX
NCBI GI
                  q2144584
BLAST score
                  329
E value
                  1.0e-30
Match length
                  142
% identity
                  51
                  trypsin inhibitor A (Kunitz) precursor - soybean
NCBI Description
                  >gi 18770 emb CAA45777 (X64447) trypsin inhibitor subtype
                  A [Glycine max]
Seq. No.
                  2351
                  1623 1.R1040
Contig ID
5'-most EST
                  uC-qmrominsoy177g08b1
Method
                  BLASTX
NCBI GI
                  q1346297
BLAST score
                  1869
E value
                  0.0e+00
Match length
                  461
% identity
                  79
                  3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 1 (HMG-COA
NCBI Description
                  REDUCTASE 1) (HMGR1) (HMGR) >gi 2117465 pir S59944
                  hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) -
```

NCBI Description

```
potato >gi_169485 (L01400) hydroxymethylglutaryl coenzyme A
reductase [Solanum tuberosum]
```

```
2352
Seq. No.
                   1623 2.R1040
Contig ID
                   zhf700958080.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1346298
                   250
BLAST score
E value
                   2.0e-21
Match length
                   143
                   43
% identity
                   3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (HMG-COA
NCBI Description
                   REDUCTASE 2) >gi 282943 pir S25316
                   hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) -
                   tomato >gi 170452 (M63642) 3-hydroxy-3-methylglutaryl
                   coenzyme A reductase [Lycopersicon esculentum]
Seq. No.
                   2353
                   1624 1.R1040
Contig ID
5'-most EST
                   LIB3028-008-Q1-B1-F1
Method
                   BLASTX
                   q4263048
NCBI GI
BLAST score
                   800
E value
                   2.0e-85
                   271
Match length
% identity
                   61
NCBI Description
                   (AC005142) putative hydrolase [Arabidopsis thaliana]
Seq. No.
                   1626 1.R1040
Contig ID
                   LIB3028-056-Q1-B1-F10
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4263791
BLAST score
                   289
                   9.0e-26
E value
                   200
Match length
                   35
% identity
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   2355
Seq. No.
                   1627 1.R1040
Contig ID
5'-most EST
                   vzy7\overline{0}0754339.h1
Seq. No.
                   2356
                   1628 1.R1040
Contig ID
                   jsh7\overline{0}1064382.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1616612
BLAST score
                   807
                   3.0e-86
E value
                   193
Match length
                   79
% identity
```

plumbaginifolia]

(Y08423) small GTP-binding protein [Nicotiana

```
2357
Seq. No.
                   1628 2.R1040
Contig ID
5'-most EST
                   LIB3040-041-Q1-E1-C9
Method
                   BLASTN
NCBI GI
                   g1184988
BLAST score
                   108
E value
                   1.0e-53
Match length
                   244
% identity
                   86
NCBI Description
                   Nicotiana tabacum GTP-binding protein NTGB2 mRNA, partial
                   2358
Seq. No.
                   1628 3.R1040
Contig ID
5'-most EST
                   asn701139847.hl
Method
                   BLASTX
NCBI GI
                   g266989
BLAST score
                   533
E value
                   2.0e-54
Match length
                   106
% identity
                   95
                   GTP-BINDING PROTEIN SAR1B >gi_322517_pir__S28603
NCBI Description
                   GTP-binding protein - Arabidopsis thaliana >gi 166734
                   (M95795) GTP-binding protein [Arabidopsis thaliana]
                   2359
Seq. No.
                   1628 5.R1040
Contig ID
                   jsh7\overline{0}1065569.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3334322
                   308
BLAST score
                   3.0e-28
E value
Match length
                   59
% identity
                   98
                   GTP-BINDING PROTEIN SAR1B >gi_2108347 (U55036) small
NCBI Description
                   GTP-binding protein Bsarlb [Brassica rapa]
Seq. No.
                   2360
                   1629 1.R1040
Contig ID
                   LIB3049-022-Q1-E1-G4
5'-most EST
                   BLASTN
Method
NCBI GI
                   g1370286
                   173
BLAST score
                   4.0e-92
E. value
Match length
                   385
% identity
                   86
                  P.sativum mRNA for pore protein
NCBI Description
                   2361
Seq. No.
                   1629 2.R1040
Contig ID
5'-most EST
                   hrw701060880.h1
Seq. No.
                   2362
                   1629 3.R1040
Contig ID
5'-most EST
                   LIB3109-033-Q1-K1-A4
                   BLASTX
Method
NCBI GI
                   g1370287
```

BLAST score

E value

576

3.0e-59

```
BLAST score
                   211
E value
                   2.0e-16
Match length
                   52
                   79
% identity
                   (273553) core protein [Pisum sativum]
NCBI Description
                   2363
Seq. No.
                   1630 1.R1040
Contig ID
5'-most EST
                   LIB3028-056-Q1-B1-C1
                   2364
Seq. No.
                   1631 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220050d12a1
                   2365
Seq. No.
                   1633 1.R1040
Contig ID
                   LIB3087-011-Q1-K1-F10
5'-most EST
Method
                   BLASTN
NCBI GI
                   g510189
BLAST score
                   445
                   0.0e + 00
E value
Match length
                   815
% identity
                   89
                   P.sativum (miranda) mRNA for chloroplast outer envelope
NCBI Description
                   protein
Seq. No.
                   2366
                   1633 3.R1040
Contig ID
                   leu7\overline{0}1144743.h1
5'-most EST
Method
                   BLASTN
                   g3293200
NCBI GI
BLAST score
                   201
E value
                   1.0e-109
                   305<sub>.</sub>
91
Match length
% identity
                   Pisum sativum GTP-binding protein (IAP34) mRNA, complete
NCBI Description
                   2367
Seq. No.
                   1634 1.R1040
Contig ID
5'-most EST
                   uC-gmropic011a08b1
                   BLASTX
Method
NCBI GI
                   g2191171
BLAST score
                   587
E value
                   2.0e-60
Match length
                   191
                   60
% identity
                   (AF007270) similar to A. thaliana DI19 mRNA (NID:g469110)
NCBI Description
                   [Arabidopsis thaliana]
                   2368
Seq. No.
                   1636 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220053f02a1
                   BLASTX
Method
NCBI GI
                   g2239262
```

```
Match length
                   212
% identity
                   51
                   (Y13285) pectin methylesterase-like protein [Zea mays]
NCBI Description
                  2369
Seq. No.
                  1637 1.R1040
Contig ID
                   fC-gmse700754179d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2961107
BLAST score
                  245
                   2.0e-20
E value
                   91
Match length
                   49
% identity
                   (AF042383) TLS-associated protein with SR repeats [Mus
NCBI Description
                  musculus] >gi 2961149 (AF047448) TLS-associated protein
                  TASR [Homo sapiens]
                  2370
Seq. No.
                  1637 2.R1040
Contig ID
5'-most EST
                  LIB3028-056-Q1-B1-C7
Seq. No.
                  2371
                  1638 1.R1040
Contig ID
                  uC-gmflminsoy069e04b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2959767
                  2370
BLAST score
                  0.0e+00
E value
                  662
Match length
                   47
% identity
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                  2372
                  1639 1.R1040
Contig ID
                  uC-qmflminsoy011c12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g886132
                  299
BLAST score
E value
                   4.0e-27
Match length
                  135
                  47
% identity
NCBI Description
                   (U28149) putative surface protein [Medicago sativa]
Seq. No.
                  2373
                  1640 1.R1040
Contig-ID
                  epx701109865.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q391604
BLAST score
                  341
                  0.0e+00
E value
Match length
                  953
                  84
% identity
NCBI Description
                  Arabidopsis thaliana ATPK15D mRNA for casein kinase II
```

catalytic subunit, complete cds

Method

```
Seq. No.
                   2374
                   1640 2.R1040
Contig ID
                  wrg700790238.h2
5'-most EST
Method
                  BLASTN
                  g391604
NCBI GI
                  134
BLAST score
                   6.0e-69
E value
Match length
                   350
% identity
                   85
                  Arabidopsis thaliana ATPK15D mRNA for casein kinase II
NCBI Description
                  catalytic subunit, complete cds
                   2375
Seq. No.
                   1640 4.R1040
Contig ID
5'-most EST
                   jC-qmle01810021e08a1
Method
                  BLASTN
                  g3169169
NCBI GI
BLAST score
                   47
E value
                   5.0e-17
                   95
Match length
                   53
% identity
                  Arabidopsis thaliana chromosome II BAC F21P24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  2376
                  1640 5.R1040
Contig ID
                  g5677543
5'-most EST
                  BLASTX
Method
NCBI GI
                  g585350
                  730
BLAST score
E value
                   2.0e-77
Match length
                  144
                   94
% identity
                  CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
NCBI Description
                  >gi 419753 pir S31099 casein kinase II (EC 2.7.1.-)
                  alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
                  >gi_391605_dbj_BAA01091_ (D10247) casein kinase II
                  catalytic subunit [Arabidopsis thaliana]
Seq. No.
                  2377
                  1642 1.R1040
Contig ID
                  jsh701067642.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4056468
BLAST score
                  359
E value
                  8.0e - 34
                  154
Match length
% identity
                   (AC005990) Contains similarity to gb X66426
NCBI Description
                  polygalacturonase from Persea americana and is a member of
                  the signal peptidase family PF 00461 and polygalacturonase
                  family PF 00295. [Arabidopsis thaliana]
                  2378
Seq. No.
                  1643 1.R1040
Contig ID
                  q5509675
5'-most EST
```

BLASTX

```
NCBI GI
                   q2497492
BLAST score
                   364
E value
                   2.0e-34
Match length
                   101
                   68
% identity
                   URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                   KINASE) >gi 1653646 dbj BAA18558 (D90915) uridine
                   monophosphate kinase [Synechocystis sp.]
                   2379
Seq. No.
                   1644 1.R1040
Contig ID
                   q5677499
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539400
BLAST score
                   824
E value
                   2.0e-88
Match length
                   208
                   75
% identity
NCBI Description
                   (AL035526) putative protein [Arabidopsis thaliana]
                   2380
Seq. No.
                   1645 1.R1040
Contig ID
5'-most EST
                   pmv700893145.h1
Method
                   BLASTX
NCBI GI
                   q1723242
BLAST score
                   152
E value
                   2.0e-09
                   74
Match length
% identity
                   50
                   HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I
NCBI Description
                   >gi 1177363 emb CAA93239 (Z69240) yeast dsk2 homolog,
                   ubiquitin-like protein [Schizosaccharomyces pombe]
Seq. No.
                   2381
Contig ID
                   1646 1.R1040
                   gsv7\overline{0}1051466.h1
5'-most EST
                   BLASTX
Method
                   g4510345
NCBI GI
BLAST score
                   355
                   4.0e-33
E value
Match length
                   164
% identity
                   45
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2382
                   1646 2.R1040
Contig ID
                   sat7\overline{0}1008658.h1
5'-most EST
                   2383
Seq. No.
                   1646 3.R1040
Contiq ID
5'-most EST
                   LIB3170-007-Q1-K1-G8
                   2384
Seq. No.
                   1646 4.R1040
Contig ID
5'-most EST
                   LIB3051-032-Q1-K1-F1
```

2385

Seq. No.

Method

BLASTN

```
1646 5.R1040
Contig ID
                   pxt700945341.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4510345
BLAST score
                   145
                   5.0e-09
E value
Match length
                   36
                   67
% identity
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                   2386
                   1646 6.R1040
Contig ID
5'-most EST
                  LIB3138-021-01-N1-H12
Seq. No.
                   2387
                   1646 8.R1040
Contig ID
5'-most EST
                  LIB3139-090-P1-N1-H4
                   BLASTX
Method
NCBI GI
                   q1172650
BLAST score
                   164
                   6.0e-11
E value
Match length
                  74
% identity
                   47
NCBI Description
                  EXTRACELLULAR METALLOPROTEASE PRECURSOR
                  >gi_95576_pir__A41048 extracellular metalloproteinase (EC
                   3.4.24.-) precursor - Erwinia carotovora subsp. carotovora
                  >qi 148480 (M36651) extracellular protease (prt) [Erwinia
                   carotovoral
Seq. No.
                   2388
                   1646 11.R1040
Contig ID
5'-most EST
                  jC-qmf102220148b01d1
Seq. No.
Contig ID
                  1646 12.R1040
5'-most EST
                  bth700844489.h1
Method
                  BLASTX
NCBI GI
                  q3123056
BLAST score
                  152
E value
                  1.0e-09
Match length
                  174
% identity
                  33
                  HYPOTHETICAL PROTEIN KIAA0039 >gi 436222 dbj BAA05039
NCBI Description
                   (D26018) KIAA0039 [Homo sapiens]
Seq. No.
                  2390
                  1646 17.R1040
Contig ID
                  LIB3\overline{1}38-001-Q1-N1-A12
5'-most EST
                  2391
Seq. No.
                  1646 18.R1040
Contig ID
                  fua701037588.h1
5'-most EST
                  2392
Seq. No.
                  1647 1.R1040
Contig ID
                  LIB3093-038-Q1-K1-A3
5'-most EST
```

Method

BLASTX

```
NCBI GI
                   q488738
BLAST score
                   233
E value
                   1.0e-128
Match length
                   777
                   82
% identity
                   G.hirsutum (DPL 62) mRNA for ribosomal protein small
NCBI Description
                   subunit 4e
Seq. No.
                   2393
                   1647 2.R1040
Contig ID
                   pmv700890611.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2262167
BLAST score
                   629
E value
                   1.0e-65
Match length
                   170
% identity
                   72
                   (ACO02329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   2394
Contig ID
                   1648 1.R1040
                   zhf700963763.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2827628
BLAST score
                   268
E value
                   2.0e-23
Match length
                   122
% identity
                   45
                   (AL021636) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2395
                   1650 1.R1040
Contig ID
5'-most EST
                   LIB3138-126-Q1-N1-B10
Method
                   BLASTN
NCBI GI
                   q1853967
BLAST score .
                   181
                   8.0e-97
E value
Match length
                   760
                   81
% identity
                  Vigna unguiculata mRNA for CPRD12 protein, complete cds
NCBI Description
                   2396
Seq. No.
                   1650 2.R1040
Contig ID
5'-most EST.
                   LIB3170-041-Q1-J1-A11
Method ·
                   BLASTN
NCBI GI
                   g1853967
BLAST score
                   66
                   1.0e-28
E value
Match length
                   138
                   87
% identity
                   Vigna unguiculata mRNA for CPRD12 protein, complete cds
NCBI Description
                   2397
Seq. No.
                   1651 1.R1040
Contig ID
                   gsv7\overline{0}1054270.h1
5'-most EST
```

```
g114181
NCBI GI
BLAST score
                    915
                    1.0e-98
E value
                    324
Match length
% identity
                    57
                    3-DEHYDROQUINATE SYNTHASE >gi_68385_pir__SYECQ
3-dehydroquinate synthase (EC 4.6.1.3) - Escherichia coli
NCBI Description
                    >gi_40968_emb_CAA27495_ (X03867) 3-dehydroquinate synthase
(aa 1-362) [Escherichia coli] >gi_41225_emb_CAA79666_
                    (Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett.
                    200:11-17(1986) [Escherichia coli] >gi_606323 (U18997)
                    3-dehydroquinate synthase [Escherichia coli] >gi 1789791
                    (AE000414) 3-dehydroquinate synthase [Escherichia coli]
Seq. No.
                    2398
                    1651 2.R1040
Contig ID
                    LIB3138-082-P1-N1-E1
5'-most EST
                    2399
Seq. No.
                    1651 3.R1040
Contig ID
5'-most EST
                    fC-gmle700875818f1
                    2400
Seq. No.
                    1652 1.R1040
Contig ID
                    LIB3139-081-P1-N1-F5
5'-most EST
                    2401
Seq. No.
                    1652 2.R1040
Contig ID
5'-most EST
                    LIB3092-015-Q1-K1-E7
Seq. No.
                    2402
                    1652 3.R1040
Contig ID
5'-most EST
                    LIB3\overline{0}92-033-Q1-K1-H10
                    2403
Seq. No.
Contig ID
                    1653 1.R1040
5'-most EST
                    LIB3138-129-Q1-N1-E3
Method
                    BLASTX
NCBI GI
                    q2465008
BLAST score
                    1115
E value
                    1.0e-122
Match length
                    339
% identity
NCBI Description
                    (AJ001445) ripening-induced protein [Fragaria vesca]
Seq. No.
Contig ID
                    1654 1.R1040
                    zhf700962965.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1076287
BLAST score
                    1503
E value
                    1.0e-167
Match length
                    419
% identity
                    67
                    amine acid permease - Arabidopsis thaliana
NCBI Description
                    >gi_510236_emb_CAA50672_ (X71787) amine acid permease
```

[Arabidopsis thaliana]

```
2405
Seq. No.
                   1654 2.R1040
Contig ID
5'-most EST
                   V4R - \overline{0}1 - Q1 - B1 - B10
                   BLASTX
Method
                   q1076287
NCBI GI
BLAST score
                   155
                   2.0e-10
E value
Match length
                   56
                   57
% identity
NCBI Description
                   amine acid permease - Arabidopsis thaliana
                   >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                   [Arabidopsis thaliana]
Seq. No.
                   2406
                   1656 1.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0980372.h1
Method
                   BLASTX
NCBI GI
                   q4056480
BLAST score
                   724
                   3.0e-91
E value
Match length
                   224
% identity
                   (AC005896) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2407
                   1656 2.R1040
Contig ID
5'-most EST
                   LIB3170-024-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   g4056480
BLAST score
                   453
E value
                   4.0e-45
Match length
                   113
% identity
NCBI Description
                   (AC005896) putative adenylate kinase [Arabidopsis thaliana]
Seq. No.
                   2408
                   1656 3.R1040
Contig ID
5'-most EST
                   uC-qmropic101b11b1
Method
                   BLASTX
NCBI GI
                   g4056480
BLAST score
                   417
                   7.0e-41
E value
                   146
Match length
                   62
% identity
                   (AC005896) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
                   2409
Seq. No.
                   1656 4.R1040
Contig ID
5'-most EST
                   sat701006284.h2
Method
                   BLASTX
                   g4056480
NCBI GI
                   227
BLAST score
                   1.0e-18
E value
Match length
                   82
% identity
                   (AC005896) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
```

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```
Seq. No.
                  2410
Contig ID
                  1657 1.R1040
5'-most EST
                  LIB3028-004-Q1-B1-G5
                  2411
Seq. No.
                  1658 1.R1040
Contig ID
5'-most EST
                  LIB3028-056-Q1-B1-B7
Method
                  BLASTX
NCBI GI
                  q4049341
BLAST score
                  380
E value
                  2.0e-36
Match length
                  175
% identity
                   41
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  2412
                  1659 1.R1040
Contig ID
5'-most EST
                  LIB3106-041-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q4335745
BLAST score
                  618
E value
                  5.0e-64
                  270
Match length
% identity
                  47
                   (AC006284) putative hydrolase (contains an
NCBI Description
                  esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.
                  2413
                  1659 2.R1040
Contig ID
                  ncj700981794.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4335745
BLAST score
                  362
E value
                  3.0e - 34
                  141
Match length
                  49
% identity
                   (AC006284) putative hydrolase (contains an
NCBI Description
                  esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                  2414
Seq. No.
                  1659 3.R1040
Contig ID
5'-most EST
                  ssr700560096.h1
                  2415
Seq. No.
                  1660 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910040d04a1
Method
                  BLASTX
NCBI GI
                  g4309757
BLAST score
                  229
                  1.0e-18
E value
Match length
                  63
% identity
NCBI Description (AC006217) hypothetical protein [Arabidopsis thaliana]
```

Match length

41

```
2416
Seq. No.
                   1665 1.R1040
Contig ID
                   LIB3170-046-Q1-J1-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2239262
BLAST score
                   1126
                   1.0e-123
E value
Match length
                   465
% identity
                   47
NCBI Description
                   (Y13285) pectin methylesterase-like protein [Zea mays]
Seq. No.
                   1665 2.R1040
Contig ID
5'-most EST
                   jC-qmf102220086f12d1
Seq. No.
                   1667_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910052a03a1
Method
                   BLASTX
NCBI GI
                   q4105798
BLAST score
                   1120
                   1.0e-122
E value
Match length
                   270
% identity
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
Seq. No.
                   2419
                   1667 2.R1040
Contig ID
5'-most EST
                   LIB3051-067-Q1-K1-D8
                   2420
Seq. No.
                   1667 3.R1040
Contig ID
                   leu701156628.h1
5'-most EST
Seq. No.
                   2421
Contig ID
                   1667 4.R1040
                   LIB3107-050-Q1-K1-F1
5'-most EST
                   2422
Seq. No.
                   1667 5.R1040
Contig ID
5'-most EST
                   g4300883
Method ·
                   BLASTX
NCBI GI
                   g4105798
BLAST score
                   416
                   8.0e-57
E value
Match length
                   171
% identity
                   56
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
Seq. No.
                   2423
                   1667 6.R1040
Contig ID
5'-most EST
                   jC-gmf102220063d05d1
                   BLASTX
Method
NCBI GI
                   g4105798
BLAST score
                   201
E value
                   1.0e-15
```

5'-most EST

```
% identity
                   83
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   2424
Seq. No.
Contig ID
                   1669 1.R1040
5'-most EST
                   eep7\overline{0}0865012.h1
                   BLASTX
Method
                   g2194132
NCBI GI
BLAST score
                   1103
E value
                   1.0e-120
Match length
                   355
% identity
                   66
                   (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                   2425
Seq. No.
                   1670 1.R1040
Contig ID
5'-most EST
                   LIB3139-116-P1-N1-E11
                   BLASTX
Method
                   g3763918
NCBI GI
                   701 .
BLAST score
E value
                   6.0e-74
Match length
                   194
                   69
% identity
NCBI Description
                   (AC004450) putative isopropylmalate dehydratase
                   [Arabidopsis thaliana]
                   2426
Seq. No.
Contig ID
                   1670 2.R1040
                  ·LIB3049-027-Q1-E1-D3
5'-most EST
Method
                   BLASTX
                   g3763918
NCBI GI
BLAST score
                   214
                   3.0e-17
E value
                   48
Match length
% identity
                   81
NCBI Description
                   (AC004450) putative isopropylmalate dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                   2427
Contig ID
                   1672 1.R1040
5'-most EST
                   wrg700788550.h1
Method
                   BLASTX
NCBI GI
                   q2262116
BLAST score
                   218
E value
                   1.0e-17
Match length
                   120
% identity
                   39
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1673 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1150051.h1
                   2429
Seq. No.
                   1673 2.R1040
Contig ID
```

jC-gmf102220127d06d1

Contig ID

```
2430
Seq. No.
                   1677 1.R1040
Contig ID
                   LIB3170-050-Q1-K1-H7
5'-most EST
                   2431
Seq. No.
                   1677 2.R1040
Contig ID
                   leu701153574.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3201613
BLAST score
                   658
E value
                   1.0e-68
Match length
                   214
% identity
                   57
                   (AC004669) glutathione S-transferase [Arabidopsis thaliana]
NCBI Description
                   2432
Seq. No.
                   1677 3.R1040
Contig ID
5'-most EST
                   uC-gmropic116g02b1
                   2433
Seq. No.
Contig ID
                   1678 1.R1040
                   kmv700743274.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2582822°
                   956
BLAST score
E value
                   1.0e-103
                   290
Match lèngth
                   67
% identity
                   (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                   Protein of 32kDa) [Solanum tuberosum]
                   2434
Seq. No.
                   1679 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220051g10a1
Method
                   BLASTX
NCBI GI
                   q2454182
BLAST score
                   1691
E value
                   0.0e + 00
Match length
                   395
% identity
NCBI Description
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
                   [Arabidopsis thaliana]
                   2435
Seq. No.
Contig ID
                   1685 1.R1040
5'-most EST
                   jsh7\overline{0}1065040.h1
Method
                   BLASTN
NCBI GI
                   g3241927
BLAST score
                   46
                   2.0e-16
E value
Match length
                   114
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   2436
```

1686 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   epx701105991.hl
Method
                   BLASTX
                   g542100
NCBI GI
BLAST score
                   718
                   6.0e-76
E value
Match length
                   165
% identity
                   82
                   H-protein - Flaveria pringlei >gi_2147453_pir__S60195
NCBI Description
                   H-protein precursor (clone HFC1) - Flaveria cronquistii
                   >gi_437993_emb_CAA81073_ (Z25854) H-protein [Flaveria
                   cronquistii] >gi_437999_emb_CAA81074_ (225855) H-protein
                   [Flaveria pringlei] >gi_3688299_emb_CAB16912_ (Z99763)
                   H-protein [Flaveria pringlei]
Seq. No.
                   2437
                   1688 1.R1040
Contig ID
                   jC-qmst02400047c03a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g113116
BLAST score
                   1475
                   1.0e-164
E value
Match length
                   503
% identity
                   55
NCBI Description
                   ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
                   >gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
                   [Rattus norvegicus]
Seq. No.
                   2438
Contig ID
                   1688 2.R1040
5'-most EST
                   LIB3170-040-Q1-K1-F8
                   BLASTX
Method
NCBI GI
                   q4406759
BLAST score
                   430
E value
                   5.0e-42
Match length
                   218
% identity
                   43
                   (AC006836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2439
                   1688 3.R1040
Contig ID
                   uC-gmrominsoy221a03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4107343
BLAST score
                   347
E value
                   1.0e-32
Match length
                   160
                   43
% identity
                   (AJ224922) ATP citrate lyase [Sordaria macrospora]
NCBI Description
Seq. No.
                   2440
                   1688 5.R1040
Contig ID
5'-most EST
                   LIB3051-001-Q1-E1-D1
                   2441
Seq. No.
```

1688 9.R1040

uC-gmrominsoy177g10b1

```
BLASTX
Method
                   g4107343
NCBI GI
BLAST score
                   140
                   8.0e-09
E value
                   61
Match length
                   48
% identity
                   (AJ224922) ATP citrate lyase [Sordaria macrospora]
NCBI Description
                   2442
Seq. No.
                   1688 12.R1040
Contig ID
5'-most EST
                   uxk7\overline{0}0667645.h1
Method
                   BLASTX
                   g1703083
NCBI GI
BLAST score
                   327
E value
                   3.0e-30
Match length
                   103
                   56
% identity
                  ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
NCBI Description
                   >gi_105392_pir__S21173 ATP citrate (pro-S)-lyase - human
                   >gi_28935_emb_CAA45614_ (X64330) ATP-citrate (pro-S-)-lyase
                   [Homo sapiens] >gi_4501865_ref_NP_001087.1_pACLY_ ATP
                   citrate lyase
                   2443
Seq. No.
                   1689 1.R1040
Contig ID
5'-most EST
                  LIB3028-054-Q1-B1-F8
Method
                   BLASTX
                   q1346701
NCBI GI
BLAST score
                   418
                   6.0e-41
E value
Match length
                   164
% identity
                  EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG)
NCBI Description
                   (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 421831 pir S34199 exopolygalacturonase (clone GBGe184)
                   - Arabidopsis thaliana >gi_313682_emb_CAA51032_ (X72291)
                   exopolygalacturonase [Arabidopsis thaliana]
                   >gi_3004440_emb_CAA76127_ (Y16230) polygalacturonase
                   [Arabidopsis thaliana]
Seq. No.
                   2444
                   1690 1.R1040
Contig ID
                   zhf700964274.h1
5'-most EST
Method
                  BLASTX
                   g2827554
NCBI GI
BLAST score
                   199
E value
                   4.0e-15
                   149
Match length
% identity
                   38
                   (AL021635) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   2445
Seq. No.
                   1690 2.R1040
Contig ID
5'-most EST
                  uC-gmropic029d08b1
```

2446

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Seq. No.

```
1690 3.R1040
Contig ID
                   uC-qmflminsoy030a12b1
5'-most EST
Seq. No.
                   1690 4.R1040
Contig ID
                   gsv701050564.hl
5'-most EST
Seq. No.
                   2448
                   1694 1.R1040
Contig ID
                   awf700840660.hl
5'-most EST
                   BLASTX
Method
                   g3738333
NCBI GI
BLAST score
                   601
E value
                   6.0e-62
                   186
Match length
% identity
                   65
                   (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2449
                   1695 1.R1040
Contig ID
                   jC-gmf102220142a10a1
5'-most EST
Method
                   BLASTX
                   g4314378
NCBI GI
BLAST score
                   277
E value
                   2.0e-24
                   101
Match length
                   59
% identity
                   (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1696 1.R1040
Contig ID
                   LIB3028-054-Q1-B1-E6
5'-most EST
Seq. No.
                   2451
                   1699 1.R1040
Contig ID
                   pcp700993505.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3449322
BLAST score
                   42
E value
                   3.0e-14
Match length
                   389
                   82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   2452
                   1700 1.R1040
Contig ID
                   leu701154008.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q1420884
BLAST score
                   186
                   1.0e-100
E value
Match length
                   481
% identity
NCBI Description
                   Phaseolus vulgaris proline-rich 14 kDa protein mRNA,
```

complete cds

```
2453
Seq. No.
                    1700 2.R1040
Contig ID
5'-most EST
                    q4298459
Method
                    BLASTX
NCBI GI
                    g462195
BLAST score
                    476
                    1.0e-47
E value
Match length
                    112
% identity
                    81
                    PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi_100682_pir__ S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                    sativa]
                    2454
Seq. No.
                    1700 3.R1040
Contig ID
5'-most EST
                     fde700877279.hl
Method
                    BLASTX
NCBI GI
                    q3659907
BLAST score
                    429
                     4.0e-42
E value
Match length
                    107
% identity
                    79
                     (AF091857) protein translation factor SUI1 homolog
NCBI Description
                     [Pimpinella brachycarpa]
                     2455
Seq. No.
                    1700 4.R1040
Contig ID
5'-most EST
                     vwf700674561.hl
Method
                    BLASTN
NCBI GI
                     g1420884
BLAST score
                    107
E value
                     5.0e-53
Match length
                     347
% identity
                     88
                     Phaseolus vulgaris proline-rich 14 kDa protein mRNA,
NCBI Description
                     complete cds
                     2456
Seq. No.
                     1700 5.R1040
Contig ID
                     vzy700753816.h1
5'-most EST
                     BLASTX
Method
                     g4140371
NCBI GI
                     402
BLAST score
E value
                     5.0e-39
Match length
                     180
                     53
% identity
                     (U43711) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                     [Morus alba]
Seq. No.
                     2457
                     1700 6.R1040
Contig ID
                     jsh7\overline{0}1063980.h1
5'-most EST
                     BLASTN
Method
```

g1420884

152

NCBI GI BLAST score

```
E value
                     1.0e-79
 Match length
                     379
 % identity
                     87
                     Phaseolus vulgaris proline-rich 14 kDa protein mRNA,
 NCBI Description
                     complete cds
                     2458
 Seq. No.
 Contig ID
                     1700 8.R1040
 5'-most EST
                     q4313847
 Method
                     BLASTX
                     q462195
 NCBI GI
 BLAST score
                     368
 E value
                     6.0e-35
 Match length
                     88
 % identity
                     81
                     PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 NCBI Description
                     >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                     sativa].
 Seq. No.
                     2459
                     1700 12.R1040
 Contig ID
                     hrw7\overline{0}1059318.h1
 5'-most EST
 Method
                     BLASTX
                     q3659907
 NCBI GI
                     167
 BLAST score
                     6.0e-12
 E value
 Match length
                     38
                     79
 % identity
                     (AF091857) protein translation factor SUI1 homolog
 NCBI Description
                     [Pimpinella brachycarpa]
                     2460
 Seq. No.
                     1701 1.R1040
 Contig ID
                     LIB3109-037-Q1-K1-E3
 5'-most EST
                     BLASTX
Method
 NCBI GI
                     q3183088
 BLAST score
                     316
                     1.0e-28
 E value
                     96
 Match length
                     56
 % identity
                     PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
 NCBI Description
                     (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                     cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                     like protein [Vigna unguiculata]
                     2461
 Seq. No.
                     1701 2.R1040
 Contig ID
 5'-most EST
                     LIB3107-040-Q1-K1-B8
 Method
                     BLASTX
 NCBI GI
                     g3183088
 BLAST score
                     309
 E value
                     6.0e-28
 Match length
                     96
 % identity
                     59
 NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
```

```
(LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

2462
1701_3.R1040
LIB3109-044-Q1-K1-G3
BLASTX
```

Method BLASTX
NCBI GI g3183088
BLAST score 208
E value 4.0e-24
Match length 96
% identity 56

Seq. No.

Contig ID

5'-most EST

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi\_629658\_pir\_\_S47084 lipid transfer like protein - cowpea >gi\_499034\_emb\_CAA56113\_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 2463

Contig ID 1701 4.R1040

5'-most EST LIB3\overline{106}-063-Q1-K1-G7

Method BLASTX
NCBI GI g3183088
BLAST score 316
E value 9.0e-29
Match length 96
% identity 56

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

(LTP) >gi\_629658\_pir\_\_S47084 lipid transfer like protein -cowpea >gi\_499034\_emb\_CAA56113\_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 2464

Contig ID 1702\_1.R1040

5'-most EST LIB3072-057-Q1-K1-C5

Method BLASTX
NCBI GI g3168840
BLAST score 292
E value 4.0e-26
Match length 67
% identity 79

NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 2465

Contig ID 1702\_3.R1040

5'-most EST LIB3040-036-Q1-E1-C2

Method BLASTX
NCBI GI g3168840
BLAST score 292
E value 3.0e-26
Match length 67
% identity 79

NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 2466

Contig ID 1703 1.R1040 5'-most EST ncj700982230.h1

```
Method
                   BLASTX
NCBI GI
                   q2244792
BLAST score
                   973
E value
                   1.0e-106
Match length
                   225
                   77
% identity
                   (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2467
Contig ID
                   1704 1.R1040
5'-most EST
                   LIB3030-009-Q1-B1-H12
Method
                   BLASTX
NCBI GI
                   q1946367
BLAST score
                   390
E value
                   6.0e-38
Match length
                   91
% identity
                   80
NCBI Description
                   (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1709 1.R1040
5'-most EST
                   smc700745026.h1
Method
                   BLASTX
NCBI GI
                   q118514
BLAST score
                   2177
E value
                   0.0e + 00
Match length
                   504
% identity
                   84
                   TURGOR-RESPONSIVE PROTEIN 26G >gi 100051_pir__ S11863
NCBI Description
                   aldehyde dehydrogenase homolog - garden pea
                   >gi_20681_emb_CAA38243_ (X54359) 508 aa peptide [Pisum
                   sativum]
Seq. No.
                   2469
Contig ID
                   1709 2.R1040
5'-most EST
                   LIB3170-039-Q1-J1-E12
Method
                   BLASTX
NCBI GI
                   g2244919
BLAST score
                   385
E value
                   8.0e-37
Match length
                   139
% identity
                   (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   2470
Seq. No.
Contig ID
                   1709 3.R1040
5'-most EST
                   jC-gmro02800026f06a1
                   BLASTX
Method
NCBI GI
                   q2980793
BLAST score
                   611
E value
                   3.0e-63
Match length
                   151
% identity
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   2471
Seq. No.
```

1709\_4.R1040

Contig ID

```
5'-most EST
                   LIB3028-020-Q1-B1-D3
Method
                   BLASTX
                   g2129774
NCBI GI
BLAST score
                   1095
E value
                   1.0e-120
Match length
                   292
                   68
% identity
NCBI Description
                   xyloglucan endotransglycosylase-related protein XTR4 -
                   Arabidopsis thaliana (fragment) >gi_1244754 (U43486)
                   xyloglucan endotransglycosylase-related protein
                   [Arabidopsis thaliana]
Seq. No.
                   2472
                   1709 5.R1040
Contig ID
                   jex7\overline{0}0905796.h1
5'-most EST
Method
                   BLASTX
                   q3980400
NCBI GI
BLAST score
                   872
E value
                   1.0e-93
Match length
                   261
% identity
                   66
                   (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                   thaliana]
                   2473
Seq. No.
                   1709 6.R1040
Contig ID
                   jC-gmle01810084f07a1
5'-most EST
Method
                   BLASTN
                   g20680
NCBI GI
BLAST score
                   180
E value
                   2.0e-96
                   344
Match length
                   88
% identity
NCBI Description
                   P.sativum mRNA of cDNA clone 26g
                   2474
Seq. No.
                   1709 7.R1040
Contig ID
5'-most EST
                   dpv701099710.hl
Method
                   BLASTX
NCBI GI
                   q2980793
BLAST score
                   506
E value
                   3.0e-51
Match length
                   161
% identity
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2475
                   1709 8.R1040
Contig ID
                   jC-qmle01810029a07d1
5'-most EST
Method
                   BLASTX
                   g2129774
NCBI GI
BLAST score
                   214
                   8.0e-17
E value
                   75
Match length
                   52
% identity
                   xyloglucan endotransglycosylase-related protein XTR4 -
NCBI Description
```

Arabidopsis thaliana (fragment) >gi\_1244754 (U43486)

NCBI GI

BLAST score

```
Seq. No.
                   2476
                   1709 10.R1040
Contig ID
5'-most EST
                   epx701109280.hl
Method
                   BLASTX
NCBI GI
                   g2129774
BLAST score
                   324
E value
                   4.0e-30
                                                      127.
Match length
                   92
% identity
NCBI Description
                   xyloglucan endotransqlycosylase-related protein XTR4 -
                   Arabidopsis thaliana (fragment) >gi 1244754 (U43486)
                   xyloglucan endotransglycosylase-related protein
                   [Arabidopsis thaliana]
Seq. No.
                   2477
Contig ID
                   1709 11.R1040
5'-most EST
                   rca701000554.hl
Method
                   BLASTX
NCBI GI
                   q2980793
BLAST score
                   322
E value
                   1.0e-29
Match length
                   118
% identity
                   58
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                   2478
Contig ID
                   1709 14.R1040
5'-most EST
                   LIB3106-003-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2980793
BLAST score
                   213
E value
                   4.0e-17
Match length
                   106
% identity
                   44
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2479
Contig ID
                   1710 1.R1040
                   fua701043156.hl
5'-most EST
Method
                   BLASTX
                   g2497539
NCBI GI
BLAST score
                   341
E value
                   2.0e-34
Match length
                   109
% identity
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703
NCBI Description
                   (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.
                   2480
                   1711 1.R1040
Contig ID
                   pmv700891332.h1
5'-most EST
Method
                  BLASTX
```

xyloglucan endotransglycosylase-related protein

[Arabidopsis thaliana]

g3559805

509

Contig ID 5'-most EST

```
E value
                   9.0e-52
Match length
                   142
% identity
                   63
                   (AJ006787) putative phytochelatin synthetase (Arabidopsis
NCBI Description
                   thaliana]
                   2481
Seq. No.
Contig ID
                   1713 1.R1040
5'-most EST
                   crh700854175.hl
Method
                   BLASTX
NCBI GI
                   q3482971
BLAST score
                   533
E value
                   6.0e-54
Match length
                   107
% identity
                   87
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   1714 1.R1040
5'-most EST
                   LIB3039-024-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                   q2780194
BLAST score
                   1713
E value
                   0.0e + 00
Match length
                   388
% identity
                   (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
Seq. No.
                   2483
                   1714 2.R1040
Contig ID
5'-most EST
                   ssr700557603.hl
Seq. No.
                   2484
Contig ID
                   1714 3.R1040
5'-most EST
                   uC-qmflminsoy064c10b1
Method
                  BLASTN
NCBI GI
                   q2780193
BLAST score
                   122
E value
                   4.0e-62
Match length
                   378
% identity
                   88
                  Lupinus albus mRNA for adenine nucleotide translocator
NCBI Description
Seq. No.
                  2485
                  1714 7.R1040
Contig ID
5'-most EST
                   kmv700741313.h1
Method
                  BLASTX
                  g2780194
NCBI GI
BLAST score
                  192
E value
                   1.0e-14
                  129
Match length
% identity
                   (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
Seq. No.
                  2486
                  1715 1.R1040
```

 $ncj7\overline{0}0975104.h1$ 

Contig ID

```
Method
                   BLASTX
NCBI GI
                   g3236259
BLAST score
                   1249
E value
                   1.0e-138
Match length
                   289
% identity
                   80
                   (AC004684) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   2487
Seq. No.
Contig ID
                   1717 1.R1040
5'-most EST
                   LIB3139-086-P1-N1-C11
                   2488
Seq. No.
Contig ID
                   1717 2.R1040
                   iex7\overline{0}0904932.h1
5'-most EST
Method
                   BLASTX
                   g3122139
NCBI GI
BLAST score
                   327
E value
                   3.0e-30
                   137
Match length
% identity
                   48
                   GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)
NCBI Description
                   (GLYCEROKINASE) (GK) (ATP-STIMULATED
                   GLUCOCORTICOID-RECEPTOR TRANSLOCATON PROMOTER) (ASTP)
                   >gi_484372_pir__JN0606 ATP-stimulated
                   glucocorticoid-receptor translocation promoter protein -
                   rat >gi_433211_dbj_BAA03677_ (D16102) ATP-stimulated
                   glucocorticoid-receptor translocaton promoter [Rattus
                   rattus]
                   2489
Seq. No.
                   1717 3.R1040
Contig ID
5'-most EST
                   fde700874271.hl
Method
                   BLASTX
NCBI GI
                   q631174
BLAST score
                   291
E value
                   1.0e-26
Match length
                   78
% identity
                   glycerol kinase - human >gi 515029 emb CAA55364 (X78711)
NCBI Description
                   glycerol kinase [Homo sapiens]
Seq. No.
Contig ID
                   1717 4.R1040
5'-most EST
                   eep7\overline{0}0863731.h1
Seq. No.
Contig ID
                   1719 1.R1040
5'-most EST
                   LIB3170-034-Q1-J1-C12
Seq. No.
                   1719 2.R1040
Contig ID
5'-most EST
                  LIB3074-031-Q1-K1-F3
                   2493
Seq. No.
```

1719 3.R1040

NCBI Description

```
LIB3170-027-Q2-K1-B8
5'-most EST
                  2494
Seq. No.
Contig ID
                  1720 1.R1040
                   rlr700900743.hl
5'-most EST
Method
                  BLASTX
                   g3885343
NCBI GI
BLAST score
                   211
E value
                   2.0e-16
                  80
Match length
% identity
                   47
NCBI Description
                   (AC005623) hypothetical protein [Arabidopsis thaliana]
                  2495
Seq. No.
Contig ID
                  1720 2.R1040
5'-most EST
                  LIB3040-027-Q1-E1-E6
Method
                  BLASTX
                  q3885343
NCBI GI
BLAST score
                  229
E value
                  7.0e-19
Match length
                  119
% identity
                   43
                  (AC005623) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  2496
Seq. No.
Contig ID
                  1723 1.R1040
5'-most EST
                  LIB3109-017-Q1-K1-E9
                  BLASTX
Method
NCBI GI
                  q498902
BLAST score
                  586
E value
                   1.0e-60
Match length
                  135
% identity
NCBI Description
                   (U10044) ribosomal protein L27 homolog [Pisum sativum]
Seq. No.
                  1723 2.R1040
Contig ID
                  LIB3073-026-Q1-K1-D11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q498902
BLAST score
                  570
E value
                  1.0e-58
Match length
                  135
% identity
                  (U10044) ribosomal protein L27 homolog [Pisum sativum]
NCBI Description
Seq. No.
                  2498
                  1723 4.R1040
Contig ID
                  zhf700959381.h1
5'-most EST
                  BLASTX
Method
                  g498902
NCBI GI
BLAST score
                  150
                  4.0e-13
E value
Match length
                  46
% identity
                  89
```

(U10044) ribosomal protein L27 homolog [Pisum sativum]

Seq. No.

2504

```
2499
Seq. No.
                   1724 1.R1040
Contig ID
5'-most EST
                  leu701148868.h1
                  BLASTX
Method
NCBI GI
                   g3334405
BLAST score
                   865
                   6.0e-93
E value
Match length
                  239
% identity
                   76
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
Seq. No.
                   2500
                   1724 2.R1040
Contig ID
5'-most EST
                  jC-gmst02400048e07a1
                  BLASTX
Method
NCBI GI
                  g3334405
BLAST score
                  920
                  2.0e-99
E value
                  232
Match length
% identity
                  81
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
                  2501
Seq. No.
                  1724 4.R1040
Contig ID
5'-most EST
                  jC-gmle01810032d08d1
Method
                  BLASTX
NCBI GI
                  g3334411
BLAST score
                  227
E value
                  1.0e-18
Match length
                  51
% identity
                  84
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi 1263911 emb CAA65581 (X96785) vacuolar H(+)-ATPase
                  [Spinacia oleracea]
Seq. No.
                  2502
                  1724 5.R1040
Contig ID
5'-most EST
                  jC-gmro02800039d11d1
                  2503
Seq. No.
Contig ID
                  1724 7.R1040
5'-most EST
                  asn701142409.h1
                  BLASTX
Method
NCBI GI
                  q3334405
BLAST score
                  471
E value
                  2.0e-47
                  107
Match length
                  89
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E
                  [Gossypium hirsutum]
```

NCBI GI

```
1724 8.R1040
Contig ID
5'-most EST
                   jC-gmro02910004a09d1
                   BLASTN
Method
                   g1263910
NCBI GI
BLAST score
                   72
                   6.0e-32
E value
Match length
                   152
                   87
% identity
                  S.oleracea mRNA for vacuolar H(+)-ATPase
NCBI Description
                   2505
Seq. No.
Contig ID
                   1725 1.R1040
                   LIB3028-054-Q1-B1-A2
5'-most EST
                   2506
Seq. No.
                   1727 1.R1040
Contig ID
                   LIB3030-001-Q1-B1-D8
5'-most EST
                   2507
Seq. No.
Contig ID
                   1728 1.R1040
                   pmv700889401.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4538987
BLAST score
                   538
                   1.0e-76
E value
Match length
                   286
                   58
% identity
                   (AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]
NCBI Description
                   2508
Seq. No.
Contig ID
                   1730 1.R1040
5'-most EST
                   q4300344
Method
                   BLASTX
NCBI GI
                   q1362093
BLAST score
                   666
E value
                   1.0e-69
Match length
                   177
% identity
                  hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                   >gi_924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.
                   1732 1.R1040
Contig ID
                   LIB3107-044-Q1-K1-D12
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2739002
BLAST score
                   1109
                   1.0e-121
E value
                   451
Match length
                   47
% identity
                   (AF022460) CYP83D1p [Glycine max]
NCBI Description
                   2510
Seq. No.
                   1735 1.R1040
Contig ID
5'-most EST
                   LIB3039-034-Q1-E1-F4
Method
                   BLASTN
```

g829118

NCBI GI

```
BLAST score
                   239
                   1.0e-131
E value
Match length
                   550
% identity
                   87
                   P.vulgaris gene for cyclophilin
NCBI Description
                   2511
Seq. No.
Contig ID
                   1735 2.R1040
5'-most EST
                   LIB3139-050-P1-N1-H3
Method
                   BLASTN
NCBI GI
                   g829118
BLAST score
                   303
E value
                   1.0e-169
Match length
                   631
% identity
                   88
NCBI Description
                   P.vulgaris gene for cyclophilin
Seq. No.
                   1735 3.R1040
Contig ID
5'-most EST
                   dpv701101486.hl
Method
                   BLASTX
NCBI GI
                   g1703292
BLAST score
                   357
E value
                   2.0e-33
Match length
                   187
% identity
                   70
                   HIGH AFFINITY AMMONIUM TRANSPORTER >qi 551219 emb CAA53473
NCBI Description
                   (X75879) amt1 [Arabidopsis thaliana]
Seq. No.
                   1735 5.R1040
Contig ID
5'-most EST
                   jC-gmro02910046f04d1
Method
                   BLASTX
NCBI GI
                   g4324714
BLAST score
                   938
E value
                   0.0e + 00
                   516
Match length
% identity
                   67
                   (AF110771) ammonium transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2514
                   1735 7.R1040
Contig ID
                   LIB3029-009-Q1-B1-G10
5'-most EST
Method '
                   BLASTX
NCBI GI
                   g1703292
BLAST score
                   762
E value
                   5.0e-81
Match length
                   225
                   64
% identity
                   HIGH AFFINITY AMMONIUM TRANSPORTER >gi 551219 emb CAA53473_
NCBI Description
                   (X75879) amt1 [Arabidopsis thaliana]
                   2515
Seq. No.
                   1735 8.R1040
Contig ID
5'-most EST
                   jC-gmle01810000c04a1
Method
                   BLASTX
```

g1703292

Seq. No.

2521

```
BLAST score
                   840
E value
                   3.0e-90
Match length
                   230
% identity
                   72
NCBI Description
                   HIGH AFFINITY AMMONIUM TRANSPORTER >gi 551219 emb CAA53473
                   (X75879) amt1 [Arabidopsis thaliana]
Seq. No.
                   1735 9.R1040
Contig ID
5'-most EST
                   jC-gmle01810029c05d1
Method
                   BLASTX
NCBI GI
                   g2392771
BLAST score
                   316
E value
                   4.0e-29
Match length
                   93
% identity
                   70
                   (AC002534) putative kinesin-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   2517
Contig ID
                   1735 14.R1040
5'-most EST
                   LIB3039-029-Q1-E1-B12
Method
                   BLASTN
NCBI GI
                   q551218
BLAST score
                   80
E value
                   5.0e-37
Match length
                   160
% identity
                   88
NCBI Description A.thaliana amt1 mRNA
                   2518
Seq. No.
                   1735 16.R1040
Contig ID
5'-most EST
                   fua701036958.h1
                   BLASTX
Method
NCBI GI
                   g4322319
BLAST score
                   194
                   8.0e-30
E value
Match length
                   89
                   74
% identity
NCBI Description (AF080541) ammonium transporter [Nepenthes alata]
                   2519
Seq. No.
                   1738 1.R1040
Contig ID
5'-most EST
                   seb7\overline{0}0648478.h1
Method
                   BLASTX
NCBI GI
                   g4240207
BLAST score
                   264
E value
                   1.0e-22
                   172
Match length
                   36
% identity
NCBI Description
                  (AB020666) KIAA0859 protein [Homo sapiens]
Seq. No.
                   2520
                   1738 2.R1040
Contig ID
5'-most EST
                   gsv7\overline{0}1056362.h1
```

```
Contig ID
                   1739 1.R1040
                   jex7\overline{0}0903805.h1
5'-most EST
Method
                   BLASTX
                   g1857447
NCBI GI
BLAST score
                   338
                   2.0e-31
E value
Match length
                   162
% identity
                   41
NCBI Description
                   (U82367) UDP-glucose glucosyltransferase [Solanum
                   tuberosum]
Seq. No.
                   2522
                   1739 2.R1040
Contig ID
                   LIB3055-011-Q1-N1-A11
5'-most EST
Method
                   BLASTX
NCBI' GI
                   q1359905
BLAST score
                 . 883
E value
                   6.0e-95
Match length
                   385
% identity
                   46
                   (X85138) homologous to glucosyltransferases [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   2523
                   1741 1.R1040
Contig ID
5'-most EST
                   q4313526
Method
                   BLASTN
NCBI GI
                   q2225882
BLAST score
                   183
E value
                   4.0e-98
Match length
                   483
% identity
NCBI Description
                   Solanum tuberosum mRNA for eukaryotic initiation factor
                   5A4, complete cds
Seq. No.
                   2524
                   1741 2.R1040
Contig ID
5'-most EST
                   epx701106183.hl
Method
                   BLASTN
NCBI GI
                   q309672
BLAST score
                   253 -
E value
                   1.0e-140
Match length
                   669
% identity
                   Pisum sativum chloroplast photosystem I 24 kDa light
NCBI Description
                   harvesting protein (lhca3) mRNA, complete cds
Seq. No.
                   2525
                   1741 3.R1040
Contig ID
                   LIB3051-055-Q1-K1-B5
5'-most EST
Method
                   BLASTN
NCBI GI
                   g309672
BLAST score
                   82
E value
                   7.0e-38
Match length
                   245
% identity
                   86
                   Pisum sativum chloroplast photosystem I 24 kDa light
NCBI Description
```

BLAST score

33

## harvesting protein (lhca3) mRNA, complete cds

```
2526
Seq. No.
                   1741 4.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy019f07b1
                   BLASTN
Method
NCBI GI
                   g309672
BLAST score
                   98
E value
                   1.0e-47
Match length
                   255
                   87
% identity
                   Pisum sativum chloroplast photosystem I 24 kDa light
NCBI Description
                   harvesting protein (lhca3) mRNA, complete cds
                   2527
Seq. No.
                   1741 11.R1040
Contig ID
                   zhf700953944.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g124224
BLAST score
                   528
E value
                   5.0e-54
Match length
                   102
% identity
                   96
                   INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi 100345 pir S21060 translation initiation factor eIF-5A
                   - common tobacco >gi 19887 emb CAA45105 (X63543)
                   eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
                   2528
Seq. No.
                   1742 1.R1040
Contig ID
                   pcp700994206.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4510406
BLAST score
                   1145
E value
                   1.0e-125
Match length
                   362
                   62
% identity
                   (AC006587) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   2529
Seq. No.
                   1742 2.R1040
Contig ID
5'-most EST
                   uC-gmropic099d01b1
Method
                   BLASTX
NCBI GI
                   g4580398
BLAST score
                   253
E value
                   1.0e-21
                   74
Match length
% identity
                   (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                   thaliana]
                   2530
Seq. No.
                   1742 3.R1040
Contig ID
5'-most EST
                   smc7\overline{0}0749001.h1
Method
                  BLASTN
                  q1209533
NCBI GI
```

```
5.0e-09
E value
Match length
                   33
                   2
% identity
                   Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2
NCBI Description
                   chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low
                   molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
                   2531
Seq. No.
                   1746_1.R1040
Contig ID
                   V4L-01-Q1-B1-G3
5'-most EST
                   2532
Seq. No.
                   1749_1.R1040
Contig ID
                   LIB3107-057-Q1-K1-F6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2384956
BLAST score
                   151
E value
                   1.0e-17
Match length
                   183
                   38
% identity
                   (AF022985) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
                   2533
Seq. No.
                   1751_1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy024e07b1
Method
                   BLASTX
NCBI GI
                   g1653622
BLAST score
                   379
E value
                   4.0e-36
Match length
                   167
% identity
                   (D90915) hypothetical protein [Synechocystis sp.]
NCBI Description
                   2534
Seq. No.
Contig ID
                   1752 1.R1040
5'-most EST
                   jC-qmle01810086c07a1
Method
                   BLASTX
NCBI GI
                   q3024908
BLAST score
                   222
E value
                   1.0e-36
Match length
                   193
                   47
% identity
                   HYPOTHETICAL 27.2 KD PROTEIN SLL0875
NCBI Description
                   >gi 1652675 dbj BAA17595 (D90907) hypothetical protein
                   [Synechocystis sp.]
Seq. No.
                   1752 2.R1040
Contig ID
5'-most EST
                   LIB3028-053-Q1-B1-H3
Seq. No.
                   2536
                   1753 1.R1040
Contig ID
                   zhf7\overline{0}0955476.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g131528
```

765

BLAST score

NCBI Description

```
5.0e-81
E value
Match length
                     442
% identity
                     16
NCBI Description
                     POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS
                     NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1) >gi_35768_emb_CAA43973_ (X62006)
                     polypirimidine tract binding protein [Homo sapiens]
                    >gi_35774_emb_CAA43056_ (X60648) polypyrimidine
tract-binding protein (pPTB) [Homo sapiens] >gi_4096061
(AC006273) PTB_HUMAN; PTB; HETEROGENEOUS NUCLEA; HNRNP I;
                     57 KD RNA-BINDING PROTEIN PPTB-1 [Homo sapiens]
                     2537
Seq. No.
                     1753 2.R1040
Contig ID
5'-most EST
                     LIB3107-064-01-K1-G1
                     BLASTX
Method
                     g91152
NCBI GI
BLAST score
                     203
                     1.0e-15
E value
Match length
                     82
                     24
% identity
                    nuclear protein, 25K - mouse
NCBI Description
Seq. No.
                     2538
                     1753 3.R1040
Contig ID
5'-most EST
                     LIB3107-008-Q1-K1-F5
Seq. No.
                     1754 2.R1040
Contig ID
5'-most EST
                     LIB3109-046-Q1-K1-F4
Seq. No.
Contig ID
                     1755 1.R1040
                     LIB3074-033-Q1-K1-A9
5'-most EST
Method
                     BLASTX
NCBI GI
                     q3023436
BLAST score
                     956
E value
                     1.0e-103
                     243
Match length
% identity
                    CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA
NCBI Description
                     3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi 857578
                     (U27116) caffeoyl-CoA 3-O-methyltransferase [Populus
                     tremuloides]
Seq. No.
                     2541
                     1755 2.R1040
Contig ID
                    leu701155444.h1
5'-most EST
Method
                    BLASTX
                     q684942
NCBI GI
BLAST score
                     1044
E value
                     1.0e-114
Match length
                    242
                     79
% identity
```

(U20736) S-adenosyl-L-methionine:trans-caffeoyl-CoA

3-O-methyltransferase [Medicago sativa subsp. sativa]

```
2542
Seq. No.
                    1755 3.R1040
Contig ID
5'-most EST
                    LIB3107-005-01-K1-H11
Method
                    BLASTX
NCBI GI
                    q533121
BLAST score
                    201
E value
                    1.0e-15
Match length
                    44
% identity
                    86
NCBI Description
                    (U13151) S-adenosyl-L-methionine:trans-caffeoyl-CoA
                    3-O-methyltransferase [Zinnia elegans]
Seq. No.
                    2543
                    1755 6.R1040
Contig ID
5'-most EST
                    q5753226
Method
                   BLASTN
NCBI GI
                    g2995933
BLAST score
                    34
E value
                    2.0e-09
Match length
                    58
% identity
                    90
NCBI Description
                   Mesembryanthemum crystallinum caffeoyl-CoA
                   O-methyltransferase mRNA, complete cds
Seq. No.
                   2544
                   1756 1.R1040
Contig ID
                   LIB3139-017-P1-N1-A11
5'-most EST
Method
                   BLASTX
                   g3860249
NCBI GI
BLAST score
                   432
E value
                    4.0e-42
                   194
Match length
                    49
% identity
NCBI Description
                    (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                   1756 3.R1040
Contig ID
5'-most EST
                   dpv701097848.h1
                   2546
Seq. No.
                   1757 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy040g12b1
Method
                   BLASTX
.NCBI GI
                   g1652601
BLAST score
                   264
E value
                   2.0e-22
Match length
                   235
% identity
                   (D90906) hypothetical protein [Synechocystis sp.]
NCBI Description
                   2547
Seq. No.
                   1757 2.R1040
Contig ID
5'-most EST
                   jsh7\overline{0}1068824.h1
Seq. No.
                   2548
Contig ID
                   1759 1.R1040.
```

rca701001537.h1

5'-most EST

```
Seq. No.
                   2549
                   1759 3.R1040
Contig ID
                   LIB3073-007-Q1-K1-B3
5'-most EST
                   2550
Seq. No.
                   1760 1.R1040
Contig ID
                   LIB3049-030-Q1-E1-E4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2983997
BLAST score
                   426
E value
                   1.0e-41
Match length
                   159
                   52
% identity
                   (AE000749) hypothetical protein [Aquifex aeolicus]
NCBI Description
                   2551
Seq. No.
                   1762 1.R1040
Contig ID
                   smc7\overline{0}0748901.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3176664
BLAST score
                   510
                   2.0e-51
E value
Match length
                   153
% identity
                   60
                   (ACO04393) Contains similarity to beta scruin gb Z47541
NCBI Description
                   from Limulus polyphemus. ESTs gb T04493 and gb AA585955
                   come from this gene. [Arabidopsis thaliana]
                   2552
Seq. No.
                   1764 1.R1040
Contig ID
                   txt700733348.hl
5'-most EST
Seq. No.
                   2553
Contig ID
                   1765 1.R1040
                   zhf700960918.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1652856
BLAST score
                   300
                   8.0e-27
E value
Match length
                   162
% identity
                   41
                  (D90909) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   2554
                   1766 1.R1040
Contig ID
5'-most EST
                   LIB3028-053-Q1-B1-E7
Method
                   BLASTX
NCBI GI
                   g4006896
BLAST score
                   162
                   2.0e-15
E value
Match length
                   76
% identity
                   (Z99708) SCARECROW-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
```

1767 1.R1040

Contig ID

```
5'-most EST
                   epx701108250.h1
Method
                   BLASTX
NCBI GI
                   q4158221
BLAST score
                   1715
E value
                   0.0e+00
Match length
                   354
                   86
% identity
NCBI Description
                   (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
Seq. No.
                   1768 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910054c10a1
Method
                   BLASTX
NCBI GI
                   q3763933
BLAST score
                   283
E value
                   5.0e-25
Match length
                   67
                   84
% identity
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
                   2557
Seq. No.
                   1769 1.R1040
Contig ID
5'-most EST
                   ncj700983042.h1
Method
                   BLASTN
NCBI GI
                   q2827081
BLAST score
                   601
E value
                   0.0e + 00
Match length
                   1016
% identity
                   91
NCBI Description
                   Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA,
                   complete cds
Seq. No.
                   2558
                   1769 2.R1040
Contig ID
5'-most EST
                   fua701043420.h1
Method
                   BLASTX
NCBI GI
                   g4115534
BLAST score
                   1466
                   1.0e-176
E value
Match length
                   400
% identity
                   (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                   mungo]
                   2559
Seq. No.
                   1769 3.R1040
Contig ID
5'-most EST
                   g4405695
Method
                   BLASTN
NCBI GI
                   g2827081
BLAST score
                   94
E value
                   4.0e-45
Match length
                   303
% identity
                   88
                   Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA,
NCBI Description
                   complete cds
```

2560

Seq. No.

5'-most EST

```
1770 1.R1040
Contig ID
5'-most EST
                   fua701036901.hl
Method
                   BLASTX
NCBI GI
                   g1209020
BLAST score
                   285
                   7.0e-25
E value
Match length
                   223
% identity
                   (U09584) PL6 protein [Homo sapiens]
NCBI Description
                   2561
Seq. No.
                   1770 2.R1040
Contig ID
                   leu701144340.h1
5'-most EST
                   2562
Seq. No.
                   1771 1.R1040
Contig ID
                   LIB3167-050-P1-K1-C12
5'-most EST
Method
                   BLASTX
                   g1363479
NCBI GI
BLAST score
                   742
E value
                   1.0e-78
Match length
                   205
                   72
% identity
                   photosystem I protein psaL - cucumber
NCBI Description
                  >gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]
Seq. No.
                   2563
                   1771 3.R1040
Contig ID
                   LIB3138-087-P1-N1-A8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1363479
BLAST score
                   254
                   3.0e-25
E value
                   100
Match length
                   63
% identity
NCBI Description
                   photosystem I protein psaL - cucumber
                   >gi 801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]
                   2564
Seq. No.
                   1771 4.R1040
Contig ID
5'-most EST
                   zhf700960439.h1
Method
                   BLASTX
NCBI GI
                   g1363479
BLAST score
                   266
                   3.0e-23
E value
Match length
                   74
% identity
                   76
                   photosystem I protein psaL - cucumber
NCBI Description
                   >gi 801740 dbj BAA09047_ (D50456) PsaL [Cucumis sativus]
Seq. No.
                   2565
Contig ID
                   1771 5.R1040
5'-most EST
                   vzy700752230.hl
                   2566
Seq. No.
                   1773 1.R1040
Contig ID
```

jC-gmro02910029d07a1

NCBI GI

```
BLASTX
Method
NCBI GI
                   g4239845
BLAST score
                   2129
                   0.0e + 00
E value
Match length
                   611
                   68
% identity
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
                   2567
Seq. No.
                   1773_2.R1040
Contig ID
5'-most EST
                   LIB3028-002-Q1-B1-F6
                   BLASTX
Method
                   g4239845
NCBI GI
BLAST score
                   611
E value
                   2.0e-63
Match length
                   144
                   84
% identity
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
                   2568
Seq. No.
Contig ID
                   1773_3.R1040
                                                           . - -
5'-most EST
                   uC-gmropic019g06b1
Method
                   BLASTX
NCBI GI
                   q4239845
                   200
BLAST score
E value
                   2.0e-15
                   58
Match length
                   67
% identity
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
Seq. No.
                   2569
                   1773 4.R1040
Contig ID
                   zhf700964078.h1
5'-most EST
                   BLASTX
Method
                   q4239845
NCBI GI
BLAST score
                   290
E value
                   7.0e-26
Match length
                   80
                   74
% identity
NCBI Description
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
Seq. No.
                   2570
Contig ID
                   1773 5.R1040
5'-most EST
                   LIB3093-058-Q1-K1-E4
                                                       . :
Method
                   BLASTX
NCBI GI
                   g4239845
BLAST score
                   205
E value
                   4.0e-16
Match length
                   59
% identity
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
                   2571
Seq. No.
                   1773 6.R1040
Contig ID
5'-most EST
                   hyd700726505.h1
Method
                   BLASTX
```

g4239845

```
BLAST score
                   254
E value
                   1.0e-21
Match length
                  101
                   49
% identity
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
                  2572
Seq. No.
                  1773 7.R1040
Contig ID
5'-most EST
                  LIB3051-037-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q4239845
                  554
BLAST score
E value
                  5.0e-57
Match length
                  144
% identity
                  75
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
                  2573
Seq. No.
                  1776 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400060h05a1
                  2574
Seq. No.
Contig ID
                  1776_2.R1040
5'-most EST
                  jC-qmst02400051g07a1
Method
                  BLASTX
                  q2967452
NCBI GI
BLAST score
                  1734
E value
                  0.0e+00
Match length
                  701
% identity
NCBI Description
                   (AB010882) hSNF2H [Homo sapiens]
                  >gi_4507075_ref_NP_003592.1_pSMARCA5_ SWI/SNF related,
                  matrix associated, actin dependent regulator of chromatin,
                  subfamily a, member
Seq. No.
                  2575
                  1776 3.R1040
Contig ID
5'-most EST
                  pxt700942642.hl
Method
                  BLASTX
NCBI GI
                  q2735256
BLAST score
                  378
                  3.0e-36
E value
                  74
Match length
% identity
                  (U89683) protein kinase [Lycopersicon esculentum]
NCBI Description
                  2576
Seq. No.
                  1778 1.R1040
Contig ID
5'-most EST
                  LIB3170-046-Q1-J1-D6
                  BLASTX
Method
NCBI GI
                  q543905
                  1023
BLAST score
                  1.0e-111
E value
                  241
Match length
                  77
% identity
NCBI Description
                  BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
```

brassinosteroid-regulated protein [Glycine max]

```
Seq. No.
                   2577
Contig ID
                   1778 2.R1040
5'-most EST
                   uC-qmflminsoy078d11b1
Method
                   BLASTX
NCBI GI
                   g543905
BLAST score
                   715
E value
                   1.0e-75
Match length
                   164
% identity
                   79
                   BRASSINOSTEROID-REGULATED PROTEIN BRU1 >qi 347459 (L22162)
NCBI Description
                   brassinosteroid-regulated protein [Glycine max]
Seq. No.
                   1778 3.R1040
Contig ID
5'-most EST
                   q5666939
Method
                   BLASTX
NCBI GI
                   g2129771
BLAST score
                   351
E value
                   4.0e-33
Match length
                   90
% identity
NCBI Description
                   xyloglucan endotransglycosylase-related protein XTR-6 -
                   Arabidopsis thaliana >gi 1244758 (U43488) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
                   >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1,
4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]
Seq. No.
                   2579
Contig ID
                   1779 1.R1040
                   asn7\overline{0}1141656.h1
5'-most EST
Seq. No.
                   2580
Contig ID
                   1780 1.R1040
5'-most EST
                   vzy700751721.h1
Method
                   BLASTX
NCBI GI
                   q4091080
BLAST score
                   520
E value
                   8.0e-53
Match length
                   141
% identity
                   70
                   (AF045571) nucleic acid binding protein [Oryza sativa]
NCBI Description
                   2581
Seq. No.
                   1784 1.R1040
Contig ID
5'-most EST
                   q4276976
Method
                   BLASTX
                   g544134
NCBI GI
                   355
BLAST score
E value
                   2.0e-33
Match length
                   183
% identity
                   22
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
NCBI Description
                   >gi 99720 pir S22863 hypothetical protein - Arabidopsis
                   thaliana >gi 421844 pir_A46260 RecA functional analog
```

DRT100 - Arabidopsis thaliana (fragment)

```
2582
Seq. No.
                   1785 1.R1040
Contig ID
                   LIB3109-036-Q1-K1-B11
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4206765
BLAST score
                   728
                   9.0e-77
E value
Match length
                   367
% identity
NCBI Description
                   (AF104329) putative type 1 membrane protein [Arabidopsis
                   thaliana]
                   2583
Seq. No.
                   1785 3.R1040
Contiq ID
5'-most EST
                   LIB3051-112-Q1-K1-B8
                   BLASTX
Method
NCBI GI
                   q4206765
BLAST score
                   194
                   5.0e-15
E value
Match length
                   86
                   57
% identity
                   (AF104329) putative type 1 membrane protein [Arabidopsis
NCBI Description
                   thaliana]
                   2584
Seq. No.
Contig ID
                   1787 1.R1040
5'-most EST
                   jC-gmro02910040b01a1
                   BLASTX
Method
NCBI GI
                   g2245012
BLAST score
                   499
E value
                   1.0e-85
Match length
                   257
                   66
% identity
NCBI Description
                   (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   2585
Contig ID
                   1789 1.R1040
5'-most EST
                   pcp700991322.hl
Method
                   BLASTX
NCBI GI
                   q1903034
BLAST score
                   1274
E value
                   1.0e-140
Match length
                   544
                   48
% identity
NCBI Description
                   (X94625) amp-binding protein [Brassica napus]
Seq. No.
                   2586
Contig ID
                   1790 1.R1040
5'-most EST
                   LIB3028-053-Q1-B1-C5
Method
                   BLASTX
NCBI GI
                   q2244956
BLAST score
                   277
E value
                   2.0e-24
Match length
                   112
% identity
                   (Z97340) strong similarity to pectinesterase [Arabidopsis
NCBI Description
```

thaliana]

NCBI GI

```
2587
Seq. No.
Contig ID
                   1791 1.R1040
5'-most EST
                   uC-qmrominsoy258e11b1
Method
                   BLASTX
NCBI GI
                   g2146732
BLAST score
                   2059
E value
                   0.0e + 00
Match length
                   541
% identity
                   74
                   FK506-binding protein - Arabidopsis thaliana >gi 1373396
NCBI Description
                   (U57838) rof1 [Arabidopsis thaliana]
Seq. No.
                   1791 2.R1040
Contig ID
5'-most EST
                   jC-qmst02400069c09a1
Method
                   BLASTN
NCBI GI
                   g1354206
BLAST score
                   76
E value
                   2.0e-34
Match length
                   212
% identity
NCBI Description
                  Arabidopsis thaliana FK506 binding protein FKBP62 (ROF1)
                  mRNA, complete cds
Seq. No.
                   2589
Contig ID
                  1791 4.R1040
5'-most EST
                   asn701140476.hl
Method
                  BLASTX
NCBI GI
                  g3023751
BLAST score
                   483
E value
                   1.0e-48
Match length
                  134
% identity
                  29
NCBI Description
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
                  ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                  >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
Seq. No.
                  2590
                  1791 5.R1040
Contig ID
                  seb700650371.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1354206
BLAST score
                  71
E value
                  2.0e-31
                  247
Match length
                  82
% identity
                  Arabidopsis thaliana FK506 binding protein FKBP62 (ROF1)
NCBI Description
                  mRNA, complete cds
                  2591
Seq. No.
                  1791 7.R1040
Contig ID
5'-most EST
                  LIB3138-007-Q1-N1-D6
Method
                  BLASTX
```

g2146731

```
487
BLAST score
                   3.0e-49
E value
Match length
                   124
% identity
                   29
                   FK506-binding protein - Arabidopsis thaliana >gi 1354207
NCBI Description
                   (U49453) rof1 [Arabidopsis thaliana]
                   2592
Seq. No.
Contig ID
                   1791 8.R1040
                   leu701150772.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3023751
                   207
BLAST score
E value
                  1.0e-16
Match length
                   63
                   47
% identity
                   70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
NCBI Description
                   ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                   >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
Seq. No.
                   2593
                   1793 1.R1040
Contig ID
                   q5510050
5'-most EST
Method
                   BLASTX
                   q3914685
NCBI GI
BLAST score
                   614
                   1.0e-63
E value
Match length
                   143
% identity
                   83
                   60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
NCBI Description
                   protein L17 [Zea mays]
Seq. No.
                   2594
Contig ID
                   1793 2.R1040
5'-most EST
                   LIB3106-075-Q1-K2-B7
Method
                   BLASTX
NCBI GI
                   q3176668
BLAST score
                   743
E value
                   1.0e-78
Match length
                   174
% identity
                   82
                   (ACO04393) Similar to ribosomal protein L17 gb_X62724 from
NCBI Description
                   Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and
                   gb Z33937 come from this gene. [Arabidopsis thaliana]
                   2595
Seq. No.
                   1793 3.R1040
Contig ID
5'-most EST
                   LIB3170-030-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   q131167
BLAST score
                   321
                   2.0e-29
E value
Match length
                   131
% identity
                   58
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
```

```
>gi_100292_pir__S18348 photosystem I chain II precursor -
                  wood tobacco >gi_19748_emb_CAA42623_ (X60008) PSI-D2
                   [Nicotiana sylvestris]
                   2596
Seq. No.
                  1793_4.R1040
Contig ID
                  LIB3028-004-Q1-B1-D11
5'-most EST
Method
                   BLASTN
NCBI GI
                  q19747
BLAST score
                   131
E value
                   5.0e-67
Match length
                   441
% identity
                  N.sylvestris psaDa gene for PSI-D2
NCBI Description
                   2597
Seq. No.
                  1793 5.R1040
Contig ID
                  LIB3170-002-Q1-K1-A4
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1806284
BLAST score
                   193
E value
                   1.0e-104
Match length
                   313
                   90
% identity
NCBI Description
                  S.rostrata mRNA coding for histone H4 homologue
Seq. No.
                   2598
                  1793 6.R1040
Contiq ID
5'-most EST
                  LIB3093-038-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                   q487046
BLAST score
                  770
E value
                   5.0e-82
Match length
                   208
% identity
NCBI Description
                  photosystem I chain II precursor - wood tobacco
                  >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
Seq. No.
                  2599
                  1793 7.R1040
Contig ID
5'-most EST
                  LIB3051-095-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g730526
BLAST score
                  502
E value
                   6.0e-90
                  192
Match length
                  84
% identity
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                  >qi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein
                   [Arabidopsis thaliana]
                  2600
Seq. No.
                  1793 8.R1040
Contig ID
                  LIB3170-013-Q1-K1-E11
5'-most EST
```

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

```
BLASTN
Method
NCBI GI
                   a2351070
BLAST score
                   115
E value
                   1.0e-57
                   303
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTH12, complete sequence [Arabidopsis thaliana]
Seq. No.
Contig ID
                   1793 9.R1040 '
5'-most EST
                  LIB3092-006-Q1-K1-H1
                  BLASTX
Method
NCBI GI
                   g131166
BLAST score
                   574
E value
                   4.0e-59
Match length
                   172
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_82100_pir_
                  photosystem I chain II precursor - tomato >gi_170492
                   (M21344) photosystem I subunit II protein precursor
                   [Lycopersicon esculentum] >gi_226544_prf__1601516A
                  photosystem I reaction center II [Lycopersicon esculentum]
Seq. No.
                  2602
Contig ID
                  1793 10.R1040
5'-most EST
                  LIB3049-007-Q1-E1-B3
Method
                  BLASTN
NCBI GI
                  g166739
BLAST score
                  97
E value
                   6.0e-47
Match length
                  209
% identity
                  87
NCBI Description
                  A.thaliana histone H4 gene, complete cds
Seq. No.
                  2603
                  1793 11.R1040
Contig ID
5'-most EST
                  LIB3167-078-P1-K2-H6
Method
                  BLASTX
NCBI GI
                  q487046
BLAST score
                  433
                  1.0e-46
E value
Match length
                  117
                  85
% identity
NCBI Description
                  photosystem I chain II precursor - wood tobacco
                  >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
                  2604
Seq. No.
                  1793 12.R1040
Contig ID
                  LIB3040-042-Q1-E1-G10
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1806284
BLAST score
                  185
E value
                  2.0e-99
```

313

Match length

```
% identity
NCBI Description S.rostrata mRNA coding for histone H4 homologue
                  2605
Seq. No.
                  1793 13.R1040
Contig ID
5'-most EST
                  LIB3106-049-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  q3914685
                  278
BLAST score
                  2.0e-24
E value
                  73
Match length
                  73
% identity
                  60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
NCBI Description
                  protein L17 [Zea mays]
                  2606
Seq. No.
                  1793 14.R1040
Contig ID
5'-most EST
                  pmv700892448.h1
                  2607
Seq. No.
                  1793 15.R1040
Contig ID
5'-most EST
                  LIB3170-021-Q1-K1-C1
                  BLASTN
Method
NCBI GI
                  g2351070
BLAST score
                  125
                  1.0e-63
E value
                  305
Match length
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTH12, complete sequence [Arabidopsis thaliana]
                  2608
Seq. No.
                  1793 16.R1040
Contig ID
5'-most EST ·
                  LIB3106-097-Q1-K1-G9
Method
                  BLASTN
NCBI GI
                  q1806284
BLAST score
                  144
E value
                  3.0e-75
Match length
                  312
% identity
                  87
NCBI Description S.rostrata mRNA coding for histone H4 homologue
                  2609
Seq. No.
Contig ID
                  1793 17.R1040
5'-most EST
                  LIB3049-032-Q1-E1-D8
Method
                  BLASTN
NCBI GI
                  g1806284
                  51
BLAST score
E value
                  8.0e-20
Match length
                  95
% identity
                  88
                  S.rostrata mRNA coding for histone H4 homologue
NCBI Description
```

1793 18.R1040 Contig ID

5'-most EST LIB3170-026-Q1-K1-B9

Method BLASTN

NCBI Description

```
NCBI GI
                   g166739
BLAST score
                   93
                   9.0e-45
E value
                   209
Match length
                   86
% identity
NCBI Description
                  A.thaliana histone H4 gene, complete cds
Seq. No.
                   2611
                  1793 19.R1040
Contig ID
                  jsh701068445.h1
5'-most EST
                  2612
Seq. No.
                  1793 22.R1040
Contig ID
5'-most EST
                  LIB3170-020-Q1-K1-H3
                  BLASTN
Method
NCBI GI
                  g1806284
BLAST score
                  83
E value
                   8.0e-39
Match length
                  203
% identity
                  85
NCBI Description S.rostrata mRNA coding for histone H4 homologue
Seq. No.
                  2613
                  1793 27.R1040
Contig ID
5'-most EST
                  gsv701051886.hl
                  BLASTN
Method
                  g1806284
NCBI GI
BLAST score
                  138
E value
                   9.0e-72
                  234
Match length
                  90
% identity
NCBI Description S.rostrata mRNA coding for histone H4 homologue
Seq. No.
                 -2614
Contig ID
                  1793 30.R1040
5'-most EST
                  vwf700676687.h1
                  BLASTX
Method
NCBI GI
                  g730450
BLAST score
                  249
                  1.0e-21
E value
Match length
                  65
                  75
% identity
                  60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                  >gi_480649_pir__S37134_cold-induced protein BnC24B - rape
                  >gi 398922 emb CAA80343 (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                  2615
Seq. No.
Contig ID
                  1793 33.R1040
5'-most EST
                  uC-gmropic004h06b1
Method
                  BLASTX
NCBI GI
                  g3935177
                  155
BLAST score
E value
                  8.0e-11
Match length
                  32
% identity
```

(AC004557) F17L21.20 [Arabidopsis thaliana]

NCBI GI

BLAST score

g20620

134

```
2616
Seq. No.
                    1794 1.R1040
Contig ID
                    pmv700888607.h1
5'-most EST
Method
                    BLASTN
                    g344003
NCBI GI
BLAST score
                    319
                    1.0e-179
E value
Match length
                    944
% identity
NCBI Description
                    Pisum sativum mRNA for precursor for 33-kDa protein of
                   photosystem II, complete cds
Seq. No.
                    2617
Contig ID
                    1794 2.R1040
                    q4396866
5'-most EST
Method
                    BLASTX
NCBI GI
                    g131384
BLAST score
                    888
E value
                    9.0e-96
Match length
                    206
% identity
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                    SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132
                   photosystem II oxygen-evolving complex protein 1 precursor
                    - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA
                   -81 to 248) [Pisum satīvum] >gi_344004_dbj_BAA02554_
                    (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving
                    complex 33kD protein [Arachis hypogaea]
Seq. No.
                    2618
Contig ID
                    1794 3.R1040
5'-most EST
                    fde7\overline{0}0876743.h1
Method
                   BLASTX
NCBI GI
                    q131384
BLAST score
                    682
E value
                    8.0e-72
Match length
                    165
                    84
% identity
NCBI Description
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132
                   photosystem II oxygen-evolving complex protein 1 precursor
                   - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_
                    (D13297) precursor for 33-kDa protein of photosystem II
                    [Pisum sativum] >gi_226937_prf__1611461A O2 evolving
                   complex 33kD protein [Arachis hypogaea]
Seq. No.
                   2619
Contig ID
                   1794 4.R1040
5'-most EST
                   LIB3170-029-Q1-J1-A9
Method
                   BLASTN
```

```
E value
                   4.0e-69
Match length
                   286
                   87
% identity
                   Pea mRNA for the 33kDa polypeptide of the water-oxidizing
NCBI Description
                   complex of photosystem II
                   2620
Seq. No.
Contig ID
                   1794 5.R1040
5'-most EST
                   jC-qmle01810047h09d1
Method
                   BLASTN
NCBI GI
                   q344003
BLAST score
                   119
E value
                   3.0e-60
Match length
                   271
% identity
                   86
                   Pisum sativum mRNA for precursor for 33-kDa protein of
NCBI Description
                   photosystem II, complete cds
Seq. No.
                   2621
Contig ID
                   1795 1.R1040
5'-most EST
                   a117\overline{0}0863141.h1
                   BLASTX
Method
NCBI GI
                   q3608152
BLAST score
                   202
E value
                   5.0e-16
Match length
                   78
% identity
                   (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   1798 1.R1040
Contig ID
5'-most EST
                   g4299089
Method
                   BLASTX
NCBI GI
                   g3152585
BLAST score
                   323
E value
                   1.0e-29
                   140
Match length
% identity
                   (AC002986) Contains similarity to auxin-induced protein
NCBI Description
                   TM018A10.6 from A. thaliana BAC gb AF013294. [Arabidopsis
                   thaliana]
                   2623
Seq. No.
                   1798 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy216f03b1
Method
                   BLASTX
NCBI GI
                   q3152585
                   278
BLAST score
                   3.0e-24
E value
Match length
                   141
                   48
% identity
                   (AC002986) Contains similarity to auxin-induced protein
NCBI Description
                   TM018A10.6 from A. thaliana BAC gb AF013294. [Arabidopsis
                   thaliana]
Seq. No.
                   2624
```

1799 1.R1040

Contig ID

```
zzp700835068.h1
 5'-most EST
Method
                    BLASTX
NCBI GI
                    q4510376
BLAST score
                    1206
E value
                    1.0e-133
Match length
                    414
 % identity
                    57
                    (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    2625
Contig ID
                    1799 2.R1040
                    uC-gmropic050d06b1
 5'-most EST
Method
                    BLASTX
NCBI GI
                    q4510376
BLAST score
                    414
                    2.0e-40
E value
Match length
                    106
                    70
 % identity
                    (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    2626
                    1800 1.R1040
Contig ID
5'-most EST
                    leu7\overline{0}1147459.h1
                    BLASTX
Method
                    g2414622
NCBI GI
BLAST score
                    585
E value
                    2.0e-60
Match length
                    169
 % identity
                    66
                    (Z99259) conserved protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                    2627
                    1800 2.R1040
Contig ID
 5'-most EST
                    ncj7\overline{0}0987772.h1
Seq. No.
                    2628
Contig ID
                    1802 1.R1040
 5'-most EST
                    zpv700761893.h1
Method
                    BLASTX
                    g3201627
NCBI GI
BLAST score
                    177
E value
                    1.0e-12
Match length
                    33
 % identity
                    (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    2629
 Contiq ID
                    1804 1.R1040
 5'-most EST
                    LIB3051-112-Q1-K1-A7
Method
                    BLASTX
NCBI GI
                    q70644
BLAST score
                    1895
E value
                    0.0e + 00
Match length
                    380
 % identity
                    53
                    ubiquitin precursor - common sunflower (fragment)
NCBI Description
```

```
Seq. No.
                   2630
                   1804 2.R1040
Contig ID
                   LIB3028-015-Q1-B1-E9
5'-most EST
                   BLASTN
Method
                   g516853
NCBI GI
BLAST score
                   726
                   0.0e + 00
E value
Match length
                   776
                   75
% identity
                   Soybean SUBI-2 gene for ubiquitin, complete cds
NCBI Description
Seq. No.
                   2631
                   1804 3.R1040
Contig ID
                   LIB3093-022-Q1-K1-G1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q516853
BLAST score
                   888
E value
                   0.0e + 00
Match length
                   1070
                   49
% identity
                   Soybean SUBI-2 gene for ubiquitin, complete cds
NCBI Description
Seq. No.
                   2632
                   1804 4.R1040
Contig ID
                   LIB3050-016-Q1-E1-D6
5'-most EST
Method
                   BLASTN
NCBI GI
                   q1684856
BLAST score
                   199
E value
                   1.0e-108
Match length
                   299
                   38
% identity
                  Phaseolus vulgaris polyubiquitin mRNA, partial cds
NCBI Description
Seq. No.
                   2633
                   1804 5.R1040
Contig ID
                   pxt700945034.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g516853
BLAST score
                   215
                   1.0e-117
E value
                   383
Match length
                   42
% identity
NCBI Description
                  Soybean SUBI-2 gene for ubiquitin, complete cds
                   2634
Seq. No.
                   1804 7.R1040
Contig ID
                   LIB3051-053-Q1-K2-H9
5'-most EST
                   BLASTN
Method
NCBI GI
                   g516853
BLAST score
                   180
                   9.0e-97
E value
                   269
Match length
                   30
% identity
                  Soybean SUBI-2 gene for ubiquitin, complete cds
NCBI Description
                   2635
Seq. No.
```

1805 1.R1040

Contig ID

```
5'-most EST
                   uC-gmrominsoy048a03b1
                   BLASTX
Method
                   g3123295
NCBI GI
                   339
BLAST score
                   2.0e-31
E value
Match length
                   136
                   52
% identity
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169
NCBI Description
                   (AF026473) calmodulin-related protein [Arabidopsis
                   thaliana]
                   2636
Seq. No.
                   1805 2.R1040
Contig ID
5'-most EST
                   LIB3028-042-Q1-B1-H10
Method
                   BLASTX
NCBI GI
                   g3123295
BLAST score
                   198
E value
                   3.0e-15
Match length
                   64
% identity
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169
NCBI Description
                   (AF026473) calmodulin-related protein [Arabidopsis
                   thaliana]
                   2637
Seq. No.
Contig ID
                   1810 1.R1040
5'-most EST
                   zhf700955314.h1
                  2638
Seq. No.
                   1811 1.R1040
Contig ID
5'-most EST
                  g4291898
Seq. No.
                  2639
                   1811 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910023d08d1
                  2640
Seq. No.
Contig ID
                  1812 1.R1040
5'-most EST
                  LIB3028-053-Q1-B1-A5
                  2641
Seq. No.
                   1814 1.R1040
Contig ID
5'-most EST
                   zhf700955022.h1
                  2642
Seq. No.
                  1815 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy275h01b1
Seq. No.
                  2643
                  1815 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy157d05b1
                  2644
Seq. No.
Contig ID
                  1815 3.R1040
5'-most EST
                  LIB3092-006-Q1-K1-C12
```

2645

Seq. No.

```
Contig ID
                   1815 6.R1040
5'-most EST
                   wrg700788505.hl
                   2646
Seq. No.
                   1817 1.R1040
Contig ID
                   LIB3028-052-Q1-B2-D9
5'-most EST
                   2647
Seq. No.
                   1818 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810014a07d1
                   2648
Seq. No.
                   1819 1.R1040
Contig ID
5'-most EST
                   dpv701097046.h1
Method
                   BLASTX
                   q3540183
NCBI GI
BLAST score
                   1022
                   1.0e-111
E value
                   304
Match length
% identity
                   (AC004122) Highly Similar to branched-chain amino acid
NCBI Description
                   aminotrańsferase [Arabidopsis thaliana]
                   2649
Seq. No.
                   1819 2.R1040
Contig ID
5'-most EST
                   uC-gmropic061b03b1
Method
                   BLASTX
NCBI GI
                   g3540185
BLAST score
                   186
                   8.0e-14
E value
                   88
Match length
                   47
% identity
                   (AC004122) Highly Similar to branched-chain amino acid
NCBI Description
                   aminotransferase [Arabidopsis thaliana]
                   2650
Seq. No.
Contig ID
                   1819 3.R1040
5'-most EST
                   xpa700794532.hl
                   BLASTX
Method
                   q2827709
NCBI GI
BLAST score
                   169
                   6.0e-12
E value
Match length
                   45
% identity
                   71
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   2651
Seq. No.
Contig ID
                   1820 1.R1040
5'-most EST
                   dkc7\overline{0}0968063.h1
                  2652
Seq. No.
                   1821 1.R1040
Contig ID
5'-most EST
                  LIB3028-052-Q1-B2-E9
                  2653
Seq. No.
                   1822 1.R1040
Contig ID
                  LIB3170-002-Q1-K1-E11
5'-most EST
```

```
Method
                   BLASTX
NCBI GI
                   g3334663
BLAST score
                   262
                   8.0e-23
E value
Match length
                   114
                   48
% identity
                  (Y10491) putative cytochrome P450 [Glycine max]
NCBI Description
                   2654
Seq. No.
                   1822 2.R1040
Contig ID
                   LIB3028-052-Q1-B1-F10
5'-most EST
Method
                   BLASTX
                   g3334663
NCBI GI
BLAST score
                   186
E value
                   5.0e-14
Match length
                   112
% identity
                   39
                  (Y10491) putative cytochrome P450 [Glycine max]
NCBI Description
Seq. No.
                   2655
                   1823 1.R1040
Contiq ID
                   LIB3170-046-Q1-J1-F3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2239262
BLAST score
                   1028
                   1.0e-111
E value
                   455
Match length
% identity
                  (Y13285) pectin methylesterase-like protein [Zea mays]
NCBI Description
                   2656
Seq. No.
                   1823 2.R1040
Contig ID
5'-most EST
                   LIB3030-002-Q1-B1-F7
                   2657
Seq. No.
                   1825 1.R1040
Contig ID
                   LIB3028-052-Q1-B2-F5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g418754
BLAST score
                   445
                   5.0e-44
E value
                   195
Match length
                   55
% identity
                  catechol oxidase (EC 1.10.3.1) precursor - fava bean
NCBI Description
                   2658
Seq. No.
                   1827 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy118b04b1
Method
                   BLASTX
                   g833835
NCBI GI
BLAST score
                   1372
                   1.0e-152
E value
                   480
Match length
% identity
                   (U26025) amygdalin hydrolase isoform AH I precursor [Prunus
NCBI Description
```

serotina]

```
2659
Seq. No.
                  1827 2.R1040
Contig ID
                  jC-gmle01810014g06d1
5'-most EST
                  BLASTX
Method
                  g2213626
NCBI GI
BLAST score
                  615
E value
                  1.0e-63
                  253
Match length
                  52
% identity
NCBI Description
                   (AC000103) F21J9.18 [Arabidopsis thaliana]
                  2660
Seq. No.
Contig ID
                  1827 3.R1040
                  smc7\overline{0}0749834.h1
5'-most EST
Seq. No.
                  2661
                  1828 1.R1040
Contig ID
                  LIB3050-018-Q1-E1-D3
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3334113
BLAST score
                  388
                  3.0e-37
E value
                  87
Match length
                  83
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
NCBI Description
                  acyl-CoA-binding protein [Gossypium hirsutum]
                  2662
Seq. No.
                  1829 1.R1040
Contig ID
5'-most EST
                  asn701133385.hl
                  BLASTN
Method
NCBI GI
                  g1162979
BLAST score
                  264
                  1.0e-146
E value
Match length
                  692
% identity
                  Spinacia oleracea nuclear-encoded chloroplast
NCBI Description
                  ribulose-5-phosphate 3-epimerase mRNA, complete cds
                  2663
Seq. No.
                  1829 2.R1040
Contig ID
5'-most EST
                  jC-gmst02400014f01d1
Method
                  BLASTN
                  g3264789
NCBI GI
BLAST score
                  81
E value
                  2.0e-37
Match length
                  161
% identity
                  Expression vector pFL505 for Spinacia oleracea chloroplast
NCBI Description
                  ribulose-phosphate 3-epimerase transit form
                  2664
Seq. No.
Contig ID
                  1830 1.R1040
5'-most EST
                  LIB3170-040-Q1-K1-G3
Method
                  BLASTX
                  g2407800
NCBI GI
```

584

BLAST score

```
E value
                   3.0e-60
Match length
                   134
                   87
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                   2665
Seq. No.
Contig ID
                   1830 2.R1040
                   leu7\overline{0}1156037.h1
5'-most EST
                   BLASTX
Method
                   g2407800
NCBI GI
BLAST score
                   179
                   3.0e-13
E value
Match length
                   62
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2666
Contig ID
                   1831 1.R1040
5'-most EST
                   LIB3049-002-Q1-E1-H1
                   BLASTN
Method
NCBI GI
                   q2598656
BLAST score
                   304
                   1.0e-170
E value
Match length
                   551
                   89
% identity
                   Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
NCBI Description
Seq. No.
Contig ID
                   1833 1.R1040
5'-most EST
                   LIB3106-006-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   q2262170
BLAST score
                   1117
E value
                   1.0e-122
Match length
                   350
% identity
                   (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                   thaliana]
                   2668
Seq. No.
Contig ID
                   1833 2.R1040
                   ssr700558633.hl
5'-most EST
Method
                   BLASTX.
                   g2262170
NCBI GI
BLAST score
                   423
                   2.0e-41
E value
Match length
                   183
% identity
                   (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   2669
Contig ID
                   1833 8.R1040
                   gsv701045546.hl
5'-most EST
Seq. No.
                   2670
```

1834 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   uC-gmflminsoy061e09b1
                   BLASTX
Method
NCBI GI
                   q1171161
BLAST score
                   1643
E value
                   0.0e+00
                   439
Match length
                   70
% identity
NCBI Description
                   (U41472) pectate lyase homolog [Medicago sativa]
                   2671
Seq. No.
                   1834 2.R1040
Contig ID
5'-most EST
                   zhf700953796.h1
Method
                   BLASTX
NCBI GI
                   q1171161
BLAST score
                   286
E value
                   2.0e-25
                   102
Match length
                   59
% identity
                  (U41472) pectate lyase homolog [Medicago sativa]
NCBI Description
                   2672
Seq. No.
                   1834 3.R1040
Contig ID
                   LIB3\overline{0}28-052-Q1-B2-B3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1171161
BLAST score
                   383
E value
                   9.0e-37
Match length
                   103
                   68
% identity
                   (U41472) pectate lyase homolog [Medicago sativa]
NCBI Description
                   2673
Seq. No.
                   1835_1.R1040
Contig ID
5'-most EST
                   LIB3170-048-Q1-J1-D7
                   BLASTX
Method
NCBI GI
                   g4204260
BLAST score
                   172
                   8.Oe-12
E value
Match length
                   62
                   50
% identity
                   (AC005223) 25568 [Arabidopsis thaliana]
NCBI Description
                   2674
Seq. No.
                   1835 2.R1040
Contig ID
5'-most EST
                   uC-gmropic045h01b1
Method
                   BLASTX
NCBI GI
                   g4204260
BLAST score
                   185
E value
                   1.0e-13
Match length
                   64
% identity
                   53
                   (AC005223) 25568 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2675
                   1835 4.R1040
Contig ID
```

fua701041703.hl

```
2676
Seq. No.
                   1836 1.R1040
Contig ID
                   zhf700954832.h1
5'-most EST
Method
                   BLASTX
                   g1495251
NCBI GI
BLAST score
                   2468
                   0.0e+00
E value
Match length
                   694
                   66
% identity
NCBI Description
                   (270314) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                   2677
                   1836 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910048e12d1
                   2678
Seq. No.
                   1837 1.R1040
Contig ID
5'-most EST
                   LIB3028-052-Q1-B2-B7
                   2679
Seq. No.
                   1839 1.R1040
Contig ID
                   seb7\overline{0}0650924.h1
5'-most EST
Method
                   BLASTX
                   g2950472 ·
NCBI GI
BLAST score
                   185
                   1.0e-13
E value
Match length
                   85
% identity
                   45
                   (AL022070) putative autophagocytosis protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   2680
Seq. No.
                   1842 1.R1040
Contig ID
                   wvk700682469.h2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1237081
BLAST score
                   336
E value
                   0.0e + 00
Match length
                   548
                   90
% identity
NCBI Description P.sativum mRNA for ADP-glucose pyrophosphorylase (agpS2)
                   2681
Seq. No.
                   1842 2.R1040
Contig ID
                   kmv700743465.h1
5'-most EST
Method
                   BLASTX
                   g1237080
NCBI GI
BLAST score
                   165
E value
                   1.0e-11
Match length
                   68
                   62
% identity
                   (X96764) ADP-glucose pyrophosphorylase [Pisum sativum]
NCBI Description
                   2682
Seq. No.
                   1843 1.R1040
Contig ID
5'-most EST
                   asn7\overline{0}1138640.h1
```

**BLASTX** 

Method

Seq. No.

```
NCBI GI
                   q1885310
BLAST score
                   298
E value
                   6.0e-27
Match length
                   99
                   59
% identity
NCBI Description
                   (X91659) Endoxyloglucan transferase (EXT) [Hordeum vulgare]
Seq. No.
Contig ID
                   1846 1.R1040
5'-most EST
                   jC-gmst02400073h02d1
Seq. No.
Contig ID
                   1846 2.R1040
5'-most EST
                   LIB3028-052-Q1-B2-D10
                   2685
Seq. No.
Contig ID
                   1847 1.R1040
5'-most EST
                   jC-gmle01810012d07a1
Method
                   BLASTX
NCBI GI
                   q2335108
BLAST score
                   1084
                   1.0e-118 🥌
E value
Match length
                   307
% identity
                   73
NCBI Description
                   (AC002339) putative isulinase [Arabidopsis thaliana]
Seq. No.
                   2686
Contig ID
                   1848 1.R1040
5'-most EST
                   LIB3107-082-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   q400515
BLAST score
                   225
E value
                   3.0e-18
Match length
                   90
% identity
                   51
NCBI Description
                   NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8)
                   (CI-B8) >gi_346540_pir__S28249 NADH dehydrogenase
                   (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine
                   >gi_246_emb_CAA44904 (X63219) NADH dehydrogenase [Bos
                   taurus]
Seq. No.
                   2687
                   1848 2.R1040
Contig ID
5'-most EST
                   LIB3039-040-Q1-E1-C7
Method
                   BLASTX
NCBI GI
                   g400515
BLAST score
                   226
E value
                   2.0e-18
                   89
Match length
% identity
NCBI Description
                   NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8)
                   (CI-B8) >gi_346540_pir_S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine
                   >gi 246 emb CAA44904 (X63219) NADH dehydrogenase [Bos
                   taurus]
```

Method

```
Contig ID
                   1850 1.R1040
                   leu701144978.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4510373
BLAST score
                   334
E value
                   5.0e-31
Match length
                   133
% identity
                   45
NCBI Description
                   (AC007017) putative harpin-induced protein [Arabidopsis
                   thaliana]
                   2689
Seq. No.
                   1851 1.R1040
Contig ID
                   leu701155612.hl
5'-most EST
Seq. No.
                   2690
Contig ID
                   1855 1.R1040
                   LIB3049-005-Q1-E1-D1
5'-most EST
                   2691
Seq. No.
Contig ID
                   1855 2.R1040
                   kmv700741440.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2894603
BLAST score
                   352
E value
                   1.0e-32
Match length
                   129
% identity
                   48
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2692
                   1855 3.R1040
Contig ID
5'-most EST
                   LIB3074-004-Q1-K1-C9
                   2693
Seq. No.
Contig ID
                   1855 6.R1040
5'-most EST
                   LIB3092-037-Q1-K1-D2
                   2694
Seq. No.
                   1855 7.R1040
Contig ID
5'-most EST
                   LIB3106-010-Q1-K1-C8
                   2695
Seq. No.
                   1855 8.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy010e06b1
Method
                   BLASTX
NCBI GI
                   g2894603
BLAST score
                   233
                   4.0e-19
E value
Match length
                   77
                   28
% identity
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                   2696
Seq. No.
Contig ID
                   1855 11.R1040
5'-most EST
                   smc700744941.h1
```

BLASTX

NCBI GI

```
g2894603
NCBI GI
BLAST score
                   189
E value
                   1.0e-14
Match length
                   56
% identity
                   22
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                   2697
Seq. No.
                   1856_1.R1040
Contig ID
5'-most EST
                   LIB3040-059-Q1-E1-H6
Method
                   BLASTX
                   g3786005
NCBI GI
BLAST score
                   845
E value
                   2.0e-90
Match length
                   363
% identity
                   40
                   (AC005499) putative phosphoethanolamine
NCBI Description
                   cytidylyltransferase [Arabidopsis thaliana]
                   2698
Seq. No.
Contig ID
                   1856_2.R1040
5 amost EST
                   jex7\overline{0}0909340.h1
Method
                   BLASTX
NCBI GI
                   g3786005
BLAST score
                   584
E value
                   4.0e-60
Match length
                   191
% identity
NCBI Description
                   (AC005499) putative phosphoethanolamine
                   cytidylyltransferase [Arabidopsis thaliana]
Seq. No.
                   1857 1.R1040
Contig ID
                  pcp700991629.hl
5'-most EST
Seq. No.
                   2700
Contig. ID
                   1859 1.R1040
5'-most EST
                  LIB3106-077-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1706082
BLAST score
                   379
                   3.0e-36
E value
Match length
                  131
% identity
NCBI Description
                  SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
                  >gi_629787_pir__S44191 serine-type carboxypeptidase (EC
                  3.4.16.1) II-3 - barley >gi_619350_bbs_153536
                  CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
                  cv. Alexis, aleurone, Peptide, 516 aa]
                  >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
                   [Hordeum vulgare]
Seq. No.
                  2701
Contig ID
                  1860 1.R1040
5'-most EST
                  LIB3087-009-Q1-K1-G2
Method
                  BLASTX
```

q4539454

Match length

```
276
BLAST score
E value
                   6.0e-24
                   208
Match length
                   37
% identity
NCBI Description
                   (AL049500) contains EST gb:AA728416 [Arabidopsis thaliana]
                   2702
Seq. No.
                   1860 2.R1040
Contig ID
                   LIB3072-052-Q1-E1-F8
5'-most EST
                   2703
Seq. No.
                   1861 1.R1040
Contig ID
5'-most EST
                   jex700904613.h1
                   2704
Seq. No.
                   1862 1.R1040
Contig ID
5'-most EST
                   LIB3107-024-Q1-K1-A10
                   2705
Seq. No.
Contig ID
                   1864 1.R1040
5'-most EST
                   LIB3028-052-Q1-B1-B12
                   2706
Seq. No.
                   1864 2.R1040
Contig ID
                   seb7\overline{0}0647923.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1439625
BLAST score
                   174
                   1.0e-12
E value
                   91
Match length
                   37
% identity
                   (U64598) weakly similar to S. cervisiae PTM1 precursor
NCBI Description
                   (SP:P32857) [Caenorhabditis elegans]
                   2707
Seq. No.
                   1865 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810028a08a1
                   2708
Seq. No.
                   1869 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy283c08b1
                   BLASTX
Method
NCBI GI
                   g4432869 ·
BLAST score
                   552
                   1.0e-56
E value
Match length
                   157
                   66
% identity
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   2709
Seq. No.
Contig ID
                   1869 2.R1040
5'-most EST
                   LIB3106-113-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   g4432869
BLAST score
                   362
E value
                   4.0e-34
```

```
% identity
                   60
NCBI Description
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  1877 1.R1040
Contig ID
5'-most EST
                  awf700842923.h1
                  2711
Seq. No.
Contig ID
                  1877 2.R1040
                  LIB3072-060-Q1-K1-F5
5'-most EST
                  2712
Seq. No.
Contig ID
                  1882 1.R1040
                  LIB3055-013-Q1-N1-A7
5'-most EST
Seq. No.
                  2713
Contig ID
                  1884 1.R1040
5'-most EST
                  rlr700898336.h1
Method
                  BLASTX
NCBI GI
                  g3128177
BLAST score
                  258
E value
                  2.0e-22
Match length
                  102
% identity
NCBI Description
                   (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  2714
Contig ID
                  1885 1.R1040
5'-most EST
                  LIB3049-027-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  q266945
BLAST score
                  893
E value
                  2.0e-96
Match length
                  192
% identity
                  90
NCBI Description
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                  >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                  >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                  >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
Seq. No.
                  2715
Contig ID
                  1885 2.R1040
5'-most EST
                  sat7\overline{0}1009469.h1
Method
                  BLASTX
NCBI GI
                  g266945
BLAST score
                  874
E value
                  3.0e-94
Match length
                  192
% identity
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                  >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                  >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                  >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
```

Seq. No. 2716

44...

```
Contig ID
                   1885 3.R1040
                   LIB3065-010-Q1-N1-G1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q266945
BLAST score
                   832
E value
                   3.0e-89
Match length
                   192
                   83
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                   >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                   >gi_20727_emb_CAA46273 (X65155) GA [Pisum sativum]
                   >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                   [Pisum sativum]
Seq. No.
                   2717
                   1885 4.R1040
Contig ID
5'-most EST
                   leu701145234.h1
Method
                   BLASTX
NCBI GI
                   g2058273
BLAST score
                   435
E value
                   6.0e-43
Match length
                   96
                   89
% identity
NCBI Description
                   (D83527) YK426 [Oryza sativa]
                   2718
Seq. No.
Contig ID
                   1886 1.R1040
5'-most EST
                   uaw700661994.hl
Method
                   BLASTX
NCBI GI
                   g3790587
BLAST score
                   691
E value
                   1.0e-72
Match length
                   254
                   56
% identity
NCBI Description
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                   thaliana]
                   2719
Seq. No.
                   1886 2.R1040
Contig ID
                   crh700850064.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3790587
BLAST score
                   313
E value
                   3.0e-28
Match length
                   101
% identity
NCBI Description
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                   thaliana]
Seq. No.
                   2720
                   1886 3.R1040
Contig ID
5'-most EST
                  LIB3109-005-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                   q3790587
BLAST score
                   300
                   3.0e-27
E value
                   66
Match length
```

Contig ID

5'-most EST

```
% identity
                   77
NCBI Description
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                   thaliana]
                   2721
Seq. No.
                   1886_5.R1040
Contig ID
                   LIB3107-079-Q1-K1-C9
5'-most EST
                   BLASTX
Method
                   g3790587
NCBI GI
BLAST score
                   590
                   6.0e-61
E value
Match length
                   167
% identity
                   66
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
NCBI Description
                   thaliana]
                   2722
Seq. No.
                   1886 6.R1040
Contig ID
                   sat701010702.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3790587
BLAST score
                   361
                   2.0e-34
E value
Match length
                   72
% identity
                   82
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
NCBI Description
                   thaliana]
                   2723
Seq. No.
                   1888 1.R1040
Contig ID
                   jC-gmro02910059b02d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455158
BLAST score
                   1148
E value
                   1.0e-126
Match length
                   255
% identity
                   83
NCBI Description
                   (AL021687) kinase-like protein [Arabidopsis thaliana]
                   2724
Seq. No.
Contig ID
                   1888 2.R1040
5'-most EST
                   q517\overline{5}304
                   BLASTX
Method.
                   g3885884
NCBI GI
                   795
BLAST score
E value
                   5.0e-85
Match length
                   164
% identity
NCBI Description
                   (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                   2725
Seq. No.
Contig ID
                   1888 3.R1040
5'-most EST
                   LIB3051-115-Q1-K1-E12
                   2726
Seq. No.
```

1888\_4.R1040 eep700869342.h1

```
BLASTX
Method
NCBI GI
                   g4454449 ·
BLAST score
                   176
                   3.0e-12
E value
Match length
                   88
                   45
% identity
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   2727
Seq. No.
                   1888_5.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy034b06b1
                   2728
Seq. No.
                   1888 6.R1040
Contig ID
5'-most EST
                   g4302443
Method
                   BLASTX
NCBI GI
                   g3885884
BLAST score
                   789
E value
                   3.0e-84
Match length
                   164
                   89
% identity
                   (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                   2729
Seq. No.
Contig ID
                   1888 7.R1040
5'-most EST
                   rca700998155.h1
Method
                   BLASTX
NCBI GI
                   g4455158
BLAST score
                   810
E value
                   2.0e-86
Match length
                   208
% identity
                   75
                   (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
                   2730
Seq. No.
                   1888 8.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy217c02b1
                   2731
Seq. No.
                   1888 9.R1040
Contig ID
5'-most EST
                   jC-gmle01810073h09a1
Seq. No.
                   2732
Contig ID
                   1888 10.R1040
5'-most EST
                   pxt700942669.hl
Seq. No.
                   2733
Contig ID
                   1888 11.R1040
5'-most EST
                   pmv7\overline{0}0892913.h1
                   2734
Seq. No.
Contig ID
                   1888 13.R1040
                   LIB3\overline{1}39-035-P1-N1-G4
5'-most EST
Method
                   BLASTX
                   g3885884
NCBI GI
BLAST score
                   501
```

7.0e-51

E value

BLAST score

```
104
Match length
% identity
                   88
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                   2735
Seq. No.
                   1891 1.R1040
Contig ID
                   leu701146963.h1
5'-most EST
                   BLASTX
Method
                   g2088651
NCBI GI
BLAST score -
                   250
                   8.0e-32
E value
                   222
Match length
                   42
% identity
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   2736
Seq. No.
                   1891 2.R1040
Contig ID
                   LIB3170-006-Q1-K1-H3
5'-most EST
                   BLASTN
Method
                   g2264316
NCBI GI
BLAST score
                   50
                   8.0e-19
E value
                   137
Match length
                  88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRO11, complete sequence [Arabidopsis thaliana]
                   2737
Seq. No.
                   1891 3.R1040
Contig ID
                   g5753333
5'-most EST
                   BLASTX
Method
                   g2088651
NCBI GI
BLAST score
                   169
                   1.0e-11
E value
                   57
Match length
                   51
% identity
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   2738
Seq. No.
                   1892 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir032g02b1
Method
                   BLASTX
                   g4006899
NCBI GI
                   410
BLAST score
                   4.0e-40
E value
Match length
                   112
% identity
                   63
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2739
                   1892 2.R1040
Contig ID
5'-most EST
                   g4294695
                   BLASTX
Method
                   g4006899
NCBI GI
```

BLAST score

```
6.0e-16
E value
Match length
                   64
% identity
                   56
NCBI Description
                   (299708) putative protein [Arabidopsis thaliana]
                   2740
Seq. No.
                   1892 4.R1040
Contig ID
                   leu7\overline{0}1155723.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4006899
BLAST score
                   619
E value
                   1.0e-64
Match length
                   156
                   71
% identity
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   2741
Seq. No.
                   1892 5.R1040
Contig ID
5'-most EST
                   fua7\overline{0}1041271.h1
                   BLASTX
Method
                   g4006899
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
                   56
Match length
% identity
                   54
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2742
                   1893 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy031g02b1
Method
                   BLASTX
NCBI GI
                   g2997591
BLAST score
                   201 .
E value
                   2.0e-15
Match length
                   63
                   71
% identity
NCBI Description
                   (AF020814) glucose-6-phosphate/phosphate-translocator
                   precursor [Pisum sativum]
                   2743
Seq. No.
Contig ID
                   1893 2.R1040
5'-most EST
                   bth700848169.h1
Method
                   BLASTX
                   g2997591
NCBI GI
BLAST score
                   212
E value
                   8.0e-17
Match length
                   68
% identity
                   (AF020814) glucose-6-phosphate/phosphate-translocator
NCBI Description
                   precursor [Pisum sativum]
                   2744
Seq. No.
                   1894 1.R1040
Contig ID
5'-most EST
                   tku700646334.h1
Method
                   BLASTX
                   g124713
NCBI GI
```

5'-most EST

```
0.0e + 00
E value
                    645
Match length
                    87
% identity
NCBI Description
                    ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID
                    SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI)
                    (VACUOLAR INVERTASE) >gi_218326_dbj_BAA01107 (D10265) invertase [Vigna radiata] >gi_384325_prf__1905412A acid
                    invertase [Vigna radiata]
Seq. No.
                    2745
Contig ID
                    1894 2.R1040
5'-most EST
                    sat701011421.h1
                    2746
Seq. No.
                    1894 3.R1040
Contig ID
                    LIB3051-059-Q1-K2-E11
5'-most EST
Method
                    BLASTN
                    g3821780
NCBI GI
BLAST score
                    36
E value
                    2.0e-10
Match length
                    36
                    100
% identity
                    Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                    2747
Contig ID
                    1894 4.R1040
                    jC-gmf102220132ad08a1
5'-most EST
Method
                    BLASTX
                    g124713
NCBI GI
BLAST score
                    308
E value
                    4.0e-28
                    115
Match length
% identity
                    54
                    ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID
NCBI Description
                    SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI)
                    (VACUOLAR INVERTASE) >gi_218326_dbj_BAA01107_ (D10265) invertase [Vigna radiata] >gi_384325_prf__1905412A acid
                    invertase [Vigna radiata]
Seq. No.
                    2748
                    1894 5.R1040
Contig ID
5'-most EST
                    jC-qmf102220138b01d1
Method
                    BLASTN
NCBI GI
                    q218325
BLAST score
                    229
E value
                    1.0e-126
Match length
                    285
% identity
NCBI Description
                    Vigna radiata mRNA for invertase, complete cds
Seq. No.
                    2749
Contig ID
                    1894 6.R1040
5'-most EST
                    LIB3170-081-Q1-K1-A1
Seq. No.
                    2750
Contig ID
                    1896 1.R1040
```

LIB3109-042-Q1-K1-H10

NCBI Description

```
2751
Seq. No.
                   1898 1.R1040
Contig ID
5'-most EST
                   leu701149544.h1
Method
                   BLASTX
                   g2129636
NCBI GI
BLAST score
                   328
                   4.0e-30
E value
                   219
Match length
% identity
                  lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase
NCBI Description
                   [Arabidopsis thaliana]
                   2752
Seq. No.
                   1899 1.R1040
Contig ID
5'-most EST
                   bth700844448.h1
                   BLASTX
Method
NCBI GI
                   q4263048
BLAST score
                   622
                   1.0e-64
E value
Match length
                   209
% identity
                   61
                   (AC005142) putative hydrolase [Arabidopsis thaliana]
NCBI Description
                   2753
Seq. No.
                   1899 2.R1040
Contig ID
5'-most EST
                   fua701038150.hl
                   BLASTX
Method
NCBI GI
                   g4263048
BLAST score
                   278
E value
                   1.0e-24
Match length
                   108
                   56
% identity
                   (AC005142) putative hydrolase [Arabidopsis thaliana]
NCBI Description
                   2754
Seq. No.
Contig ID
                   1900 1.R1040
5'-most EST
                  LIB3107-061-Q1-K1-G1
Method
                   BLASTN
NCBI GI
                   g456567
                   275
BLAST score
E value
                   1.0e-153
Match length
                   451
% identity
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                  cds
Seq. No.
                   2755
Contig ID
                   1900 3.R1040
                  LIB3049-023-Q1-E1-B9
5'-most EST
Method
                  BLASTN
NCBI GI
                  q456567
BLAST score
                   67
                   3.0e-29
E value
Match length
                  187
% identity
```

Pisum sativum ubiquitin conjugating enzyme (UBC4), complete

Seq. No. Contig ID

```
2756
Seq. No.
                   1900 4.R1040
Contig ID
5'-most EST
                   bth700846257.h1
                   BLASTN
Method
NCBI GI
                   g456567
BLAST score
                   65
E value
                   4.0e-28
Match length
                   178
                   90
% identity
NCBI Description
                   Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
                   2757
Seq. No.
Contig ID
                   1901 1.R1040
                   ujr7\overline{0}0646501.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4193381
BLAST score
                   85
E value
                   8.0e-40
Match length
                   261
                   83
% identity
                   Arabidopsis thaliana ribosomal protein S27 (ARS27A) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   2758
                   1901 2.R1040
Contig ID
5'-most EST
                   LIB3106-088-Q1-K1-G8
                   BLASTN
Method
NCBI GI
                   g4193381
BLAST score
                   91
E value
                   2.0e-43
Match length
                   239
                   85
% identity
NCBI Description
                   Arabidopsis thaliana ribosomal protein S27 (ARS27A) mRNA,
                   complete cds
                   2759
Seq. No.
                   1901_3.R1040
Contig ID
5'-most EST
                   g5606680
Method
                   BLASTX
NCBI GI
                   g4193382
BLAST score
                   367
                   4.0e-35
E value
Match length
                   83
                   84
% identity
NCBI Description
                   (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
                   >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                   thaliana]
                   2760
Seq. No.
Contig ID
                   1902 1.R1040
5'-most EST
                   LIB3049-016-Q1-E1-D12
                   2761
```

cds

1902 2.R1040

NCBI GI

```
5'-most EST
                   bth700849686.h1
                   2762
Seq. No.
                   1902 3.R1040
Contig ID
                   LIB3107-006-Q1-K1-C9
5'-most EST
                   2763
Seq. No.
                   1902 5.R1040
Contig ID
                   LIB3139-006-P1-N1-H2
5'-most EST
                  2764 🌁 .
Seq. No.
                   1905 1.R1040
Contig ID
                   LIB3049-011-Q1-E1-F10
5'-most EST
                   BLASTX
Method
                   g3608481
NCBI GI
BLAST score
                   610
                   3.0e-63
E value
Match length
                   146
                   78
% identity
                   (AF088913) ribosomal protein L27a [Petunia x hybrida]
NCBI Description
                   2765
Seq. No.
                   1905 3.R1040
Contig ID
                   txt700735894.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g1881580
BLAST score
                   60
E value
                   4.0e-25
                   124
Match length
% identity
                   Drosophila melanogaster ribosomal protein RpL27a gene,
NCBI Description
                   complete cds
                   2766
Seq. No.
                   1906 1.R1040
Contig ID
                   LIB3028-051-Q1-B1-F9
5'-most EST
                   2767
Seq. No.
                   1907 1.R1040
Contig ID
                   k117\overline{0}1208895.h1
5'-most EST
                   BLASTX
Method
                   g2583108
NCBI GI
BLAST score .
                   643
                   9.0e-67
E value
Match length
                   311
% identity
                   (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                   2768
Seq. No.
                   1907 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400070b04d1
                   2769
Seq. No.
                   1908 1.R1040
Contig ID
                   fua701042926.hl
5'-most EST
                   BLASTX
Method
```

g2129648

```
729
BLAST score
                   6.0e-77
E value
                   295
Match length
                   55
% identity
                   MYB-related protein 33,3K - Arabidopsis thaliana
NCBI Description
                   >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein
                   [Arabidopsis thaliana]
                   2770
Seq. No.
                   1908 2.R1040
Contig ID
5'-most EST
                   LIB3028-013-Q1-B1-C2
Method
                   BLASTX
NCBI GI
                   q2129648
                   223
BLAST score
                   8.0e-18
E value
                   177
Match length
                   36
% identity
                   MYB-related protein 33,3K - Arabidopsis thaliana
NCBI Description
                   >gi 1263095_emb_CAA90809_ (Z54136) MYB-related protein
                   [Arabidopsis thaliana]
                   2771
Seq. No.
                   1908 3.R1040
Contig ID
5'-most EST
                   crh700852179.h1
Method
                   BLASTX
NCBI GI
                   q2642435
                   559
BLAST score
                   1.0e-57
E value
                   112
Match length
% identity
                   (AC002391) MYB-related protein [Arabidopsis thaliana]
NCBI Description
                   2772
Seq. No.
                   1909 1.R1040
Contig ID
                   hrw7\overline{0}1061638.h1
5'-most EST
Method
                   BLASTN
                   g1326162
NCBI GI
BLAST score
                   340
E value
                   0.0e + 00
                   536
Match length
% identity
                   Phaseolus vulgaris stress related protein PvSRP mRNA,
NCBI Description
                   complete cds
                   2773
Seq. No.
                   1909 2.R1040
Contig ID
5'-most EST
                   LIB3051-043-Q1-K1-A4
Method
                   BLASTN
NCBI GI
                   q1326162
                   324
BLAST score
                   0.0e + 00
E value
                   536
Match length
% identity
                   Phaseolus vulgaris stress related protein PvSRP mRNA,
NCBI Description
                   complete cds
```

Seq. No.

```
Contig ID
                   1909 3.R1040
                   LIB3\overline{0}93-040-Q1-K1-F9
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1326162
BLAST score
                   139
E value
                   6.0e-72
Match length
                   267
                   88
% identity
NCBI Description
                   Phaseolus vulgaris stress related protein PvSRP mRNA,
                   complete cds
2775
Seq. No.
Contig ID
                   1912 1.R1040
5'-most EST
                   LIB3107-075-Q1-K1-C9
                   BLASTX
Method
NCBI GI
                   q3077640
BLAST score
                   852
E value
                   1.0e-91
Match length
                   268
                   63
% identity
NCBI Description
                   (AJ223151) O-methyltransferase [Prunus dulcis]
                   2776
Seq. No.
                   1912 2.R1040
Contig ID
5'-most EST
                   zhf700954691.h1
                   BLASTX
Method
                   g1174621
NCBI GI
BLAST score
                   879
E value
                   1.0e-94
Match length
                   330
                   52
% identity
                   T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                   (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing
                   cytosolic chaperonin (CCT) theta chain - mouse
                   >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit
                   of the chaperonin containing TCP-1 (CCT) [Mus musculus]
Seq. No.
                   2777
Contig ID
                   1915 1.R1040
                   zhf700952177.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2739389
BLAST score
                   1268
                   1.0e-140
E value
                   450
Match length
% identity
NCBI Description
                   (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
Seq. No.
                   2778
Contig ID
                   1916 1.R1040
                   leu7\overline{0}1150759.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4559334
BLAST score
                   1197
                   1.0e-132
E value
Match length
                   326
```

% identity

```
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
                   2779
Seq. No.
                   1917 1.R1040
Contig ID
                   LIB3109-046-Q1-K1-H11
5'-most EST
                   BLASTX
Method
                   g559330
NCBI GI
                   276
BLAST score
                   8.0e-24
E value
                   306
Match length
                   26
% identity
                   (D38521) The ha0919 gene product is novel. [Homo sapiens]
NCBI Description
                   2780
Seq. No.
                   1918 1.R1040
Contig ID
                   LIB3028-035-Q1-B1-A7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2213629
BLAST score
                   675
                   7.0e-71
E value
                   190
Match length
                   66
% identity
                   (AC000103) F21J9.21 [Arabidopsis thaliana]
NCBI Description
                   2781
Seq. No.
                   1919 1.R1040
Contig ID
5'-most EST
                   LIB3106-049-Q1-K1-H7
Method
                   BLASTX
                   g4049349
NCBI GI
                   399
BLAST score
                   1.0e-38
E value
                   122
Match length
% identity
                   63
                   (AL034567) ubiquinol-cytochrome c reductase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   2782
Contig ID
                   1920 1.R1040
5'-most EST
                   LIB3028-051-Q1-B1-E1
                   2783
Seq. No.
                   1922 1.R1040
Contig ID
                   LIB3109-022-Q1-K1-A9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4432814
BLAST score
                   305
E value
                   3.0e-27
Match length
                   238
                   33
% identity
NCBI Description
                   (AC006593) unknown protein [Arabidopsis thaliana]
                   2784
Seq. No.
                   1924 1.R1040
Contig ID
                   jex700907752.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455192
```

BLAST score

```
E value
                   3.0e-20
Match length
                   126
% identity
                   22
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   2785
Seq. No.
                   1925 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy026b09b1
Method
                   BLASTX
                   g400890
NCBI GI
BLAST score
                   662
                   4.0e-69
E value
                   247
Match length
                   60
% identity
                   PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
                   >gi 282837 pir S26953 photosystem II 22K protein precursor
                   - spinach >gi 21307 emb CAA48557 (X68552) 22kD-protein of
                   PSII [Spinacia oleracea] >gi 260917 bbs_119338 (S49864)
                   photosystem II 22 kda polypeptide [spinach, Peptide, 274
                   aa] [Spinacia oleracea]
                   2786
Seq. No.
                   1925_2.R1040
Contig ID
5'-most EST
                   jC-gmle01810064a12a1
Method
                   BLASTX
NCBI GI
                  g1709846
BLAST score
                   285
                   7.0e-34
E value
                   132
Match length
                   43
% identity
                   PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
NCBI Description
                   22 kDa component of photosystem II [Lycopersicon
                   esculentum]
                   2787
Seq. No.
                   1925 3.R1040
Contig ID
5'-most EST
                  LIB3138-079-P1-N1-H6
Method
                  BLASTN
NCBI GI
                   q21306
BLAST score
                   45
E value
                   5.0e-16
                  117
Match length
                   85
% identity
                  S.oleracea mRNA for photosystem II 22kDa protein
NCBI Description
                  2788
Seq. No.
                  1925 7.R1040
Contig ID
5'-most EST
                  ncj700981872.hl
                   2789
Seq. No.
                   1925 8.R1040
Contig ID
5'-most EST
                   kmv700741481.h1
                  2790
Seq. No.
                  1927 1.R1040
Contig ID
                   km \sqrt{700739216.h1}
5'-most EST
Method
                  BLASTX
```

```
g2499553
NCBI GI
BLAST score
                   1797
                   0.0e+00
E value
                   476
Match length
                   75
% identity
                   CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
NCBI Description
                   >gi_629524_pir__S39058 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana
                   >gi_442529_bbs_139743 (S66907) flavin-type blue-light
                   photoreceptor, HY4=DNA photolyase/tropomyosin A homolog
                    [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa]
                    [Arabidopsis thaliana]
                   2791
Seq. No.
                   1927 2.R1040
Contig ID
5'-most EST
                   kl1701204912.hl
Method
                   BLASTX
NCBI GI
                   g4325368
BLAST score
                   271
                   1.0e-23
E value
                   157
Match length
% identity
                   46
                   (AF128396) Arabidopsis thaliana flavin-type blue-light
NCBI Description
                   photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2,
                   E=2.6e-226, N=1) [Arabidopsis thaliana]
Seq. No.
                   2792
                   1927 3.R1040
Contig ID
                   LIB3\overline{0}93-018-Q1-K1-E1
5'-most EST
                   2793
Seq. No.
Contig ID
                   1929 1.R1040
                   leu7\overline{0}1146395.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2222777
BLAST score
                   301
E value
                   3.0e-27
Match length
                   106
                   58
% identity
                   (Y13986) GTP-binding protein [Ostertagia circumcincta]
NCBI Description
                   2794
Seq. No.
Contig ID
                   1930 1.R1040
5'-most EST
                   LIB3028-051-Q1-B1-B4
Method
                   BLASTX
NCBI GI
                   g3426036
BLAST score
                   239
E value
                   5.0e-20
Match length
                   128
                   47
% identity
                   (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   2795
Seq. No.
Contig ID
                   1931 1.R1040
                   LIB3028-019-Q1-B1-A3
5'-most EST
```

Seq. No.

Match length

```
Contig ID
                   1933 1.R1040
                   LIB3028-051-Q1-B1-B7
5'-most EST
Seq. No.
                   2797
                   1934 1.R1040
Contig ID
5'-most EST
                   LIB3028-051-Q1-B1-B8
                   BLASTX
Method
                   g4309969
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   89
Match length
                   52
% identity
                   (AC002983) putative phosphoglyceride transfer protein
NCBI Description
                   [Arabidopsis thaliana]
                   2798
Seq. No.
Contig ID
                   1934 2.R1040
5'-most EST
                   LIB3049-045-Q1-E1-F12
                   2799
Seq. No.
                  1936 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1155657.h1
                   BLASTX
Method
                   g100347
NCBI GI
BLAST score
                   383
                   9.0e-37
E value
Match length
                   141
% identity
                   53
                   monosaccharide transport protein MST1 - common tobacco
NCBI Description
                   >gi 19885_emb_CAA47324_ (X66856) monosaccharid transporter
                   [Nicotiana tabacum]
                   2800
Seq. No.
                   1936 2.R1040
Contig ID
                   uC-gmflminsoy079f01b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g100347
BLAST score
                   312
                   1.0e-28
E value
                   98
Match length
                   59
% identity
                  monosaccharide transport protein MST1 - common tobacco
NCBI Description
                   >gi 19885 emb CAA47324 (X66856) monosaccharid transporter
                   [Nicotiana tabacum]
                   2801
Seq. No.
                   1940 1.R1040
Contig ID
5'-most EST
                   LIB3170-078-Q1-J1-D1
                   2802
Seq. No.
                   1941 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy180d02b1
Method
                   BLASTX
NCBI GI
                   g3860263
BLAST score
                   1554
                   1.0e-173
E value
```

NCBI GI

```
% identity
NCBI Description
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
                   thaliana]
                   2803
Seq. No.
                   1941 2.R1040
Contig ID
                   uC-gmrominsoy243e12b1
5'-most EST
                   BLASTX
Method
                   g3860263
NCBI GI
BLAST score
                   658 ·
                   5.0e-70
E value
Match length
                   241
                   58
% identity
NCBI Description
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
                   thaliana]
                   2804
Seq. No.
                   1941 4.R1040
Contig ID
                   LIB3092-058-Q1-K1-E8
5'-most EST
Method
                   BLASTX
                   g3860263
NCBI GI
BLAST score
                   288
                   8.0e-26
E value
                   91
Match length
                   59
% identity
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
                   2805
Seq. No.
                   1942 1.R1040
Contig ID
                   LIB3028-043-Q1-B1-E4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244956
                   307
BLAST score
                   1.0e-27
E value
                   146
Match length
                   43
% identity
NCBI Description
                   (Z97340) strong similarity to pectinesterase [Arabidopsis
                   thaliana]
                   2806
Seq. No.
                   1942 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220130e04d1
                   2807
Seq. No.
                   1944_1.R1040
Contig ID
                   LIB3107-044-Q1-K1-E9
5'-most EST
                   2808 .
Seq. No.
                   1944_3.R1040
Contig ID
                   zhf700964515.h1
5'-most EST
                   2809
Seq. No.
Contig ID
                   1946 1.R1040
                   sat7\overline{0}1015379.h1
5'-most EST
Method
                   BLASTX
```

g2760320

Method

NCBI GI

BLASTN

g463251

```
BLAST score
                   504
                   2.0e-50
E value
                   211
Match length
% identity
                   49
                   (AC002130) F1N21.4 [Arabidopsis thaliana]
NCBI Description
                   2810
Seq. No.
                   1946 2.R1040
Contig ID
                   jC-gmst02400054f03d1
5'-most EST
                   2811
Seq. No.
                   1946 3.R1040
Contig ID
                   rlr7\overline{0}0897008.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2760320
BLAST score
                   203
                   3.0e-17
E value
Match length
                   112
                   54
% identity
                   (AC002130) F1N21.4 [Arabidopsis thaliana]
NCBI Description
                   2812
Seq. No.
                   1946 5.R1040
Contig ID
                   zsg701118627.hl
5'-most EST
                  2813
Seq. No.
                   1946 6.R1040
Contig ID
5'-most EST
                   smc700746556.hl
                   2814
Seq. No.
                   1947 1.R1040
Contig ID
                   qsv7\overline{0}1046102.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g463251
                   245
BLAST score
                   1.0e-135
E value
                   553
Match length
                   86
% identity
                   M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5
NCBI Description
                   2815
Seq. No.
                   1947 2.R1040
Contig ID
                   LIB3040-025-Q1-E1-H8
5'-most EST
Method
                   BLASTN
                   q1944341
NCBI GI
BLAST score
                   340
                   0.0e+00
E value
                   507
Match length
% identity
                   92
                   Glycine max DNA for cysteine proteinase inhibitor, complete
NCBI Description
                   2816
Seq. No.
Contig ID
                   1947 3.R1040
                   uC-gmropic108c03b1
5'-most EST
```

```
BLAST score
                  162
                  1.0e-85
E value
Match length
                  354
% identity
                  86
                  M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5
NCBI Description
Seq. No.
                  2817
                  1947 4.R1040
Contig ID
                  LIB3028-009-Q1-B1-F12
5'-most EST
                  BLASTN
Method
                  g4512656
NCBI GI
BLAST score
                  67
                  4.0e-29
E value
                  115
Match length
                  90
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  2818
Seq. No.
                  1947 5.R1040
Contig ID
                  LIB3170-016-Q1-K1-G1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g463251
BLAST score
                  241
                  1.0e-133
E value
Match length
                  553
                  86
% identity
                  M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5
NCBI Description
                  2819
Seq. No.
                  1947 7.R1040
Contig ID
                  LIB3040-019-Q1-E1-F10
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1173055
BLAST score
                  462
                  3.0e-46
E value
                  124
Match length
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497
                  ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                  RL5 ribosomal protein - alfalfa >gi_463252 emb CAA55090_
                   (X78284) RL5 ribosomal protein [Medicago sativa]
                  2820
Seq. No.
                  1947 9.R1040
Contig ID
                  zzp700829957.h1
5'-most EST
Method
                  BLASTN
                  g1944341
NCBI GI
BLAST score
                  87
                  3.0e-41
E value
Match length
                  147
                  90
% identity
                  Glycine max DNA for cysteine proteinase inhibitor, complete
NCBI Description
                  cds
```

1947 12.R1040

Seq. No.

Contig ID

BLAST score

```
5'-most EST
                   gsv701046130.hl
Method
                   BLASTN
                   g463251
NCBI GI
BLAST score
                   102
                   3.0e-50
E value
Match length
                   250
                   85
% identity
                   M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5
NCBI Description
                   2822
Seq. No.
                   1948 1.R1040
Contig ID
5'-most EST
                   LIB3049-010-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   g3402711
BLAST score
                   779
                   1.0e-82
E value
Match length
                   360
                   50
% identity
                   (AC004261) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   2823
Seq. No.
                   1948 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy045h11b1
Seq. No.
                   2824
Contig ID
                   1948 5.R1040
                   uC-gmflminsoy043e03b1
5'-most EST
Seq. No.
                   2825
                   1949 1.R1040
Contig ID
5'-most EST
                   LIB3065-007-Q1-N1-B3
Method
                   BLASTX
NCBI GI
                   g2244744
BLAST score
                   311
E value
                   5.0e-28
Match length
                   139
% identity
                   50
                   (Y13676) bZIP DNA-binding protein [Antirrhinum majus]
NCBI Description
                   2826
Seq. No.
                   1949 2.R1040
Contig ID
5'-most EST
                   1eu7\overline{0}1155981.h1
                   BLASTN
Method
NCBI GI
                   g394735
BLAST score
                   44
E value
                   2.0e-15
Match length
                   52
                   96
% identity
NCBI Description
                   Rice lip19 mRNA for basic/leucine zipper protein
Seq. No.
                   2827
                   1950 1.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0982269.h1
Method
                   BLASTX
NCBI GI
                   q1778376
```

```
0.0e + 00
E value
                   374
Match length
                   89
% identity
NCBI Description
                   (U81288) PsRT17-1 [Pisum sativum]
                   2828
Seq. No.
                   1950_2.R1040
Contig ID
                   jC-gmst02400050d06a1
5'-most EST
                   BLASTN
Method
                   g1778375
NCBI GI
BLAST score
                   50
                   7.0e-19
E value
                   86
Match length
                   90
% identity
NCBI Description Pisum sativum PsRT17-1 mRNA, complete cds
                   2829
Seq. No.
                   1950_5.R1040
Contig ID
                   LIB3065-006-Q1-N1-E7
5'-most EST
                   BLASTN
Method
                   g1778375
NCBI GI
BLAST score
                   36
                   7.0e-11
E value
                   74
Match length
                   93
% identity
                  Pisum sativum PsRT17-1 mRNA, complete cds
NCBI Description
                   2830
Seq. No.
                   1950 6.R1040
Contig ID
                   zhf700962217.h1
5'-most EST
                   BLASTN
Method
                   g1778375
NCBI GI
                   159
BLAST score
                   4.0e-84
E value
                   377
Match length
                   87
% identity
NCBI Description
                   Pisum sativum PsRT17-1 mRNA, complete cds
                   2831
Seq. No.
                   1950 9.R1040
Contig ID
                   wrg700786756.h2
5'-most EST
                   2832
Seq. No.
                   1951 1.R1040
Contig ID
                   LIB3\overline{1}39-087-P1-N1-D6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2654358
BLAST score
                   494
E value
                   1.0e-49
                   175
Match length
                   54
% identity
                   (Y15522) MNUDC protein [Mus musculus]
NCBI Description
                   >gi_2808636_emb_CAA57201_ (X81443) Sig 92 [Mus musculus]
                   2833
Seq. No.
```

1951 2.R1040

 $leu7\overline{0}1151540.h1$ 

Contig ID

5'-most EST

% identity

```
2834
Seq. No.
                   1952 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910062e09a1
Method
                   BLASTN
NCBI GI
                   g18729
BLAST score
                   36
                   1.0e-10
E value
                   40
Match length
                   97
% identity
                   Soybean (Glycine max) 18S ribosomal RNA
NCBI Description
                   2835
Seq. No.
Contig ID
                   1952 2.R1040
                   LIB3028-051-Q1-B1-A12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3927831
BLAST score
                   740
                   3.0e-78
E value
Match length
                   199
% identity
                   69
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   2836
Seq. No.
Contig ID
                   1952 3.R1040
5'-most EST
                   g5607045
Method
                   BLASTX
NCBI GI
                   g3927831
BLAST score
                   419
                   6.0e-41
E value
Match length
                   163
                   54
% identity
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   2837
Contig ID
                   1952 4.R1040
                   rlr700896407.hl
5'-most EST
                   BLASTX
Method
                   g3927831
NCBI GI
BLAST score
                   336
E value
                   4.0e-31
Match length
                   175
                   45
% identity
NCBI Description
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                   thaliana]
                   2838
Seq. No.
Contig ID
                   1955_1.R1040
                   LIB3094-070-Q1-K1-F5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3482979
BLAST score
                   548
                   3.0e-56
E value
Match length
                   127
```

Seq. No.

Contig ID

```
(AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4567258 gb_AAD23672.1_AC007070_21 (AC007070)
                  hypothetical protein [Arabidopsis thaliana]
                   2839
Seq. No.
                   1956 1.R1040
Contig ID
                   crh700854558.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q133872
BLAST score
                   1491
E value
                   1.0e-166
                   363
Match length
                   80
% identity
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                   >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                  spinach >gi_322404_pir__A44121 small subunit ribosomal
                   protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
Seq. No.
                   2840
Contig ID
                   1956 2.R1040
5'-most EST
                  LIB3106-006-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   q133872
BLAST score
                   469
                   5.0e-47
E value
                   101
Match length
% identity
NCBI Description
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
                   >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404_pir__A44121 small subunit ribosomal
                   protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >qi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
                   2841
Seq. No.
                   1957 1.R1040
Contig ID
                   bth700848861.h1
5'-most EST
Method
                   BLASTX
                   q1076610
NCBI GI
BLAST score
                   1404
                   1.0e-156
E value
                   355
Match length
% identity
                   70
                   cathepsin B-like cysteine proteinase (EC 3.4.22.-) - Aztec
NCBI Description
                   tobacco >gi_609175_emb_CAA57522_ (X81995) cathepsin B-like
                   cysteine proteinase [Nicotiana rustica]
Seq. No.
                   2842
Contia ID
                   1957 2.R1040
5'-most EST
                   jC-qmf102220056d01d1
```

1957\_3.R1040

5'-most EST

```
jC-gmle01810009b12a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   a1652807
BLAST score
                   261
                   3.0e-22
E value
                   114
Match length
                   45
% identity
NCBI Description
                   (D90908) hypothetical protein [Synechocystis sp.]
Seq. No.
Contig ID
                   1957 4.R1040
5'-most EST
                   uC-qmrominsoy176c09b1
Method
                   BLASTX
NCBI GI
                   q2842493
BLAST score
                   483
                   3.0e-48
E value
                   187
Match length
% identity
                   50
                   (AL021749) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2845
                   1957_5.R1040
Contig ID
5'-most EST
                   jC-gmle01810037h10a2
Method
                   BLASTN
                   q21952
NCBI GI
BLAST score
                   95
E value
                   8.0e-46
Match length
                   175
                   89
% identity
                   T.repens mRNA for cyanogenic beta-glucosidase (linamarase)
NCBI Description
                   2846
Seq. No.
                   1957_6.R1040
Contig ID
5'-most EST
                   jC-qmle01810001c03a1
                   BLASTN
Method
NCBI GI
                   g21952
BLAST score
                   89
                   5.0e-42
E value
Match length
                   153
% identity
                  T.repens mRNA for cyanogenic beta-glucosidase (linamarase)
NCBI Description
                   2847
Seq. No.
                   1957 8.R1040
Contig ID
5'-most EST
                   uC-gmropic097d08b1
                  BLASTX
Method
NCBI GI
                   q2842493
BLAST score
                   193
E value
                   1.0e-14
Match length
                   53
% identity
                   62
NCBI Description
                   (AL021749) predicted protein [Arabidopsis thaliana]
Seq. No.
                   1957 12.R1040
Contig ID
```

 $zsg7\overline{0}1129432.h1$ 

5'-most EST

```
Seq. No.
                   2849
                   1958 1.R1040
Contig ID
5'-most EST
                   LIB3028-051-Q1-B1-A8
Method
                   BLASTX
                   q3256035
NCBI GI
BLAST score
                   956
                   1.0e-107
E value
Match length
                   458
                   46
% identity
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                   bicolor)
                   2850
Seq. No.
                   1958 2.R1040
Contig ID
5'-most EST
                   fC-gmse700855803a1
Method
                   BLASTX
                   q2980770
NCBI GI
BLAST score
                   576
                   5.0e-59
E value
Match length
                   284
% identity
                   45
                   (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2851
                   1958_4.R1040
Contig ID
                   uC-gmropic107g01b1
5'-most EST.
Seq. No.
                   2852
                   1958 5.R1040
Contig ID
                   seb700653353.h1
5'-most EST
                   2853
Seq. No.
Contig ID
                   1958 6.R1040
5'-most EST
                   6HC - \overline{0}1 - Q1 - B1 - E11
                   BLASTX
Method
                   g1777312
NCBI GI
BLAST score
                   153
                   7.0e-10
E value
Match length
                   45
% identity
NCBI Description
                   (D30622) novel serine/threonine protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   2854
                   1958 8.R1040
Contig ID
                   jC-gmro02910020g05d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2980770
BLAST score
                   183
                   2.0e-13
E value
Match length
                   65
% identity
                   (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   2855
Seq. No.
                   1959 1.R1040
Contig ID
```

LIB3028-051-Q1-B1-A9

```
Method
                    BLASTX
                    g3080391
NCBI GI
BLAST score
                    679
                    5.0e-71
E value
Match length
                    292
% identity
                    67
                    (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                    2856
Seq. No.
                    1961_1.R1040
Contig ID
                    wvk700681379.h2
5'-most EST
                    BLASTX
Method -
                    g3341899
NCBI GI
BLAST score
                    185
                    4.0e-13
E value
Match length
                    110
% identity
                    45
                    (AB009285) BCNT [Homo sapiens]
NCBI Description
                    2857
Seq. No.
                    1962 1.R1040
Contig ID
                    jC-gmro02800033c10a1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g2129956
BLAST score
                    467
                    2.0e-46
E value
Match length
                    155
                    55
% identity
                    photoassimilate-responsive protein PAR-1c precursor -
NCBI Description
                    common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y
                    expressed in sugar-accumulating plants [Nicotiana tabacum]
                    2858
Seq. No.
                    1962 2.R1040
Contig ID
5'-most EST
                    ncj7\overline{0}0982510.h1
Method
                    BLASTX
NCBI GI
                    g2129956
BLAST score
                    353
                    2.0e-33
E value
Match length
                    115
% identity
                    photoassimilate-responsive protein PAR-1c precursor -
NCBI Description
                    common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y
                    expressed in sugar-accumulating plants [Nicotiana tabacum]
Seq. No.
                    2859
Contig ID
                    1962 3.R1040
                    q4437054
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4544412
BLAST score
                    384
E value
                    1.0e-36
Match length
                    173
                    40
% identity
                    (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

NCBI GI

```
2860
Seq. No.
                   1965 1.R1040
Contig ID
                   epx7\overline{0}1106858.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4388726
                   1425
BLAST score
                   1.0e-158
E value
Match length
                   383
                   71
% identity
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
                   2861
Seq. No.
                   1965 2.R1040
Contig ID
                   pmv700893580.h1
5'-most EST
                   BLASTX
Method
                   q4388726
NCBI GI
BLAST score
                   811
                   7.0e-87
E value
                   198
Match length
                   76
% identity
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
                   2862
Seq. No.
Contig ID
                   1965 3.R1040
                   LIB3170-037-Q1-J1-C12
5'-most EST
                   2863
Seq. No.
                   1965 4.R1040
Contig ID
5'-most EST
                   LIB3109-009-Q1-K1-G10
Method
                   BLASTX
                   g4388726
NCBI GI
                   390
BLAST score
                   9.0e-38
E value
Match length
                   97
% identity
                   76
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
                   2864
Seq. No.
Contig ID
                   1966 1.R1040
5'-most EST
                   vzy7\overline{0}0756786.h1
                   BLASTX
Method
                   g4220512
NCBI GI
BLAST score
                   229
E value
                   3.0e-19
                   57
Match length
                   72
% identity
                   (AL035356) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2865
Contig ID
                   1967 1.R1040
                   LIB3\overline{0}28-052-Q1-B2-E1
5'-most EST
Method
                   BLASTX
```

g3608412

5'-most EST

```
662
BLAST score
                   2.0e-69
E value
                   179
Match length
                   73
% identity
                   (AF079355) protein phosphatase-2c [Mesembryanthemum
NCBI Description
                   crystallinum]
                   2866
Seq. No.
Contig ID
                   1969 1.R1040
                  LIB3028-040-Q1-B1-A7
5'-most EST
Method
                  BLASTX
                   g4510395
NCBI GI
BLAST score
                   342
                   3.0e-42
E value
Match length
                   114
% identity
                   75
                   (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   2867
Seq. No.
Contig ID
                  1970_1.R1040
5'-most EST
                  LIB3028-050-Q1-B1-G11
Method
                  BLASTX
NCBI GI
                  g3386614
                   359
BLAST score
E value
                   3.0e-34
                  88
Match length
                   41
% identity
                   (AC004665) putative transcription factor SF3 [Arabidopsis
NCBI Description
                  thaliana]
                  2868
Seq. No.
                  1972 1.R1040
Contig ID
5'-most EST
                  gsv701044495.hl
                  2869
Seq. No.
Contig ID
                  1972 2.R1040
5'-most EST
                  uC-gmropic103c02b1
                  2870
Seq. No.
                  1973 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910022c04a1
Method
                  BLASTX
NCBI GI
                  q3329368
BLAST score
                  251
E value
                  1.0e-21
Match length
                  61
% identity
NCBI Description
                   (AF031244) nodulin-like protein [Arabidopsis thaliana]
                  2871
Seq. No.
                  1973 2.R1040
Contig ID
5'-most EST
                  zhf700954080.h1
Seq. No.
                  2872
Contig ID
                  1973 4.R1040
```

jC-gmle01810077d06d1

```
2873
Seq. No.
Contig ID
                   1975 1.R1040
                   uC-gmrominsoy302h05b1
5'-most EST
                   BLASTX
Method
                   q4262233
NCBI GI
BLAST score
                   460
                   1.0e-45
E value
                   246
Match length
                   46
% identity
                   (AC006200) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   2874
Seq. No.
                   1976 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910046b07a1
                   BLASTX
Method
                   g4567281
NCBI GI
                   201
BLAST score
                   3.0e-15
E value
Match length
                   114
                   43
% identity
                   (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                   2875
Seq. No.
                   1976 3.R1040
Contig ID
5'-most EST
                   leu701150855.h1
                   2876
Seq. No.
                   1977 1.R1040
Contig ID
5'-most EST
                  LIB3028-050-Q1-B1-G9
                   2877
Seq. No.
                   1979_1.R1040
Contig ID
5'-most EST
                  LIB3028-026-Q1-B1-H2
                  BLASTX
Method
NCBI GI
                   g4204466
BLAST score
                   582
E value
                   8.0e-60
                  222
Match length
% identity
NCBI Description
                   (AF067417) mannose lectin [Dolichos lablab]
                   2878
Seq. No.
Contig ID
                   1980 1.R1040
                   epx701107594.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3551246
BLAST score
                   181
E value
                   6.0e-97
                   499
Match length
                   85
% identity
                  Daucus carota mRNA for 181, partial cds
NCBI Description
Seq. No.
                   2879
                  1983_1.R1040
Contig ID
                   jC-gmle01810018c12a2
5'-most EST
```

BLASTX

Method

```
NCBI GI
                   g2911799
BLAST score
                   1303
E value
                   1.0e-144
Match length
                   328
% identity
                   75
NCBI Description
                   (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera
                   subsp. trichocarpa X Populus deltoides]
                   2880
Seq. No.
Contig ID
                   1984 1.R1040
5'-most EST
                   zhf700956267.h1
Method
                   BLASTX
NCBI GI
                   g2262110
BLAST score
                   235
E value
                   7.0e-20
Match length
                   65
                   63
% identity
NCBI Description
                   (AC002343) zinc finger protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   2881
                   1986 1.R1040
Contig ID
                   asn701131155.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2970050
BLAST score
                   380
E value
                   0.0e + 00
Match length
                   692
                   89
% identity
NCBI Description
                   Vigna radiata mRNA for ARG10, complete cds
                   2882
Seq. No.
                   1986 2.R1040
Contig ID
5'-most EST
                   pxt700944387.hl
                   2883
Seq. No.
Contig ID
                   1986_3.R1040
5'-most EST
                   zzp700833378.hl
Method
                   BLASTN
                   g2970050
NCBI GI
BLAST score
                   320
E value
                   1.0e-180
Match length
                   727
% identity
                  Vigna radiata mRNA for ARG10, complete cds
NCBI Description
Seq. No.
                   2884
Contig ID
                   1986 4.R1040
5'-most EST
                   fua701040205.hl
Method
                   BLASTN
NCBI GI
                  q2970050
BLAST score
                   215
E value
                   1.0e-117
Match length
                   351
                   90
% identity
```

NCBI Description Vigna radiata mRNA for ARG10, complete cds

NCBI Description

```
Seq. No.
                   2885
                   1986 9.R1040
Contig ID
5'-most EST
                   jC-gmf102220097h01a1
Method
                   BLASTN
                   g2970050
NCBI GI
                   78
BLAST score
E value
                   9.0e-36
Match length
                   355
                   87
% identity
                   Vigna radiata mRNA for ARG10, complete cds
NCBI Description
Seq. No.
                   2886
                   1987 1.R1040
Contig ID
5'-most EST
                   g5753538
Method
                   BLASTX
NCBI GI
                   g2967456
BLAST score
                   473
                   2.0e-47
E value
Match length
                   164
% identity
                   54
                   (AB012048) sulfate transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2887
                   1988 1.R1040
Contig ID
5'-most EST
                   LIB3028-040-Q1-B1-G1
                   2888
Seq. No.
Contig ID
                   1988 2.R1040
5'-most EST
                   zsg701118956.hl
                   2889
Seq. No.
                   1989 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910024d07a1
Method
                   BLASTX
                   g3193330
NCBI GI
BLAST score
                   510
E value
                   2.0e-51
Match length
                   208
% identity
                   55
                   (AF069299) contains similarity to Medicago sativa corC
NCBI Description
                   (GB:L22305) [Arabidopsis thaliana]
                   2890
Seq. No.
Contig ID
                   1989 2.R1040
5'-most EST
                   6HA - \overline{0}1 - Q1 - B1 - G3
                   2891
Seq. No.
                   1989 4.R1040
Contig ID
                   zhf700962925.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3738316
BLAST score
                   156
E value
                   1.0e-10
Match length
                   42
                   74
% identity
```

(AC005170) unknown protein [Arabidopsis thaliana]

```
2892
Seq. No.
                   1991 1.R1040
Contig ID
                   zzp700830841.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3790581
                   237
BLAST score
                   3.0e-19
E value
Match length
                   157
                   37
% identity
NCBI Description
                   (AF079179) RING-H2 finger protein RHBla [Arabidopsis
                   thaliana)
                   2893
Seq. No.
                   1991 2.R1040
Contig ID
                   LIB3051-102-Q1-K1-C7
5'-most EST
Method
                   BLASTX
                   g3790581
NCBI GI
BLAST score
                   214
E value
                   6.0e-17
Match length
                   111
                   38
% identity
                   (AF079179) RING-H2 finger protein RHBla [Arabidopsis
NCBI Description
                   thaliana]
                   2894
Seq. No.
                   1991 3.R1040
Contig ID
5'-most EST
                   sat7\overline{0}1009081.h1
                   2895
Seq. No.
                   1993 1.R1040
Contig ID
                   LIB3039-048-Q1-E1-D8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4512671
BLAST score
                   381
E value
                   3.0e-36
Match length
                   162
% identity
                   57
NCBI Description
                   (AC006931) unknown protein [Arabidopsis thaliana]
                   2896
Seq. No.
Contig ID
                   1993 2.R1040
5'-most EST
                   LIB3039-006-Q1-E1-H10
                   2897
Seq. No.
Contig ID
                   1993 3.R1040
                   asn7\overline{0}1138996.h1
5'-most EST
Method '
                   BLASTX
NCBI GI
                   g4512671
BLAST score
                   333
E value
                   1.0e-30
Match length
                   146
% identity
                   47
NCBI Description
                   (AC006931) unknown protein [Arabidopsis thaliana]
                   2898
Seq. No.
                   1994 1.R1040
Contig ID
```

leu701150696.h1

5'-most EST

```
Method
                   BLASTN
NCBI GI
                   g1658196
BLAST score
                   475
                   0.0e+00
E value
Match length
                   1107
                   86
% identity
                  Ricinus communis calreticulin mRNA, complete cds
NCBI Description
                   2899
Seq. No.
                   1994 2.R1040
Contig ID
5'-most EST
                  LIB3087-001-Q1-K1-A11
Method
                  BLASTX
                   g4467153
NCBI GI
BLAST score
                   550
                   3.0e-56
E value
Match length
                   126
                   78
% identity
                   (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   2900
Seq. No.
                   1997 1.R1040
Contig ID
                  LIB3040-042-Q1-E1-A8
5'-most EST
                  BLASTN
Method
                  g2465009
NCBI GI
BLAST score
                  98
E value
                   1.0e-47
Match length
                  170
                  89
% identity
                  Fragaria vesca mRNA for putative acyl carrier protein
NCBI Description
Seq. No.
                  2901
                  1997 2.R1040
Contig ID
5'-most EST
                   g5607168
                  BLASTN
Method
NCBI GI
                   g1838960
BLAST score
                   91
E value
                   3.0e-43
                  215
Match length
% identity
                  C.glauca mRNA for acyl carrier protein
NCBI Description
                  2902
Seq. No.
                  1998 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir037d06b1
                  2903
Seq. No.
Contig ID
                  1998 2.R1040
5'-most EST
                   zzp700832963.hl
                  2904
Seq. No.
                  1999 1.R1040
Contig ID
5'-most EST
                  LIB3028-050-Q1-B1-F1
Method
                  BLASTX
NCBI GI
                  q4249386
BLAST score
                  166
```

1.0e-11

E value

Match length 37 % identity 86 (AC005966) Strong similarity to gb AF061286 gamma-adaptin 1 NCBI Description from Arabidopsis thaliana. EST gb H37393 comes from this gene. [Arabidopsis thaliana] 2905 Seq. No. Contig ID 2002 1.R1040 5'-most EST LIB3028-050-Q1-B1-A8 BLASTX Method NCBI GI g3928089 BLAST score 670 E value 4.0e-70 Match length 188 % identity NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana] Seq. No. Contig ID 2002 2.R1040 5'-most EST LIB3049-014-Q1-E1-H9 BLASTX Method NCBI GI g3928089 BLAST score 390 E value 2.0e-37 Match length 101 % identity (AC005770) putative osr40 [Arabidopsis thaliana] NCBI Description 2907 Seq. No. Contig ID 2003 1.R1040 5'-most EST LIB3139-094-P1-N1-B6 Method BLASTX NCBI GI q2191150 BLAST score 852 E value 1.0e-149 Match length 355 45 % identity (AF007269) similar to mitochondrial carrier family NCBI Description [Arabidopsis thaliana] 2908 Seq. No. 2003 2.R1040 Contig ID LIB3170-073-Q1-K1-G9 5'-most EST Method BLASTX g2191150 NCBI GI 345 BLAST score 2.0e-32 E value Match length 81 % identity 37 (AF007269) similar to mitochondrial carrier family NCBI Description

[Arabidopsis thaliana]

Seq. No. 2909 Contig ID 2003 3.R1040

5'-most EST LIB3106-090-Q1-K1-C6

Method BLASTX NCBI GI g2191150

```
BLAST score
                   263
                   8.0e-23
E value
                   91
Match length
                   67
% identity
                   (AF007269) similar to mitochondrial carrier family
NCBI Description
                   [Arabidopsis thaliana]
                   2910
Seq. No.
                   2004 1.R1040
Contig ID
                   LIB3030-009-Q1-B1-H9
5'-most EST
                   BLASTX
Method
                   g728867
NCBI GI
                   736
BLAST score
                   1.0e-77
E value
                   325
Match length
% identity
                   44
                   ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR
NCBI Description
                   >gi_99694_pir__S21961 proline-rich protein APG -
                   Arabidopsis thaliana >gi 22599 emb_CAA42925_ (X60377) APG
                   [Arabidopsis thaliana]
                   2911
Seq. No.
                   2005 1.R1040
Contig ID
                   vwf700674514.h1
5'-most EST
                   BLASTX
Method
                   g2583108
NCBI GI
                   218
BLAST score
E value
                   2.0e-17
                   79
Match length
% identity
                   (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                   2912
Seq. No.
                   2005 2.R1040
Contig ID
                   LIB3106-004-Q1-K1-E8
5'-most EST
                   BLASTX
Method
                   g2507093
NCBI GI
BLAST score
                   340
                   3.0e-31
E value
                   154
Match length
                   2
% identity
                   PERIOD CLOCK PROTEIN >gi 1196649 (M12039) ORF starts at 87,
NCBI Description
                   first start codon is found at 210.; putative [Mus musculus]
                   2913
Seq. No.
                   2005 3.R1040
Contig ID
                   LIB3094-048-Q1-K1-H6
5'-most EST
                   BLASTX
Method
                   g2583108
NCBI GI
                   765
BLAST score
                   2.0e-81
E value
Match length
                   233
                   65
% identity
                   (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                   2914
Seq. No.
```

2006 1.R1040

Contig ID

Match length

132

```
5'-most EST
                   eep700870025.hl
Method
                  BLASTX
                   g1707074
NCBI GI
BLAST score
                  316
E value
                   1.0e-28
                   243
Match length
                   33
% identity
                   (U80450) M01E11.2 [Caenorhabditis elegans]
NCBI Description
Seq. No.
                  2915
Contig ID
                  2010 1.R1040
5'-most EST
                  LIB3107-072-Q1-K1-C4
Method
                  BLASTX
                  g4510421
NCBI GI
                  196
BLAST score
                  1.0e-14
E value
                  264
Match length
% identity
                  27
                   (AC006929) unknown protein [Arabidopsis thaliana]
NCBI Description
                  2916
Seq. No.
                  2011 1.R1040
Contig ID
                  LIB3028-050-Q1-B1-C10
5'-most EST
                  2917
Seq. No.
                  2012 1.R1040
Contig ID
5'-most EST
                  LIB3028-050-Q1-B1-C11
Method
                  BLASTX
                  g1888357
NCBI GI
BLAST score
                  444
                  4.0e-44
E value
Match length
                  141
                  58
% identity
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  2918
                  2014 1.R1040
Contig ID
                  jC-gmf102220142c10a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2842480
BLAST score
                  1456
E value
                  1.0e-162
Match length
                  359
% identity
                   (ALO21749) ADP, ATP carrier-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  2919
Seq. No.
                  2014 2.R1040
Contig ID
                  jC-gmle01810061d02a1
5'-most EST
Method
                  BLASTX
                  g2842480
NCBI GI
                  548
BLAST score
                  5.0e-56
E value
```

Method

**BLASTX** 

```
% identity
                   82
                   (ALO21749) ADP, ATP carrier-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   2920
Seq. No.
                   2014 3.R1040
Contig ID
                   uC-gmrominsoy129b01b1
5'-most EST
Method
                   BLASTX
                   g2842480
NCBI GI
BLAST score
                   502
E value
                   8.0e-51
                   134
Match length
                   50
% identity
                   (AL021749) ADP, ATP carrier-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   2921
Seq. No.
                   2014 5.R1040
Contig ID
                   q5688431
5'-most EST
                   BLASTN
Method
                   g1297067
NCBI GI
BLAST score
                   58
E value
                   1.0e-23
                   170
Match length
                   84
% identity
NCBI Description
                   T.turgidum ant gene (1494bp)
                   2922
Seq. No.
                   2016 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{1}39-095-P1-N1-G6 .
                   BLASTX
Method
NCBI GI
                   q2828280
BLAST score
                   651
                   4.0e-68
E value
                   184
Match length
                   70
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2832633_emb_CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
                   2923
Seq. No.
                   2016 3.R1040
Contig ID
                   zsg7\overline{0}1119357.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2828280
BLAST score
                   208
                   1.0e-16
E value
Match length
                   48
                   83
% identity
NCBI Description
                   (AL021687) putative protein [Arabidopsis thaliana]
                   >gi_2832633_emb_CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
                   2924
Seq. No.
                   2017 1.R1040
Contig ID
5'-most EST
                   LIB3106-022-Q1-K1-E10
```

```
NCBI GI
                   g3953473
BLAST score
                   504
                   9.0e-51
E value
                   140
Match length
                   71
% identity
                   (AC002328) F2202.18 [Arabidopsis thaliana]
NCBI Description
                   2925
Seq. No.
                   2017 3.R1040
Contig ID
5'-most EST.
                   LIB3106-043-Q1-K1-F4
Method
                   BLASTX
                   g131194
NCBI GI
BLAST score
                   387
                   3.0e-37
E value
                   89
Match length
                   85
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 72686 pir F1SP5
                   photosystem I chain V precursor - spinach
                   >gi 21299 emb CAA31524 (X13134) PSI subunit V preprotein
                   (AA -69 to 98) [Spinacia oleracea] >gi 226167 prf 1413236B
                   photosystem I reaction center V [Spinacia oleracea]
Seq. No.
                   2926
                   2017 4.R1040
Contig ID
                   LIB3138-010-Q1-N1-H6
5'-most EST
Seq. No.
                   2927
                   2019 1.R1040
Contig ID
                   LIB3028-050-Q1-B1-C8
5'-most EST
Method
                   BLASTX
                   g1076398
NCBI GI
BLAST score
                   186
                   8.0e-14
E value
                   48
Match length
                   73
% identity
                   ribosomal protein L2 - Arabidopsis thaliana
NCBI Description
                   >gi_572523_emb_CAA57902_ (X82556) ribosomal protein L2
                   [Arabidopsis thaliana]
                   2928
Seq. No.
                   2021 1.R1040
Contig ID
5'-most EST
                   LIB3051-012-Q1-E1-H12
Method
                   BLASTX
                   g2498973
NCBI GI
                   288
BLAST score
E value
                   3.0e-25
Match length
                   270
                   31
% identity
                   SURFEIT LOCUS PROTEIN 1 >gi_1362943_pir__ S57749 SURF-1 protein - human >gi_895849_emb_CAA84476_ (Z35093) SURF-1
NCBI Description
                   [Homo sapiens] >gi 4507319 ref NP 003163.1 pSURF1 surfeit
Seq. No.
                   2929
```

2022 1.R1040

LIB3028-049-Q1-B1-H6

Contig ID 5'-most EST

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2930
Seq. No.
                   2024 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400048g07a1
                   2931
Seq. No.
                   2024 2.R1040
Contig ID
5'-most EST
                   jsh7\overline{0}1066682.h1
                   2932
Seq. No.
Contig ID
                   2025_1.R1040
5'-most EST
                   uC-gmrominsoy271f10b1
Method
                   BLASTX
NCBI GI
                   g1362093
BLAST score
                   675
                   1.0e-70
E value
Match length
                   212
                   63
% identity
                   hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                   >gi 924632 (U20595) unknown [Solanum lycopersicum]
                   2933
Seq. No.
                   2025_2.R1040
Contig ID
                   LIB3106-112-Q1-K1-G9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1362093
BLAST score
                   222
E value
                   1.0e-17
Match length
                   100
                   64
% identity
                   hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                   >gi 924632 (U20595) unknown [Solanum lycopersicum]
                   2934
Seq. No.
                   2025 3.R1040
Contig ID
                   awf7\overline{0}0842920.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g924631
                   59
BLAST score
E value
                   2.0e-24
Match length
                   119
                   87
% identity
NCBI Description
                   Solanum lycopersicum predominantly pistil-, sepal-, and
                   fruit-expressed unknown protein mRNA, partial cds
                   2935
Seq. No.
Contig ID
                   2025 4.R1040
5'-most EST
                   uC-gmrominsoy243b12b1
Method
                   BLASTX
NCBI GI
                   g1362093
BLAST score
                   636
E value
                   3.0e-66
Match length
                   163
% identity
                   72
NCBI Description
                   hypothetical protein (clone TPP15) - tomato (fragment)
                   >gi_924632 (U20595) unknown [Solanum lycopersicum]
```

Seq. No.

```
2025 5.R1040
Contig ID
                   LIB3106-049-Q1-K1-G2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g924631
BLAST score
                   51
                   2.0e-19
E value
                   119
Match length
                   86
% identity
NCBI Description
                   Solanum lycopersicum predominantly pistil-, sepal-, and
                   fruit-expressed unknown protein mRNA, partial cds
Seq. No.
                   2937
                   2025 7.R1040
Contig ID
5'-most EST
                   LIB3139-085-P4-N4-F12
                   2938
Seq. No.
                   2028 2.R1040
Contig ID
                   jex7\overline{0}0909111.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1834288
BLAST score
                   149
                   2.0e-09
E value
                   149
Match length
% identity
                   (AB000475) S.pombe TFA2 homolog [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   2939
                   2030 1.R1040
Contig ID
                   jC-gmf102220073c06a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2832625
BLAST score
                   337
                   4.0e-31
E value
                   194
Match length
                   38
% identity
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
                   2940
Seq. No.
                   2030 2.R1040
Contig ID
5'-most EST
                   LIB3039-032-Q1-E1-D4
                   BLASTX
Method
NCBI GI
                   q2832625
BLAST score
                   605
E value
                   1.0e-62 .
Match length
                   257
% identity
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
                   2941
Seq. No.
Contig ID
                   2032 1.R1040
                   LIB3028-049-Q1-B1-H11
5'-most EST
                   2942
Seq. No.
Contig ID
                   2034 1.R1040
                  LIB3106-060-Q1-K1-F3
5'-most EST
```

Seq. No.

```
Contig ID
                   2035 1.R1040
5'-most EST
                   g5688044
                   BLASTN
Method
NCBI GI
                   g2564046
BLAST score
                   37
                   7.0e-11
E value
                   269
Match length
                   86
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MGI19, complete sequence [Arabidopsis thaliana]
                   2944
Seq. No.
Contig ID
                   2035 2.R1040
5'-most EST
                   LIB3028-010-Q1-B1-G3
                   BLASTN
Method
NCBI GI
                   g2564046
BLAST score
                   37
E value
                   5.0e-11
Match length
                   150
                   90
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MGI19, complete sequence [Arabidopsis thaliana]
                   2945
Seq. No.
                   2037 1.R1040
Contig ID
                   LIB3051-104-Q1-K1-H3
5'-most EST
Method
                   BLASTX
                   g1841355
NCBI GI
                   411
BLAST score
                   8.0e-40
E value
                   91
Match length
                   79
% identity
                   (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
                   2946
Seq. No.
Contig ID
                   2037 2.R1040
5'-most EST
                   ncj700983001.hl
Method
                   BLASTX
                   g1841355
NCBI GI
BLAST score
                   173
E value
                   3.0e-12
Match length
                   48
                   69
% identity
                   (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   2947
                   2038 1.R1040
Contig ID
5'-most EST
                   has700548129.h1
Method
                   BLASTX
NCBI GI
                   q4063747
BLAST score
                   595
E value
                   2.0e-61
Match length
                   143
% identity
NCBI Description
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
```

```
2948
Seq. No.
                   2040 1.R1040
Contig ID
                   LIB3028-020-Q1-B1-A1
5'-most EST
Method
                   BLASTX
                   g419963
NCBI GI
BLAST score
                   285
                   4.0e-25
E value
                   85
Match length
                   59
% identity
                   snRNP protein B - fruit fly (Drosophila melanogaster)
NCBI Description
                   >gi 290272 (L02919) ribonucleoprotein [Drosophila
                   melanogaster]
                   2949
Seq. No.
                   2040 2.R1040
Contig ID
5'-most EST
                   g4397638
                   BLASTN
Method
NCBI GI
                   g3510341
BLAST score
                   46
                   1.0e-16
E value
Match length
                   114
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MFC16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   2950
                   2042 1.R1040
Contig ID
                   LIB3039-014-Q1-E1-A3
5'-most EST
                   BLASTX
Method
                   g2565429
NCBI GI
BLAST score
                   144
                   1.0e-08
E value
Match length
                   36
                   75
% identity
                   (AF027686) glycine-rich protein [Onobrychis viciifolia]
NCBI Description
Seq. No.
                   2951
                   2042 2.R1040
Contig ID
5'-most EST
                   LIB3039-035-Q1-E1-H4
Method
                   BLASTX
NCBI GI
                   g2565429
BLAST score
                   150
E value
                   2.0e-09
Match length
                   61
                   49
% identity
                   (AF027686) glycine-rich protein [Onobrychis viciifolia]
NCBI Description
                   2952
Seq. No.
                   2043 1.R1040
Contig ID
                   uC-gmropic027h11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1706130
BLAST score
                   830
                   6.0e-89
E value
                   189
Match length
```

% identity

BLAST score

E value

192 2.0e-14

```
NCBI Description CDPK-RELATED PROTEIN KINASE (PK421) >gi 2129917 pir S60052
                   calcium-dependent protein kinase homolog - carrot
                   >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein
                   kinase [Daucus carota]
                   2953
Seq. No.
                   2043 2.R1040
Contig ID
                   fC-g\overline{m}st700895016d3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1706130
BLAST score
                   228
                   1.0e-18
E value
Match length
                   49
                   86
% identity
                   CDPK-RELATED PROTEIN KINASE (PK421) >gi 2129917 pir S60052
NCBI Description
                   calcium-dependent protein kinase homolog - carrot
                   >gi 1103386_emb_CAA58750_ (X83869) CDPK-related protein
                   kinase [Daucus carota]
                  2954
Seq. No.
Contig ID
                   2044 1.R1040
5'-most EST
                   jC-gmf102220137h06a1
                   2955
Seq. No.
Contig ID
                   2044_2.R1040
5'-most EST
                   uC-gmropic100g07b1
                   2956
Seq. No.
Contig ID
                   2045 1.R1040
5'-most EST
                   LIB3028-049-Q1-B1-G9
                   BLASTX
Method
NCBI GI
                   g2651310
BLAST score
                   434
                   7.0e-43
E value
Match length
                   111
% identity
                   (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
                   2957
Seq. No.
                   2046 1.R1040
Contig ID
5'-most EST
                   qsv7\overline{0}1052103.h1
Method
                   BLASTX
NCBI GI
                   g4455280
BLAST score
                   468
                   1.0e-46
E value
Match length
                   106
                   70
% identity
                   (AL035527) putative protein [Arabidopsis thaliana]
NCBI Description
                   2958
Seq. No.
                   2047 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400041q03a1
Method
                   BLASTX
                   g2760325
NCBI GI
```

E value

```
118
Match length
                   44
% identity
                   (AC002130) F1N21.10 [Arabidopsis thaliana]
NCBI Description
                   2959
Seq. No.
                   2047 2.R1040
Contig ID
                   LIB3170-047-Q1-J1-A2
5'-most EST
                   BLASTX
Method
                   g2648692
NCBI GI
                   160
BLAST score
                   2.0e-10
E value
                   262
Match length
                   28
% identity
                   (AE000975) NADH oxidase (noxA-5) [Archaeoglobus fulgidus]
NCBI Description
Seq. No.
                   2960
                   2047 3.R1040
Contig ID
                   pcp700995722.hl
5'-most EST
                   2961
Seq. No.
                   2047 4.R1040
Contig ID
5'-most EST
                   jC-gmro02910067h12a1
                   2962
Seq. No.
                   2048 1.R1040
Contig ID
5'-most EST
                   LIB3028-049-Q1-B1-E5
Method
                   BLASTX
NCBI GI
                   g3377517
BLAST score
                   346
                   2.0e-32
E value
                   149
Match length
% identity
                   (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
NCBI Description
                   2963
Seq. No.
                   2050 1.R1040
Contig ID
5'-most EST
                   LIB3028-049-Q1-B1-E8
                   2964
Seq. No.
                   2051 1.R1040
Contig ID
                   dpv7\overline{0}1101734.h1
5'-most EST
                   BLASTX
Method
                   g4262236
NCBI GI
                   830
BLAST score
                   4.0e-92
E value
                   256
Match length
                   66
% identity
NCBI Description
                   (AC006200) putative ribose 5-phosphate isomerase
                   [Arabidopsis thaliana]
                   2965
Seq. No.
                   2051 2.R1040
Contig ID
                   jC-gmle01810073a01a1
5'-most EST
Method
                   BLASTX
                   g4262236
NCBI GI
BLAST score
                   362
```

3.0e-34

Method

NCBI GI

BLASTX

g2232254

```
106
Match length
                   73
% identity
                   (AC006200) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
                   2966
Seq. No.
                   2053 1.R1040
Contig ID
5'-most EST
                   LIB3072-021-Q1-E1-B12
Seq. No.
                   2967
                   2053 2.R1040
Contig ID
5'-most EST
                   LIB3050-003-Q1-E1-B7
                   2968
Seq. No.
                   2054 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy244e12b1
Method
                   BLASTN
NCBI GI
                   q4159704
                   50
BLAST score
                   8.0e-19
E value
Match length
                   320
% identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MCB17, complete sequence [Arabidopsis thaliana]
                   2969
Seq. No.
Contig ID
                   2054 2.R1040
5'-most EST
                   LIB3028-049-Q1-B1-F11
Method
                   BLASTN
                   g4159704
NCBI GI
BLAST score
                   50
E value
                   6.0e-19
Match length
                   187
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MCB17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   2970
                   2054 3.R1040
Contig ID
                   1eu7\overline{0}1152121.h1
5'-most EST
                  2971
Seq. No.
Contig ID
                   2055 1.R1040
5'-most EST
                   LIB3.092-041-Q1-K1-G3
                   BLASTX
Method
NCBI GI
                   g1854443
BLAST score
                   1598
E value
                   1.0e-179
Match length
                   376
% identity
                   (D83970) CPRD8 protein [Vigna unguiculata]
NCBI Description
                   2972
Seq. No.
                   2055 2.R1040
Contig ID
                  LIB3051-068-Q1-K1-A4
5'-most EST
```

```
BLAST score
                   553
                   8.0e-57
E value
Match length
                   125
                   ·82
 % identity
                    (AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
NCBI Description
                   2973
 Seq. No.
                   2055 4.R1040
Contig ID
                   uC-gmrominsoy113c06b1
 5'-most EST
                   BLASTX
Method
                   g1854443
NCBI GI
BLAST score
                   433
                   6.0e-48
E value
                   111
Match length
 % identity
                   85
                   (D83970) CPRD8 protein [Vigna unguiculata]
NCBI Description
Seq. No.
                   2974
                   2056 1.R1040
Contig ID
                   LIB3051-018-Q1-E1-G2
5'-most EST
                   2975
Seq. No.
Contig ID
                   2058 1.R1040
5'-most EST
                   LIB3106-010-Q1-K1-D7
                   BLASTX
Method
                   g1710424
NCBI GI
BLAST score
                   455
E value
                   5.0e-45
                   199
Match length
                   52
% identity
                   50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
NCBI Description
                   >gi 2129718 pir S71282 ribosomal protein L21 - Arabidopsis
                   thaliana >gi 1149573 emb CAA89887 (Z49787) chloroplast
                   ribosomal large subunit protein L21 [Arabidopsis thaliana]
                   2976
Seq. No.
                   2059 1.R1040
· Contig ID
5'-most EST
                   k117\overline{0}1214615.h1
Method
                   BLASTX
                   g2982463
NCBI GI
                   843
BLAST score
                   1.0e-90
E value
                   209
Match length
% identity
                   78
                    (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   2977
Seq. No.
                   2059 2.R1040
Contig ID
                   LIB3028-018-Q1-B1-H10
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g2982463
BLAST score
                   237
E value
                   8.0e-20
Match length
                   86
% identity
                   58
```

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

```
2978
Seq. No.
                   2059 3.R1040
Contig ID
                   txt700734209.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2982463
BLAST score
                   146
                   2.0e-09
E value
                   37
Match length
                   76
% identity
NCBI Description
                   (AL022223) putative protein [Arabidopsis thaliana]
                   2979
Seq. No.
Contig ID
                   2060 1.R1040
5'-most EST
                   LIB3109-014-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   q4580397
                   498
BLAST score
                   3.0e-50
E value
                   204
Match length
                   50
% identity
                   (AC007171) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
                   2980
Seq. No.
                   2061 1.R1040
Contig ID
5'-most EST
                   zhf700962048.h1
                   2981
Seq. No.
                   2061 3.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1156542.h1
                   BLASTN
Method
NCBI GI
                   g1924955
BLAST score
                   57
E value
                   2.0e-23
Match length
                   57
                   100
% identity
NCBI Description
                   L.luteus 5S rRNA gene
Seq. No.
                   2982
Contig ID
                   2061 5.R1040
                   zhf700954372.h1
5'-most EST
                   2983
Seq. No.
Contig ID
                   2061 6.R1040
5'-most EST
                   jC-gmst02400040c11a1
                   2984
Seq. No.
Contig ID
                   2063_1.R1040
5'-most EST
                   fC-gmf1700905086f4
Method
                   BLASTX
                   g2598587
NCBI GI
BLAST score
                   2091
                   0.0e + 00
E value
Match length
                   464
% identity
                   80
                   (Y15366) cycloartenol synthase [Medicago truncatula]
NCBI Description
```

Seq. No.

5'-most EST

```
Contig ID
                   2065 1.R1040
5'-most EST
                   LIB3028-048-Q1-B1-F7
                   2986
Seq. No.
Contig ID
                   2068 1.R1040
5'-most EST
                   LIB3028-049-Q1-B1-D7
                   2987
Seq. No.
                   2069 1.R1040
Contig ID
                   sat701009654.h1
5'-most EST
                   2988
Seq. No.
Contig ID
                   2070 1.R1040
5'-most EST
                   g5510085
                   2989
Seq. No.
                   2070 2.R1040
Contig ID
5'-most EST
                   g4396899
Method
                   BLASTX
NCBI GI
                   g2583123
BLAST score
                   525
                   2.0e-53
E value
Match length
                   145
% identity
NCBI Description
                   (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                   thaliana]
                   2990
Seq. No.
                   2073 1.R1040
Contig ID
5'-most EST
                   LIB3028-039-Q1-B2-C1
                   2991
Seq. No.
                   2074 1.R1040
Contig ID
5'-most EST
                   LIB3028-049-Q1-B1-B4
Method
                   BLASTX
NCBI GI
                   g4468979
BLAST score
                   590
E value
                   9.0e-61
Match length
                   243
% identity
                   55
NCBI Description
                   (AL035605) putative protein [Arabidopsis thaliana]
                   2992
Seq. No.
                   2074 2.R1040
Contig ID
                   fua701041905.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4468979
BLAST score
                   416
E value
                   7.0e-41
Match length
                   86
                   90
% identity
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   2993
Seq. No.
                   2075 1.R1040
Contig ID
```

LIB3028-049-Q1-B1-B5

Match length

225

```
2994
Seq. No.
                   2076 1.R1040
Contig ID
                   vzy700751843.hl
5'-most EST
                   BLASTX
Method
                   g3136057
NCBI GI
                   199
BLAST score
                   3.0e-15
E value
                   138
Match length
                   39
% identity
NCBI Description
                   (AL023592) actin-like protein [Schizosaccharomyces pombe]
                   2995
Seq. No.
                   2077 1.R1040
Contig ID
                   LIB3028-049-Q1-B1-B8
5'-most EST
Method
                   BLASTN
                   g1431738
NCBI GI
                   56
BLAST score
                   2.0e-22
E value
Match length
                   168
                   88
% identity
                   Soybean (Glycine max) low MW heat shock protein gene
NCBI Description
                   (Gmhsp17.5-M)
                   2996
Seq. No.
Contig ID
                   2078 1.R1040
5'-most EST
                   LIB3028-049-Q1-B1-C10
Method
                   BLASTX
NCBI GI
                   g4204793
BLAST score
                   693
                   3.0e-73
E value
Match length
                   152
                   43
% identity
                   (U52079) P-glycoprotein [Solanum tuberosum]
NCBI Description
                   2997
Seq. No.
Contig ID
                   2079 1.R1040
5'-most EST
                   LIB3028-049-Q1-B1-C11
                   2998
Seq. No.
                   2080 1.R1040
Contig ID
5'-most EST
                   hrw701062141.h1
                   BLASTX
Method
NCBI GI
                   g2894599
BLAST score
                   800
E value
                   3.0e-85
Match length
                   229
                   69
% identity
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                   2999
Seq. No.
Contig ID
                   2080 2.R1040
                  bth700846937.hl
5'-most EST
Method
                  BLASTX
                   g2894599
NCBI GI
BLAST score
                  822
                   8.0e-88
E value
```

NCBI Description

```
% identity
                   71
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                   3000
                   2080 3.R1040
Contig ID
                   LIB3051-086-Q1-K1-A10 .
5'-most EST
Method
                   BLASTX
                   g2894599
NCBI GI
                   539
BLAST score
                   4.0e-55
E value
                   120
Match length
% identity
                   80
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3001
Contig ID
                   2080 4.R1040
5'-most EST
                   g4396557
Method
                   BLASTX
NCBI GI
                   g2894599
BLAST score
                   295
                   1.0e-26
E value
Match length
                   63
% identity
                   78
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   3002
Seq. No.
                   2080 9.R1040
Contig ID
5'-most EST
                   jex700909422.hl
Method
                  BLASTX
                  g2894599
NCBI GI
                   298
BLAST score
                   4.0e-27
E value
Match length
                   65
% identity
                   78
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   3003
Seq. No.
                   2080 10.R1040
Contig ID
                   zsg701127602.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2894599
BLAST score
                   279
                   4.0e-25
E value
Match length
                   58
                  81
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   3004
Seq. No.
                   2082 1.R1040
Contig ID
                   leu701151978.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3819099
BLAST score
                  1152
                   1.0e-126
E value
Match length
                  264
% identity
                  77
```

(AJ009825) copper amine oxidase [Cicer arietinum]

```
3005
Seq. No.
 Contig ID
                    2083 1.R1040
 5'-most EST
                    hyd700724953.hl
                    BLASTX
 Method
                    g3292814
 NCBI GI
 BLAST score
                    1095
                    1.0e-120
 E value
 Match length
                    317
 % identity
                    70
                    (AL031018) putative protein [Arabidopsis thaliana]
 NCBI Description
                    3006
 Seq. No.
                    2083 2.R1040
 Contig ID
 5'-most EST
                    LIB3138-059-Q1-N1-C8
 Method
                    BLASTX
                    g3292814
 NCBI GI
 BLAST score
                    452
                    6.0e-45
 E value
 Match length
                    128
                    70
 % identity
                    (AL031018) putative protein [Arabidopsis thaliana]
 NCBI Description
                    3007
 Seq. No.
                    2083 3.R1040
 Contig ID
                    LIB3028-049-Q1-B1-B3
 5'-most EST
 Seq. No.
                    3008
 Contig ID
                    2083 4.R1040
 5'-most EST
                    q5606500
 Method
                    BLASTX
 NCBI GI
                    q3292814
 BLAST score
                    316
                    4.0e-29
 E value
                    94
 Match length
                    68 .
 % identity
                    (AL031018) putative protein [Arabidopsis thaliana]
 NCBI Description
                    3009
 Seq. No.
                    2085 1.R1040
 Contig ID
                    k117\overline{0}1203522.h2
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g4457221
 BLAST score
                    372
                    5.0e-35
 E value
 Match length
                    161
                    56
 % identity
                    (AF127797) putative bZIP DNA-binding protein [Capsicum
 NCBI Description
                    chinense]
                    3010
 Seq. No.
                    2085 2.R1040
 Contig ID
                    LIB3087-011-Q1-K1-C12
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g4457221
 BLAST score
                    361
```

7.0e-34

E value

NCBI Description

```
Match length
                   98
                   77
% identity
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
NCBI Description
                   chinense]
                   3011
Seq. No.
                   2085 3.R1040
Contig ID
                   LIB3049-006-Q1-E1-A5
5'-most EST
Method
                   BLASTX
                   g4457221
NCBI GI
BLAST score
                   385
                   1.0e-36
E value
                   101
Match length
% identity
                   77
NCBI Description
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
                   chinense]
Seq. No.
                   3012
                   2085 4.R1040
Contig ID
5'-most EST
                   LIB3093-008-Q1-K1-F4
                   3013
Seq. No.
                   2085 5.R1040
Contig ID
5'-most EST
                   jC-gmst02400047b01d1
                   3014
Seq. No.
                   2087 1.R1040
Contig ID
                   jC-gmro02800040d02a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2190542
BLAST score
                   573
                   5.0e-59
E value
Match length
                   211
% identity
                   (AC001229) F5I14.5 gene product [Arabidopsis thaliana]
NCBI Description
                   3015
Seq. No.
Contig ID
                   2089 1.R1040
5'-most EST
                   vzy700750788.hl
Method
                   BLASTX
NCBI GI
                   g3158476
BLAST score
                   1232
                   1.0e-136
E value
                   285
Match length
                   82
% identity
                   (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                   3016
Seq. No.
                   2089 2.R1040
Contig ID
5'-most EST
                  LIB3050-014-Q1-E1-H4
Method
                   BLASTX
NCBI GI
                   q3158476
BLAST score
                   628
E value
                   1.0e-65
Match length
                  145
% identity
```

(AF067185) aquaporin 2 [Samanea saman]

BLAST score

E value

1913 0.0e+00

```
3017
Seq. No.
Contig ID
                   2094 1.R1040
5'-most EST
                   LIB3093-001-Q1-K1-E6
Method
                   BLASTX
                   g3608137
NCBI GI
BLAST score
                   660
                   1.0e-68
E value
                   333
Match length
                  .43
% identity
                   (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3018
Seq. No.
                   2094 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910037h07d1
                   3019
Seq. No.
Contig ID
                   2095 1.R1040
                   sat701009411.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4263722
BLAST score
                   1724
E value
                   0.0e+00
Match length
                   635
% identity
                   (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3020
Contig ID
                   2096 1.R1040
                   fC-gmro700865146f1
5'-most EST
Method
                   BLASTN
                  g3641864
NCBI GI
                   260
BLAST score
                   1.0e-144
E value
Match length
                  697
                  84
% identity
                  Cicer arietinum mRNA for beta-galactosidase, clone
NCBI Description
                  CanBGal-4
                   3021
Seq. No.
Contig ID
                   2096 2.R1040
                   zhf700955904.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3126969
BLAST score
                   729
                   4.0e-77
E value
                  223
Match length
% identity
NCBI Description
                   (AF061808) chalcone isomerase [Elaeagnus umbellata]
                  3022
Seq. No.
Contig ID
                  2096 3.R1040
                  uC-gmflminsoy003e05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3641863
```

NCBI GI

```
496
Match length
                   75
% identity
                   (AJ005042) beta-galactosidase [Cicer arietinum]
NCBI Description
                   3023
Seq. No.
                   2096 4.R1040
Contig ID
                   uC-gmflminsoy001a11b1
5'-most EST
                   BLASTX
Method
                   g3860420
NCBI GI
BLAST score
                   1813
                   0.0e+00
E value
Match length
                   383
                   84
% identity
                   (AJ011047) exo galactanase [Lupinus angustifolius]
NCBI Description
Seq. No.
                   3024
Contig ID
                   2096 5.R1040
5'-most EST
                   uC-gmflminsoy034h12b1
                   3025
Seq. No.
                   2096 6.R1040
Contig ID
5'-most EST
                   LIB3072-052-Q1-E1-D10
Method
                   BLASTN
                   g3860419
NCBI GI
                   65
BLAST score
E value
                   6.0e-28
Match length
                   117
% identity
                   90
                   Lupinus angustifolius mRNA for exo galactanase
NCBI Description
                   3026
Seq. No.
                   2096 8.R1040
Contig ID
                   sat7\overline{0}1007604.h1
5'-most EST
                   BLASTN
Method
                   g3860419
NCBI GI
BLAST score
                   119
E value
                   3.0e-60
Match length
                   199
                   90
% identity
                   Lupinus angustifolius mRNA for exo galactanase
NCBI Description
                   3027
Seq. No.
Contig. ID
                   2097 1.R1040
5'-most EST
                   LIB3028-048-Q1-B1-G12
                   BLASTX
Method
                   g2760326
NCBI GI
BLAST score
                   1178
E value
                   1.0e-129
                   531
Match length
                   46
% identity
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                   3028
Seq. No.
Contig ID
                   2097 2.R1040
5'-most EST
                   g5676937
Method
                   BLASTX
```

g2760326

```
BLAST score
                   130
                   5.0e-12
E value
Match length
                   73
% identity
                   55
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                   3029
Seq. No.
                   2097 4.R1040
Contig ID
                   zhf700953819.h1
5'-most EST
                   BLASTX
Method
                   g2760326
NCBI GI
BLAST score
                   176
                   1.0e-12
E value
Match length
                   100
% identity
                   40
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3030
                   2098 1.R1040
Contig ID
                   fC-gmse700674243f2
5'-most EST
Method
                   BLASTX
                   g4056500
NCBI GI
BLAST score
                   165
                   3.0e-11
E value
                   52
Match length
% identity
                   (AC005896) putative acetyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   3031
Seq. No.
                   2098 2.R1040
Contig ID
                   LIB3028-048-Q1-B1-G3
5'-most EST
                   BLASTX
Method
                   g1653293
NCBI GI
                   175
BLAST score
                   1.0e-22
E value
                   96
Match length
                   59
% identity
                   (D90912) ornithine acetyltransferase [Synechocystis sp.]
NCBI Description
                   3032
Seq. No.
                   2099 1.R1040
Contig ID
                   vwf700675854.h1
5'-most EST
                   3033
Seq. No.
                   2100 1.R1040
Contig ID
                   zhf700957066.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g516248
BLAST score
                   146
E value
                   4.0e-76
Match length
                   310
                   87
% identity
                   A.thaliana gene for porphobilinogen deaminase
NCBI Description
Seq. No.
                   3034
```

2100 2.R1040

Contig ID

```
jC-gmro02800036a04d1
5'-most EST
                   BLASTN
Method
                   g516248
NCBI GI
                   97
BLAST score
                   4.0e-47
E value
Match length
                   177
                   89
% identity
                   A.thaliana gene for porphobilinogen deaminase
NCBI Description
                   3035
Seq. No.
                   2102 1.R1040
Contig ID
                   LIB3049-042-Q1-E1-A8
5'-most EST
                   3036
Seq. No.
                   2102 2.R1040
Contig ID
                   LIB3049-004-Q1-E1-G5
5'-most EST
                   3037 .
Seq. No.
                   2103 1.R1040
Contig ID
                   LIB3093-029-Q1-K1-E5
5'-most EST
                   BLASTN
Method
                   g3928149
NCBI GI
BLAST score
                   412
                   0.0e+00
E value
Match length
                   852
                   87
% identity
                   Cicer arietinum mRNA for hypothetical protein
NCBI Description
                   3038
Seq. No.
                   2103 2.R1040
Contig ID
                   uC-gmropic028g12b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3928150
                   230
BLAST score
                   2.0e-40
E value
                   124
Match length
                   72
% identity
                   (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                   3039
Seq. No.
                   2103 3.R1040
Contig ID
                   k117\overline{0}1203849.h1
5'-most EST
                   BLASTN
Method
                   g3928149
NCBI GI
                   69
BLAST score
                   1.0e-30
E value
                   197
Match length
                   84
% identity
                   Cicer arietinum mRNA for hypothetical protein
NCBI Description
                   3040
Seq. No.
                   2105 1.R1040
Contig ID
                   txt7\overline{0}0735241.h1
5'-most EST
                   BLASTX
Method
                   g3641837
NCBI GI
                   1027
BLAST score
```

0.0e+00

E value

```
Match length
                   550
% identity
                   86
NCBI Description
                   (AL023094) Nonclathrin coat protein gamma - like protein
                   [Arabidopsis thaliana]
                   3041
Seq. No.
Contig ID
                   2105 4.R1040
                   hrw701058021.hl
5'-most EST
Method
                   BLASTX
                   g3641837
NCBI GI
BLAST score
                   262
E value
                   6.0e-23
Match length
                   55
% identity
                   91
                   (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   3042
Contig ID
                   2106 1.R1040
5'-most EST
                   LIB3109-014-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g4539001
BLAST score
                   1288
E value
                   1.0e-142
Match length
                   318
% identity
                   (AL049481) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3043
                   2109 1.R1040
Contig ID
                   zhf700961869.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2160165
BLAST score
                   220
E value
                   9.0e-18
Match length
                   69
% identity
                   59
                   (AC000132) F21M12.11 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3044
Contig ID
                   2110 1.R1040
                   uC-gmropic080d08b1
5'-most EST
Method
                   BLASTX
                   q2894598
NCBI GI
BLAST score
                   625
                   1.0e-102
E value
                   335
Match length
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   3045
Seq. No.
                   2111 1.R1040
Contig ID
                   epx701109255.h1
5'-most EST
                   3046
Seq. No.
                   2112 1.R1040
Contig ID
```

zzp700833245.hl

5'-most EST

BLAST score

E value

195 1.0e-14

```
Method
                   BLASTX
                   g3377850
NCBI GI
BLAST score
                   325
                   9.0e-30
E value
Match length
                   133
% identity
                   72
                   (AF076274) contains simlarity to Canis familiaris signal
NCBI Description
                   peptidase complex 25 kDa subunit (GB:U12687) [Arabidopsis
                   thaliana]
                   3047
Seq. No.
Contig ID
                   2113 1.R1040
                   LIB3109-038-Q1-K1-B10
5'-most EST
Method
                   BLASTX
NCBI GI
                   q549010
BLAST score
                   1992
E value
                   0.0e + 00
Match length
                   433
% identity
                   89
                   EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)
NCBI Description
                   (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)
                   >gi 322554 pir S31328 omnipotent suppressor protein SUP1
                   homolog (clone G18) - Arabidopsis thaliana
                   >gi_16514_emb_CAA49172_ (X69375) similar to yeast
                   omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis
                   thaliana] >gi 1402882_emb_CAA66813_ (X98130) eukaryotic
                   early release factor subunit 1-like protein [Arabidopsis
                   thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3
                   [Arabidopsis thaliana]
                   3048
Seq. No.
                   2113 3.R1040
Contig ID
                   trc700563986.hl
5'-most EST
                   3049
Seq. No.
                   2116 1.R1040
Contig ID
                   LIB3139-098-P1-N1-G1
5'-most EST
Seq. No.
                   3050
Contig ID
                   2119 1.R1040
·5'-most EST
                   uC-qmflminsoy063c12b1
                   BLASTX
Method
                   g2435522
NCBI GI
BLAST score
                   1333
                   1.0e-147
E value
                   388
Match length
                   64
% identity
                   (AF024504) contains similarity to other AMP-binding enzymes
NCBI Description
                   [Arabidopsis thaliana]
                   3051
Seq. No.
                   2119 2.R1040
Contig ID
                   uC-gmropic010b07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1903034
```

NCBI Description

```
94
Match length
% identity
                   43
                   (X94625) amp-binding protein [Brassica napus]
NCBI Description
                   3052
Seq. No.
                   2120 1.R1040
Contig ID
                   jC-gmst02400060f04a1
5'-most EST
                   3053
Seq. No.
                   2120 2.R1040
Contig ID
                   uC-gmflminsoy028d12b1
5'-most EST
                   BLASTX
Method
                   g3063710
NCBI GI
                   208
BLAST score
                   3.0e-16
E value
                   150
Match length
                   37
% identity
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   3054
Seq. No.
                   2123 1.R1040
Contig ID
                   zsg7\overline{0}1123264.h1
5'-most EST
                   BLASTX
Method
                   g3319340
NCBI GI
BLAST score
                   231
                   5.0e-19
E value
Match length
                   91
                   54
% identity
                   (AF077407) contains similarity to E. coli cation transport
NCBI Description
                   protein ChaC (GB:D90756) [Arabidopsis thaliana]
                   3055
Seq. No.
                   2125 1.R1040
Contig ID
                   uC-gmflminsoy078e04b1
5'-most EST
                   3056
Seq. No.
                   2126 1.R1040
Contig ID
5'-most EST
                   LIB3028-048-Q1-B1-D9
Method
                   BLASTX
                   q3513738
NCBI GI
                   149
BLAST score
                   2.0e-09
E value
Match length
                   37
% identity
                   (AF080118) similar to the GDSL family of lipolytic enzymes
NCBI Description
                   [Arabidopsis thaliana]
                   3057
Seq. No.
                   2131_1.R1040
Contig ID
5'-most EST
                   LIB3087-009-Q1-K1-E1
Method
                   BLASTX
                   g2618721
NCBI GI
BLAST score
                   716
E value
                   2.0e-75
Match length
                   231
% identity
                   67
```

(U49072) IAA16 [Arabidopsis thaliana]

```
3058
Seq. No.
                   2131 2.R1040
Contig ID
                  LIB3039-034-Q1-E1-F1
5'-most EST
                  BLASTX
Method
                   g114734
NCBI GI
BLAST score
                   655 .
                   2.0e-68
E value
                   226
Match length
                   65
% identity
                  AUXIN-INDUCED PROTEIN AUX28 >gi 81759 pir A28993 aux28
NCBI Description
                  protein - soybean >gi 169921 (J03919) auxin-regulated
                  protein (Aux28) [Glycine max]
                   3059
Seq. No.
                   2131 3.R1040
Contig ID
                  LIB3107-066-Q1-K1-D4
5'-most EST
Method
                  BLASTX
                  q2618721
NCBI GI
                   660
BLAST score
                   6.0e-69
E value
Match length
                  234
                   61
% identity
                   (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                   3060
Seq. No.
                   2131 4.R1040
Contig ID
                   sat7\overline{0}1006155.h1
5'-most EST
Method
                  BLASTX
                  g2618721
NCBI GI
BLAST score
                   116
                   1.0e-08
E value
Match length
                  69
% identity
                   (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                   3061
Seq. No.
Contig ID
                  .2132 1.R1040
                  LIB3028-048-Q1-B1-C8
5'-most EST
                  BLASTX
Method
                  g2352492
NCBI GI
BLAST score
                   488
                   6.0e-49
E value
Match length
                  115
                   78
% identity
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
                   3062
Seq. No.
                   2132 2.R1040
Contig ID
                  uC-gmrominsoy125g04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2352492
                   329
BLAST score
                  2.0e-30
E value
```

Match length

Method

NCBI GI

BLASTX q2495179

```
% identity
NCBI Description
                   (AF005047) transport inhibitor response 1 [Arabidopsis
                   thaliana] >gi 2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
Seq. No.
                   3063
Contig ID
                   2134 1.R1040
                   LIB3139-039-P1-N1-H4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2947062
BLAST score
                   550
E value
                   8.0e-56
Match length
                   534
                   35
% identity
NCBI Description
                   (AC002521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   3064
Contig ID
                   2134 2.R1040
5'-most EST
                   uC-gmropic083d02b1
Seq. No.
                   3065
Contig ID
                   2134 3.R1040
5'-most EST
                   pmv700894820.h1
Seq. No.
                   3066
Contig ID
                   2135 1.R1040
5'-most EST
                   LIB3167-023-P4-K4-B8
Method
                   BLASTX
NCBI GI
                   g2495180
BLAST score
                   1073
E value
                   1.0e-117
Match length
                   251
% identity
                   84
NCBI Description
                   PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
                   (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                   SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane
                   synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278
                   hydroxymethylbilane synthase (EC 4.3.1.8) precursor -
                   garden pea chloroplast >gi 313724 emb CAA51820 (X73418)
                   hydroxymethylbilane synthase [Pisum sativum]
Seq. No.
                   3067
Contig ID
                   2135 2.R1040
                   LIB3028-048-Q1-B1-D10
5'-most EST
Method
                   BLASTN
                   g313723
NCBI GI
BLAST score
                   134
                   3.0e-69
E value
Match length
                   322
% identity
                   P.sativum hemC mRNA for hydroxymethylbilane synthase
NCBI Description
Seq. No.
                   3068
                   2135 5.R1040
Contig ID
                   qsv701054125.hl
5'-most EST
```

4

```
268
BLAST score
                  1.0e-37
E value
                  146
Match length
% identity
                  79
NCBI Description
                  PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
                  (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                  SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane
                  synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana
                  >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane
                  synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_
                  (X73839) hydroxymethylbilane synthase [Arabidopsis
                  thaliana]
                  3069
Seq. No.
                  2135 6.R1040
Contig ID
                  ncj700975534.h1
5'-most EST
Method
                  BLASTX
                  g2495180
NCBI GI
BLAST score
                  271
                  5.0e-36
E value
Match length
                  89
                  90
% identity
                  PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
NCBI Description
                  (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                  SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane
                  synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278
                  hydroxymethylbilane synthase (EC 4.3.1.8) precursor -
                  garden pea chloroplast >gi 313724 emb CAA51820 (X73418)
                  hydroxymethylbilane synthase [Pisum sativum]
                  3070
Seq. No.
Contig ID
                  2136 1.R1040
                  LIB3138-022-Q1-N1-D5
5'-most EST
                  BLASTN
Method
                  g1381085
NCBI GI
BLAST score
                  322
E value
                  0.0e + 00
Match length
                  578
                  89
% identity
                  Pisum sativum imidazoleglycerol-phosphate dehydratase
NCBI Description
                  (PSHIS3) mRNA, complete cds
Seq. No.
                  3071
                  2137 1.R1040
Contig ID
5'-most EST
                  LIB3028-048-Q1-B1-D12
                  3072
Seq. No.
Contig ID
                  2138_1.R1040
5'-most EST
                  LIB3093-027-Q1-K1-B1
Method
                  BLASTN
                  g3885514
NCBI GI
BLAST score
                  178
E value
                  3.0e-95
Match length
                  334
% identity
                  88
```

NCBI Description Medicago sativa clone MS56 unknown mRNA

```
Seq. No.
                   3073
                   2138 2.R1040
Contig ID
5'-most EST
                   LIB3040-036-Q1-E1-A7
Method
                   BLASTN
                   g3885514
NCBI GI
                   189
BLAST score
E value
                   1.0e-102
Match length
                   369
                   88
% identity
                   Medicago sativa clone MS56 unknown mRNA
NCBI Description
Seq. No.
                   3074
                   2138 4.R1040
Contig ID
                   asn701132221.h2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3885514
                   86
BLAST score
E value
                   2.0e-40
                   186
Match length
                   87
% identity
NCBI Description Medicago sativa clone MS56 unknown mRNA
Seq. No.
                   3075
                   2138 5.R1040
Contig ID
                   LIB3040-018-Q1-E1-H12
5'-most EST
Method
                   BLASTN
                   g3885514
NCBI GI
BLAST score
                   163
E value
                   2.0e-86
Match length
                   311
                   88
% identity
                   Medicago sativa clone MS56 unknown mRNA
NCBI Description
Seq. No.
                   3076
                   2139 1.R1040
Contig ID
5'-most EST
                   LIB3028-048-Q1-B1-D3
Method
                   BLASTX
NCBI GI
                   g4371290
BLAST score
                   512
E value
                   1.0e-51
Match length
                   190
% identity
                   (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3077
Seq. No.
                   2139 2.R1040
Contig ID
                   LIB3049-051-Q1-E1-B8
5'-most EST
Method
                   BLASTX
                   g4371290
NCBI GI
BLAST score
                   374
                   8.0e-36
E value
Match length
                   89
% identity
                   72
                   (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3078
Seq. No.
```

2140 1.R1040

Contig ID

```
5'-most EST
                  awf700843415.h1
Method
                  BLASTX
NCBI GI
                  q464987
BLAST score
                  776
                  1.0e-82
E value
Match length
                  149
% identity
                  97
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi_421858_pir__S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >gi 297878 emb CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi 349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
Seq. No.
                  3079
                  2140 2.R1040
Contig ID
5'-most EST
                  LIB3050-003-Q1-E1-F12
Method
                  BLASTN
NCBI GI
                  q297877
BLAST score
                  179
                  1.0e-95
E value
Match length
                  443
                  85
% identity
                  A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme
NCBI Description
                  homolog >gi 349212 gb L00640 ATHUBCC Arabidopsis thaliana
                  ubiquitin conjugating enzyme mRNA, complete cds
Seq. No.
                  3080
                  2140 3.R1040
Contig ID
                  leu701147536.hl
5'-most EST
Method
                  BLASTN
                  q297877
NCBI GI
BLAST score
                  175
                  3.0e-93
E value
                  447
Match length
                  85
% identity
NCBI Description
                  A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme
                  homolog >gi 349212 gb L00640 ATHUBCC Arabidopsis thaliana
                  ubiquitin conjugating enzyme mRNA, complete cds
                  3081
Seq. No.
                  2140 5.R1040
Contig ID
5'-most EST
                  jC-qmro02910066q10a1
Method
                  BLASTN
                  g388206
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
Match length
                  69
% identity
                  Lycopersicon esculentum ubiquitin carrier protein (Ubc)
NCBI Description
                  mRNA, complete cds. >gi 2086269 gb I38279 I38279 Sequence
                  109 from patent US
                  3082
Seq. No.
```

2140 6.R1040

LIB3092-003-Q1-K1-D3

Contig ID

5'-most EST

```
Method
                  BLASTN
NCBI GI
                  g297877
BLAST score
                  102
                  5.0e-50
E value
                  290
Match length
                  84
% identity
                  A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme
NCBI Description
                  homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana
                  ubiquitin conjugating enzyme mRNA, complete cds
                  3083
Seq. No.
                  2141 1.R1040
Contig ID
                  k11701212974.h1
5'-most EST
                  BLASTX
Method
                  g2464855
NCBI GI
                  551
BLAST score
                  2.0e-56
E value
                  176
Match length
                  66
% identity
                   (Z99707) myb-related protein [Arabidopsis thaliana]
NCBI Description
                  3084
Seq. No.
                  2144 2.R1040
Contig ID
5'-most EST
                  jC-gmf102220108a01a1
                  3085
Seq. No.
Contig ID
                  2144_3.R1040
5'-most EST
                  jC-gmf102220090d03a1
Method
                  BLASTN
NCBI GI
                  g3033512
BLAST score
                  557
                  0.0e+00
E value
Match length
                  1251
                  87
% identity
                  Phaseolus vulgaris rubisco activase (Rcal) mRNA, complete
NCBI Description
                  cds
Seq. No.
                  3086
                  2144 4.R1040
Contig ID
                  LIB3138-105-Q1-N1-F11
5'-most EST
                  BLASTN
Method
                  q4406529
NCBI GI
BLAST score
                  499
                  0.0e + 00
E value
                  1411
Match length
% identity
                  Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                  encoding chloroplast protein, complete cds
                  3087
Seq. No.
Contig ID
                  2148 1.R1040
5'-most EST
                  uC-gmrominsoy176b07b1
Method
                  BLASTX
                  g4115925
NCBI GI
                  798
BLAST score
```

6.0e-85

270

E value

Match length

E value

```
% identity
                   60
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
                   3088
Seq. No.
                   2148_2.R1040
Contig ID
                   jC-gmst02400014a06a1
5'-most EST
                   BLASTX
Method
                   g4115925
NCBI GI
BLAST score
                   683
                   9.0e-72
E value
Match length
                   231
                   43
% identity
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                  >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
                   3089
Seq. No.
Contig ID
                   2150 1.R1040
                   pmv700894902.hl
5'-most EST
                   3090
Seq. No.
Contig ID
                   2150 2.R1040
5'-most EST
                   sat701013106.hl
                   3091
Seq. No.
                   2151_1.R1040
Contig ID
                   dpv7\overline{0}1103482.h1
5'-most EST
                   BLASTX
Method
                   g2462927
NCBI GI
BLAST score
                   178
                   6.0e-13
E value
Match length
                   64
                   52
% identity
NCBI Description
                   (Y10342) putative amidase [Arabidopsis thaliana]
                   3092
Seq. No.
                   2152 1.R1040
Contig ID
5'-most EST
                   k117\overline{0}1205744.h1
                   BLASTX
Method
NCBI GI
                   g285741
BLAST score
                   694
E value
                   1.0e-72
Match length
                   376
% identity
                   45
                   (D14550) EDGP precursor [Daucus carota]
NCBI Description
                   3093
Seq. No.
                   2152 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910034c10d1
Method
                   BLASTX
                   g285741
NCBI GI
BLAST score
                   320
```

2.0e-29

BLAST score

282

```
104
Match length
% identity
NCBI Description
                   (D14550) EDGP precursor [Daucus carota]
Seq. No.
                   3094
                   2152 3.R1040
Contig ID
5'-most EST
                   uC-gmropic116e09b1
                   3095
Seq. No.
                   2153 1.R1040
Contig ID
                   has700548121.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4006816
BLAST score
                   166
                   4.0e-11
E value
Match length
                   99
                   43
% identity
                   (AC005970) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
                   3096
Seq. No.
                   2153 2.R1040
Contig ID
5'-most EST
                   ncj700984512.hl
                   3097
Seq. No.
                   2154 1.R1040
Contig ID
                   LIB3028-048-Q1-B1-B2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3201619
BLAST score
                   557
E value
                   4.0e-57
Match length
                   163
% identity
                   65
                   (AC004669) dihydroxypolyprenylbenzoate methyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   3098
Seq. No.
                   2155 1.R1040
Contig ID
5'-most EST
                   g4294625
Seq. No.
                   3099
Contig ID
                   2156 1.R1040
5'-most EST '
                   uC-gmrominsoy173a11b1
                   BLASTX
Method
NCBI GI
                   q2181180
BLAST score
                   1149
E value
                   1.0e-125
Match length
                   699
% identity
NCBI Description
                   (Z84377) xylosidase [Aspergillus niger]
                   3100
Seq. No.
Contig ID
                   2158 1.R1040
5'-most EST
                   zhf700955352.h1
Method
                   BLASTX
NCBI GI
                   q4115547
```

```
E value
                   7.0e-32
Match length
                   155
% identity
                   51
                   (AB012634) lectin [Robinia pseudoacacia]
NCBI Description
Seq. No.
                   3101
Contig ID
                   2161 1.R1040
                   jC-gmle01810044a01d1
5'-most EST
Method
                   BLASTX
                   g1388078
NCBI GI
BLAST score
                   307
E value
                   1.0e-27
                   104
Match length
                   47
% identity
                   (U35826) thioredoxin h [Arabidopsis thaliana]
NCBI Description
                   3102
Seq. No.
Contig ID
                   2161 2.R1040
                   uC-gmrominsoy101a09b1
5'-most EST
Method
                   BLASTX
                   q1388078
NCBI GI
BLAST score
                   265
E value
                   7.0e-23
Match length
                   106
% identity
                   42
                   (U35826) thioredoxin h [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3103
                   2161 3.R1040
Contig ID
                   zsq7\overline{0}1119390.h1
5'-most EST
                   BLASTX
Method
                   q129960
NCBI GI
BLAST score
                   494
                   2.0e-49
E value
                   282
Match length
                   42
% identity
NCBI Description
                   4-NITROPHENYLPHOSPHATASE (PNPPASE)
Seq. No.
                   3104
                   2161 4.R1040
Contig ID
                   LIB3\overline{1}39-033-P1-N1-F1
5'-most EST
                   BLASTX
Method
                   g1388078
NCBI GI
BLAST score
                   269
                   1.0e-23
E value
Match length
                   88
                   57
% identity
                   (U35826) thioredoxin h [Arabidopsis thaliana]
NCBI Description
                   3105
Seq. No.
Contig ID
                   2163 1.R1040
5'-most EST
                   g4297823
Method
                   BLASTX
                   g3372230
NCBI GI
                   461
BLAST score
                   9.0e-46
E value
```

140

Match length

NCBI Description

```
% identity
                   62
                   (AF017074) RNA polymerase I, II and III 16.5 kDa subunit
NCBI Description
                   [Arabidopsis thaliana]
                   3106
Seq. No.
                   2164 1.R1040
Contig ID
5'-most EST
                   LIB3049-050-Q1-E1-B5
Method
                   BLASTX
                   g1041825
NCBI GI
BLAST score
                   228
                   4.0e-18
E value
Match length
                   283
                   25
% identity
                   (U26175) LPG2 [Leishmania donovani]
NCBI Description
                   >gi 1583457 prf 2120442A LPG2 gene [Leishmania donovani]
                   3107
Seq. No.
Contig ID
                   2166 1.R1040
                   txt700735601.h1
5'-most EST
                   3108
Seq. No.
                   2167 1.R1040
Contig ID
5'-most EST
                   LIB3028-047-Q1-B1-H1
                   3109
Seq. No.
                   2168 1.R1040
Contig ID
                   LIB3170-057-Q1-K1-A4
5'-most EST
Seq. No.
                   3110
                   2168 2.R1040
Contig ID
                   jC-gmf102220104a05a1
5'-most EST
                   3111
Seq. No.
Contig ID
                   2168 3.R1040
                   LIB3039-046-Q1-E1-E4
5'-most EST
                   3112
Seq. No.
                   2169 1.R1040
Contig ID
                   jC-gmst02400026h10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4115386
BLAST score
                   317
E value
                   3.0e-29
Match length
                   120
                   62
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3113
                   2169 3.R1040
Contig ID
5'-most EST
                   g4396207
Method
                   BLASTX
NCBI GI
                   g4115386
BLAST score
                   212
                   7.0e-17
E value
                   59
Match length
                   76
% identity
```

(AC005967) unknown protein [Arabidopsis thaliana]

```
3114
Seq. No.
                  2171 1.R1040
Contig ID
                  LIB3109-048-Q1-K1-A2
5'-most EST
Method
                  BLASTX
                  q2288981
NCBI GI
BLAST score
                  512
                  7.0e-52
E value
Match length
                  148
% identity
                   67
NCBI Description
                   (AC002335) calcium binding protein isolog [Arabidopsis
                  thaliana] >gi 3763938 (AC004450) putative calcium binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  3115
Contig ID
                  2171 2.R1040
                  dpv701099410.h1
5'-most EST
Method
                  BLASTX
                  g2288981
NCBI GI
BLAST score
                  527
                  3.0e-53
E value
Match length
                  148
% identity
                   69
                   (AC002335) calcium binding protein isolog [Arabidopsis
NCBI Description
                  thaliana] >gi 3763938 (AC004450) putative calcium binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  3116
                  2171 3.R1040
Contig ID
                  rca701000403.hl
5'-most EST
                  3117
Seq. No.
Contig ID
                  2174 1.R1040
                  LIB3040-061-Q1-E1-H9
5'-most EST
Method
                  BLASTX
                  g4512699
NCBI GI
                  1164
BLAST score
E value
                  1.0e-128
                  300
Match length
% identity
                   (AC006569) putative NADH-ubiquinone oxireductase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  3118
Contig ID
                  2175 1.R1040
5'-most EST
                  LIB3028-047-Q1-B1-H7
                  BLASTX
Method
                  g2088650
NCBI GI
BLAST score
                  244
E value
                  2.0e-20
                  74
Match length
% identity
                   (AF002109) peroxisomal ATP/ADP carrier protein isolog
NCBI Description
                   [Arabidopsis thaliana]
```

3119

2176 1.R1040

Seq. No.

Contig ID

```
5'-most EST
                   LIB3028-040-Q1-B1-A11
                   BLASTX
Method
NCBI GI
                   g2281334
                   409
BLAST score
                   9.0e-40
E value
                   174
Match length
% identity
                   51
                   (U83619) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
                   3120
Seq. No.
                   2177 1.R1040
Contig ID
                   k117\overline{0}1210975.h1
5'-most EST
Method
                   BLASTX
                   q4544449
NCBI GI
BLAST score
                   831
E value
                   3.0e-89
Match length
                   203
% identity
                   76
                   (AC006592) putative peroxidase [Arabidopsis thaliana]
NCBI Description
                   3121
Seq. No.
                   2179 1.R1040
Contig ID
                   jC-gmro02910030d10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g543867
BLAST score
                   1284
                   1.0e-142
E value
Match length
                   313
% identity.
                   84
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor - sweet potato
                   >gi 303626 dbj BAA03526 (D14699) F1-ATPase gammma subunit
                   [Ipomoea batatas]
                   3122
Seq. No.
                   2179 2.R1040
Contig ID
                   leu7\overline{0}1152070.h1
5'-most EST
Method
                   BLASTN
                   g397554
NCBI GI
                   159
BLAST score
                   7.0e-84
E value
                   287
Match length
% identity
                  N.sylvestris psaH gene for photosystem I psaH protein
NCBI Description
Seq. No.
                   3123
                   2179 4.R1040
Contig ID
                   LIB3051-045-Q1-K1-A10
5'-most EST
                   BLASTX
Method
NCBI GI
                   g543867
BLAST score
                   433
E value
                   1.0e-42
Match length
                   114
                   81
% identity
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi 1076684 pir A47493 H+-transporting ATP synthase (EC
```

```
[Ipomoea batatas]
                   3124
Seq. No.
                   2179 5.R1040
Contig ID
                   LIB3073-015-Q1-K1-C10
5'-most EST
                   BLASTN
Method
                   g397556
NCBI GI
                   158
BLAST score
                   2.0e-83
E value
Match length
                   306
                   88
% identity
                  N.tabacum psaH gene for photosystem I psaH protein
NCBI Description
Seq. No.
                   3125
                   2179 6.R1040
Contig ID
5'-most EST
                  LIB3073-016-Q1-K1-B2
Method
                   BLASTN
NCBI GI
                   q397554
BLAST score
                   124
                   5.0e-63
E value
Match length
                   284
% identity
                  86
                  N.sylvestris psaH gene for photosystem I psaH protein
NCBI Description
                   3126
Seq. No.
Contig ID
                   2179 7.R1040
5'-most EST
                   LIB3074-004-Q1-K1-H1
Method
                   BLASTN
                   g397554
NCBI GI
BLAST score
                   85
E value
                   9.0e-40
Match length
                   249
% identity
                   85
                  N.sylvestris psaH gene for photosystem I psaH protein
NCBI Description
                   3127
Seq. No.
Contig ID
                   2179 8.R1040
                   g5677856
5'-most EST
                   3128
Seq. No.
                   2179 9.R1040
Contig ID
                   jC-gmro02910030a06d1
5'-most EST
Method
                   BLASTN
                   g286033
NCBI GI
BLAST score
                   44
                   2.0e-15
E value
                   104
Match length
% identity
                   Ipomoea batatas (sweet potato) mRNA for F1-ATPase
NCBI Description
                   gamma-subunit
                   3129
Seq. No.
                   2179 11.R1040
Contig ID
```

3.6.1.34) gamma chain precursor - sweet potato

>gi 303626 dbj BAA03526 (D14699) F1-ATPase gammma subunit

pmv700892366.hl

BLASTN

5'-most EST

Method

```
NCBI GI
                   g397556
BLAST score
                   92
E value
                   3.0e-44
Match length
                   160
                   89
% identity
                  N.tabacum psaH gene for photosystem I psaH protein
NCBI Description
Seq. No.
                   3130
                   2179 13.R1040
Contig ID
                   fua7\overline{0}1042954.h1
5'-most EST
Seq. No.
                   3131
Contig ID
                   2183 1.R1040
                   LIB3139-091-P1-N1-C10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2662375
BLAST score
                   934
E value
                   1.0e-101
Match length
                   443
% identity
                  (D89060) oligosaccharyltransferase [Homo sapiens]
NCBI Description
Seq. No.
                   3132
                   2184 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy069g07b1
Method
                   BLASTX
                   g2505879
NCBI GI
BLAST score
                   252
E value
                   4.0e-29
Match length
                   268
% identity
                   37
                   (Y12776) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3133
                   2185 1.R1040
Contig ID
                   LIB3028-030-Q1-B1-G10
5'-most EST
Method
                   BLASTX
                   g4539301
NCBI GI
BLAST score
                   252
E value
                   2.0e-21
Match length
                   142
% identity
                   (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                   thaliana] 🦈
                   3134
Seq. No.
                   2185 2.R1040
Contig ID
                   LIB3093-027-Q1-K1-A11
5'-most EST
Seq. No.
                   3135
                   2186 1.R1040
Contig ID
                   q5606255
5'-most EST
Method
                   BLASTX
                   g4455223
NCBI GI
                   1033
BLAST score
                   1.0e-112
E value
```

291

Match length

BLAST score

229

```
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   3136
Seq. No.
                   2186 2.R1040
Contig ID
                   LIB3\overline{0}28-012-Q1-B1-C9
5'-most EST
Method
                   BLASTX
                   g4455223
NCBI GI .
BLAST score
                   651
                   8.0e-68
E value
Match length
                   180
                   45
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   3137
Seq. No.
Contig ID
                   2186 3.R1040
                   pcp700991124.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4455223
BLAST score
                   424
E value
                   4.0e-59
Match length
                   209
% identity
                   32
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3138
                   2186 4.R1040
Contig ID
                   LIB3167-023-P4-K4-G9
5'-most EST
                   BLASTX
Method
                   g1899188
NCBI GI
BLAST score
                   266
                   4.0e-23
E value
                   72
Match length
                   23
% identity
                   (U90212) DNA binding protein ACBF [Nicotiana tabacum]
NCBI Description
Seq. No.
                   3139
                   2186 5.R1040
Contig ID
                   uC-gmropic068b09b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4455223
BLAST score
                   331
E value
                   3.0e-31
                   100
Match length
% identity
NCBI Description
                   (AL035440) putative DNA binding protein [Arabidopsis
                   thaliana]
                   3140
Seq. No.
                   2186 7.R1040
Contig ID
5'-most EST
                   uxk700669935.hl
Method
                   BLASTX
                   q4455223
NCBI GI
```

Contig ID

5'-most EST

```
E value
                   5.0e-19
Match length
                   63
% identity
                   37
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
Seq. No.
                   3141
                   2187 1.R1040
Contig ID
                   zpv700759026.hl
5'-most. EST
                   3142
Seq. No.
Contig ID
                   2190 1.R1040
                   jC-gmle01810035e07a2
5'-most EST
Seq. No.
                   3143
Contig ID
                   2191 1.R1040
5'-most EST
                   LIB3028-047-Q1-B1-F8
Seq. No.
                   3144
Contig ID
                   2193 1.R1040
5'-most EST
                   LIB3050-004-Q1-E1-E12
Method
                   BLASTX
NCBI GI
                   g4263712
BLAST score
                   486
E value
                   1.0e-48
Match length
                   119
% identity
                   76
NCBI Description
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
                   thaliana]
                   3145
Seq. No.
                   2193 2.R1040
Contig ID
                   k117\overline{0}1212032.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4263712
BLAST score
                   488
E value
                   6.0e-49
Match length
                   119
% identity
                   76
                   (ACO06223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   3146
Seq. No.
                   2193 3.R1040
Contig ID
5'-most EST
                   leu701155992.h1
Method
                   BLASTX
                   g4263712
NCBI GI
BLAST score
                   356
                   9.0e-34
E value
Match length
                   84
                   79
% identity
                   (ACO06223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   3147
Seq. No.
                   2193 4.R1040
```

bth700848563.h1

NCBI Description

```
BLASTX
Method
NCBI GI
                   q4263712
BLAST score
                   373
E value
                   4.0e-38
Match length
                   107
                   74
% identity
                   (ACO06223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   3148
Seq. No.
Contig ID
                   2193 5.R1040
5'-most EST
                   LIB3139-075-P1-N1-D5
Method
                   BLASTX
                   q4263712
NCBI GI
BLAST score
                   401
                   9.0e-39
E value
Match length
                   121
% identity
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   3149
Seq. No.
Contig ID
                   2193 7.R1040
5'-most EST
                   LIB3040-009-Q1-E1-A6
Seq. No.
Contig ID
                   2194 1.R1040
5'-most EST
                   fua701040372.h1
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   2838
E value
                   0.0e + 00
Match length
                   865
% identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   3151
Seq. No.
                   2194 2.R1040
Contig ID
5'-most EST
                   rlr700899150.hl
Method
                   BLASTN
NCBI GI
                   g2369713
BLAST score
                   54
E value
                   2.0e-21
Match length
                   162
% identity
                   85
                  Beta vulgaris cDNA for elongation factor
NCBI Description
Seq. No.
                   3152
                   2194 4.R1040
Contig ID
5'-most EST
                   LIB3093-010-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   208
                   3.0e-16
E value
                   55
Match length
% identity
                   73
                   (297178) elongation factor 2 [Beta vulgaris]
```

BLAST score

65

```
Seq. No.
                   3153
                   2196 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy199h08b1
Method
                   BLASTX
NCBI GI
                   g2492519
                   2180
BLAST score
                   0.0e+00
E value
                   426
Match length
                   99
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
Seq. No.
                   3154
                   2196 2.R1040
Contig ID
5'-most EST
                   jC-qmro02910005d08d1
Method
                   BLASTN
NCBI GI
                   q1395190
BLAST score
                   45
                   5.0e-16
E value
Match length
                   85
                   88
% identity
                   Spinacia oleracea L. mRNA for 26S proteasome ATPase
NCBI Description
                   subunit, complete cds
Seq. No.
                   3155
                   2196 3.R1040
Contig ID
5'-most EST
                   rca701001049.hl
                   BLASTX
Method
NCBI GI
                   q2492519
BLAST score
                   272
                   3.0e-24
E value
                   58
Match length
                   90
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
Seq. No.
                   3156
                   2196 4.R1040
Contig ID
5'-most EST
                   zzp7\overline{0}0831319.h1
                   BLASTN
Method
                   g1395190
NCBI GI
BLAST score
                   46
E value
                   7.0e-17
                   86
Match length
                   88
% identity
                   Spinacia oleracea L. mRNA for 26S proteasome ATPase
NCBI Description
                   subunit, complete cds
Seq. No.
                   3157
                   2197 1.R1040
Contig ID
5'-most EST
                   epx7\overline{0}1110235.h1
Method
                   BLASTN
                   g1707656
NCBI GI
```

NCBI GI

```
E value
                   5.0e-28
                   105
Match length
                   90
% identity
                   P.sativum mRNA for DnaJ-like protein
NCBI Description
                   3158
Seq. No.
                   2198 1.R1040
Contig ID
                   LIB3109-014-Q1-K1-D7
5'-most EST
                   BLASTX
Method
                   g4106538
NCBI GI
BLAST score
                   1078
                   1.0e-118
E value
                   282
Match length
                   72
% identity
                   (AF104220) gamma-tocopherol methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3159
                   2198 2.R1040
Contig ID
                   taw700655856.hl
5'-most EST
Method
                   BLASTX
                   g4106538
NCBI GI
BLAST score
                   244
                   1.0e-20
E value
Match length
                   60
                   75
% identity
                   (AF104220) gamma-tocopherol methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   3160
Seq. No.
                   2200 1.R1040
Contig ID
                   vwf7\overline{0}0678153.h1
5'-most EST
Method
                   BLASTX
                   g1350680
NCBI GI
BLAST score
                   1614
                   1.0e-180
E value
Match length
                   404
% identity
                   76
NCBI Description
                   60S RIBOSOMAL PROTEIN L1
Seq. No.
                   3161
                   2200 3.R1040
Contig ID
                   gsv701051391.hl
5'-most EST
Method
                   BLASTX
                   g2459420
NCBI GI
BLAST score
                   716
                   1.0e-75
E value
Match length
                   140
                   98
% identity
NCBI Description
                   (AC002332) putative ribosomal protein L17 [Arabidopsis
                   thaliana]
Seq. No.
                   3162
                   2200 4.R1040
Contig ID
                   LIB3106-005-Q1-K1-D8
5'-most EST
Method
                   BLASTN
```

17.

g310932

```
BLAST score
                   161
                   4.0e-85
E value
Match length
                   421
                   85
% identity
                  Nicotiana tabacum ribosomal protein L17 mRNA, complete cds
NCBI Description
Seq. No.
                   3163
                   2200 5.R1040
Contig ID
                   LIB3051-015-Q1-E1-G11
5'-most EST
                   BLASTN
Method
                   g310932
NCBI GI
BLAST score
                   145
                   1.0e-75
E value
                   413
Match length
% identity
                   84
                   Nicotiana tabacum ribosomal protein L17 mRNA, complete cds
NCBI Description
Seq. No.
                   2200 8.R1040
Contig ID
                   kwa701015594.hl
5'-most EST
Seq. No.
                   3165
Contig ID
                   2201 1.R1040
                   LIB3\overline{0}93-044-Q1-K1-G2
5'-most EST
Method
                   BLASTX
                   g3249071
NCBI GI
                   560
BLAST score
E value
                   3.0e-57
Match length
                   164
% identity
                   (AC004473) Contains similarity to protein-tyrosine
NCBI Description
                   phosphatase 2 gb L15420 from Dictyostelium discoideum. EST
                   gb N38718 comes from this g [Arabidopsis thaliana]
                   3166
Seq. No.
                   2201 2.R1040
Contig ID
                   asn7\overline{0}1134505.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3249071
BLAST score
                   155
E value
                   1.0e-10
Match length
                   41
% identity
                   (AC004473) Contains similarity to protein-tyrosine
NCBI Description
                   phosphatase 2 gb_L15420 from Dictyostelium discoideum. EST
                   gb N38718 comes from this g [Arabidopsis thaliana]
                   3167
Seq. No.
Contig ID
                   2204 1.R1040
                   ssr7\overline{0}0561073.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q938299
BLAST score
                   690
                   0.0e + 00
E value
Match length
                   1290
% identity
                   89
NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)
```

```
Seq. No.
                   3168
Contig ID
                  2204 4.R1040
5'-most EST
                  g5509857
                  3169
Seq. No.
Contig ID
                  2204 6.R1040
                  zsq701119048.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g938299
BLAST score
                  114
E value
                  2.0e-57
                  158
Match length
                  93
% identity
NCBI Description
                  V.ungiculata mRNA for unknown protein (A3 gene)
Seq. No.
                  3170
Contig ID
                  2205 1.R1040
5'-most EST
                  LIB3028-047-Q1-B1-D8
Seq. No.
                  3171
Contig ID
                  2206 1.R1040
5'-most EST
                  LIB3092-007-Q1-K1-C7
Method
                  BLASTN
NCBI GI
                  g1370204
BLAST score
                  391
                  0.0e+00
E value
Match length
                  615
% identity
                  91
NCBI Description L. japonicus mRNA for small GTP-binding protein, RAN1B
Seq. No.
                  3172
                  2206 2.R1040
Contig ID
5'-most EST
                  hrw701058039.h1
Method
                  BLASTN
                  g1370204
NCBI GI
BLAST score
                  125
                  1.0e-63
E value
Match length
                  226
% identity
                  92
                  L.japonicus mRNA for small GTP-binding protein, RAN1B
NCBI Description
                  3173
Seq. No.
                  2206 3.R1040
Contig ID
                  smc700745908.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g1370202
BLAST score
                  207
                  1.0e-112
E value
Match length
                  347
                  90
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1A
                  3174
Seq. No.
                  2206 5.R1040
Contig ID
                  leu701145214.h1
5'-most EST
```

i.

BLASTX

Method

NCBI GI

```
NCBI GI
                   g2149051
BLAST score
                   631
E value
                   1.0e-116
Match length
                   222
% identity
                   93
                   (U73810) small Ras-like GTP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   3175
Seq. No.
                   2206 10.R1040
Contig ID
                   pxt700944036.hl
5'-most EST
Method
                   BLASTN
                   g1370202
NCBI GI
BLAST score
                   149
                   3.0e-78
E value
Match length
                   209
                   93
% identity
NCBI Description
                  L. japonicus mRNA for small GTP-binding protein, RAN1A
Seq. No.
                   3176
Contig ID
                   2206 11.R1040
5'-most EST
               hrw701060904.hl
Method
                   BLASTN
NCBI GI
                   g1370202
BLAST score
                   112
                   4.0e-56
E value
                   234
Match length
% identity
                   94
NCBI Description
                  L.japonicus mRNA for small GTP-binding protein, RAN1A
                   3177
Seq. No.
                   2206 13.R1040
Contig ID
                   uxk700672208.hl
5'-most EST
Method
                   BLASTN
                   g1370204
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
                   153
Match length
% identity
                   92
                  L.japonicus mRNA for small GTP-binding protein, RAN1B
NCBI Description
                   3178
Seq. No.
                   2208 1.R1040
Contig ID
5'-most EST
                   LIB3039-031-Q1-E1-A3
Method
                   BLASTX
                   g4538897
NCBI GI
                   539
BLAST score
                   5.0e-55
E value
Match length
                   154
% identity
                   63
                   (AL049482) AX110P-like protein [Arabidopsis thaliana]
NCBI Description
                   3179
Seq. No.
                   2210 1.R1040
Contig ID
5'-most EST
                   sat7\overline{0}1007262.h2
Method
                   BLASTX
```

q2505876

```
BLAST score
                   336
                   4.0e-31
E value
Match length
                   89
% identity
                   75
                   (Y12776) MYB-related protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3180
                   2211 1.R1040
Contig ID
                   leu701155294.hl
5'-most EST
Method
                   BLASTX
                   g3176684
NCBI GI
BLAST score
                   365
                   1.0e-34
E value
Match length
                   148
% identity
                   51
NCBI Description
                   (AC003671) Contains similarity to equilibratiave nucleoside
                   transporter 1 qb U81375 from Homo sapiens. ESTs qb N65317,
                   qb T20785, qb AA586285 and qb AA712578 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   3181
                   2213 1.R1040
Contig ID
5'-most EST
                   gsv701047793.h1
Method
                  BLASTX
NCBI GI
                  g464365
BLAST score
                  1212
                   1.0e-133
E value
Match length
                   296
% identity
                  78
                  PEROXIDASE P7 >gi 66306 pir OPNB7 peroxidase (EC 1.11.1.7)
NCBI Description
                  - turnip
                  3182
Seq. No.
Contig ID
                  2214 1.R1040
                  LIB3072-049-Q1-K1-B6
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3608481
BLAST score
                   623
E value
                  7.0e-65
Match length
                  148
                  79
% identity
                   (AF088913) ribosomal protein L27a [Petunia x hybrida]
NCBI Description
Seq. No.
                  3183
                  2214 2.R1040
Contig ID
5'-most EST
                  LIB3093-012-Q1-K1-F8
Method
                  BLASTX
                  g1710530
NCBI GI
BLAST score
                  455
                  3.0e-45
E value
Match length
                  148
% identity
                  60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
NCBI Description
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
```

```
Seq. No.
                   3184
                   2216 1.R1040
Contig ID
                  pxt700943374.h1
5'-most EST
                   3185
Seq. No.
                   2217 1.R1040
Contig ID
                  LIB3051-050-Q1-K1-A10
5'-most EST
                  BLASTX
Method
                   g4263722
NCBI GI
BLAST score
                   766
                   1.0e-81
E value
                   203
Match length
                   70
% identity
                   (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3186
                   2218 1.R1040
Contig ID
                   LIB3039-049-Q1-E1-D2
5'-most EST
                   BLASTX
Method
                   q4185505
NCBI GI
                   266
BLAST score
                   6.0e-23
E value
                   91
Match length
% identity
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
Seq. No.
                   3187
Contig ID
                   2220 1.R1040
                   q5752955
5'-most EST
                   BLASTX
Method
                   q549750
NCBI GI
                   233
BLAST score
                   5.0e-19
E value
                   96
Match length
                   48
% identity
                   HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
NCBI Description
                   >gi_539221_pir__S38045 hypothetical protein YKL207w - yeast
                   (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_
                   (Z28207) ORF YKL207w [Saccharomyces cerevisiae]
                   3188
Seq. No.
                   2220 2.R1040
Contig ID
                   LIB3\overline{0}51-028-Q1-K1-G7
5'-most EST
                   3189
Seq. No.
                   2220 3.R1040
Contig ID
                   kl1701209834.hl
5'-most EST
                   BLASTX
Method
                   g549750
NCBI GI
                   218
BLAST score
                   2.0e-17
E value
                   147
Match length
                   37
% identity
                   HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
NCBI Description
                   >gi_539221_pir__S38045 hypothetical protein YKL207w - yeast
```

(Saccharomyces cerevisiae) >gi\_486369\_emb\_CAA82052\_

Match length

% identity

172 49

## (Z28207) ORF YKL207w [Saccharomyces cerevisiae]

```
Seq. No.
                  3190
                  2220 4.R1040
Contig ID
                  sat7\overline{0}1004550.h1
5'-most EST
                  3191
Seq. No.
                  2220 5.R1040
Contig ID
                  LIB3050-024-Q1-K1-D10
5'-most EST
                  3192
Seq. No.
                  2221 1.R1040
Contig ID
                  LIB3028-049-Q1-B1-A12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3142301
BLAST score
                  1220
                  1.0e-134
E value
Match length
                  497
% identity
                  53
                   (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                  molecule 2, large isoform precursor gb M76710 from Xenopus
                  laevis, and beta transducin from S. cerevisiae gb_Q05946.
                  ESTs gb N65081 gb Z30910, gb Z34190, gb Z34611, gb R30101,
                  gb_H3630
                  3193
Seq. No.
                  2222 1.R1040
Contig ID
5'-most EST
                  zsg701121747.hl
Method
                  BLASTX
                  g2351374
NCBI GI
BLAST score
                  821
                  5.0e-88
E value
                  180
Match length
% identity
                   (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                   [Arabidopsis thaliana]
                  3194
Seq. No.
Contig ID
                  2224 1.R1040
                  crh700850891.h1
5'-most EST
Method
                  BLASTX
                  q3269287
NCBI GI
                  751
BLAST score
E value
                  5.0e-80
                  177
Match length
% identity
                   (AL030978) GH3 like protein [Arabidopsis thaliana]
NCBI Description
                  3195
Seq. No.
                  2225 1.R1040
Contig ID
5'-most EST
                  zhf700955393.hl
                  BLASTX
Method
                  q3819099
NCBI GI
BLAST score
                  450
E value
                  1.0e-44
```

```
NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]
                   3196
Seq. No.
Contig ID
                   2226 1.R1040
5'-most EST
                   kl1701205002.h1
                   BLASTX
Method
NCBI GI
                   q2829911
BLAST score
                   1328
E value
                   1.0e-147
Match length
                   363
% identity
                   70
NCBI Description
                   (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   2226 2.R1040
5'-most EST
                   LIB3051-067-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   g2829911
BLAST score
                   212
E value
                   9.0e-17
Match length
                   87
% identity
NCBI Description
                   (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   3198
Contig ID
                   2226 4.R1040
5'-most EST
                   q4291800
Method
                   BLASTX
NCBI GI
                   q2829911
BLAST score
                   788
E value
                   5.0e-84
Match length
                   206
% identity
                   44
NCBI Description
                   (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   3199
Contig ID
                   2226 5.R1040
5'-most EST
                   jC-gmf102220063d08a1
Method
                   BLASTX
NCBI GI
                   g2829911
BLAST score
                   296
                   8.0e-27
E value
Match length
                   105
% identity
NCBI Description
                   (AC002291) Unknown protein [Arabidopsis thaliana]
                   3200
Seq. No.
Contig ID
                   2226 6.R1040
5'-most EST
                   LIB3049-004-Q1-E1-E12
Method
                   BLASTX
NCBI GI
                   g2829911
BLAST score
                   125
E value
                   8.0e-12
```

(AC002291) Unknown protein [Arabidopsis thaliana]

77

57

Match length

NCBI Description

% identity

```
Seq. No.
                   3201
                   2227 1.R1040 -
Contig ID
5'-most EST
                   uC-gmropic009b10b1
Method
                   BLASTX
NCBI GI
                   q2065531
BLAST score
                   2076
                   0.0e+00
E value
Match length
                   484
                   77
% identity
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   3202
                   2227 2.R1040
Contig ID
                   sat7\overline{0}1012015.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2065531
BLAST score
                   1055
                   1.0e-154
E value
Match length
                   365
% identity
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   3203
                   2227 3.R1040
Contig ID
                   LIB3\overline{0}51-041-Q1-K1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2065531
BLAST score
                   363
                   3.0e-34
E value
Match length
                   92
% identity
                   71
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   3204
                   2229 1.R1040
Contig ID
                   asn7\overline{0}1139633.h1
5'-most EST
Method
                   BLASTN
                   g3366929
NCBI GI
BLAST score
                   35
E value
                   5.0e-10
Match length
                   71
% identity
                   Solanum tuberosum putative phosphatidylinositol 4-kinase
NCBI Description
                   (PI4KI) mRNA, partial cds
                   3205
Seq. No.
                   2230 1.R1040
Contig ID
                   jex7\overline{0}0908180.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q118158
BLAST score
                   1697
                   0.0e + 00
E value
Match length
                   362
                   87
% identity
                   VIGNAIN PRECURSOR (BEAN ENDOPEPTIDASE) (CYSTEINE
NCBI Description
                   PROTEINASE) (SULFHYDRYL-ENDOPEPTIDASE) (SH-EP)
                   >gi 82006 pir S12581 cysteine proteinase (EC 3.4.22.-) -
```

```
sulfhydryl-pre-endopeptidase (AA -20 to 342) [Vigna mungo]
                  >gi 22066 emb CAA36181 (X51900) sulfhydryl-endopeptidase
                   [Vigna mungo]
                   3206
Seq. No.
Contig ID
                  2230 2.R1040
5'-most EST
                  jC-qmst02400066a10a2
Seq. No.
Contig ID
                  2231 1.R1040
5'-most EST
                  uC-qmrominsoy221g11b1
Method
                  BLASTX
NCBI GI
                  q2769566
BLAST score
                  922
                   2.0e-99
E value
Match length
                   362
% identity
                   (Y10477) chloroplast thylakoidal processing peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
Contig ID
                  2231 2.R1040
5'-most EST
                  rlr700900371.h1
                  3209
Seq. No.
Contig ID
                  2231 4.R1040
5'-most EST
                  LIB3093-038-Q1-K1-G5
Seq. No.
                  3210
Contig ID
                  2231 5.R1040
5'-most EST
                  jsh701068480.hl
Method
                  BLASTX
NCBI GI
                  q2769566
BLAST score
                  246
                   3.0e-21
E value
Match length
                  62
% identity
NCBI Description
                   (Y10477) chloroplast thylakoidal processing peptidase
                   [Arabidopsis thaliana]
Seq. No.
                  3211
                  2234 1.R1040
Contig ID
                  uC-qmflminsoy071f11b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g729882
BLAST score
                  417
                  1.0e-40
E value
                  111
Match length
% identity
                  74
                  CASEIN KINASE II BETA' CHAIN (CK II)
NCBI Description
                  >gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta
                  chain CKB2 - Arabidopsis thaliana >gi 467975 (U03984)
                  casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                  >gi 2245122 emb CAB10544 (Z97343) unnamed protein product
                   [Arabidopsis thaliana]
```

black gram >gi 22062 emb CAA33753\_ (X15732)

```
3212
Seq. No.
Contig ID
                   2234 2.R1040
                   zsg7\overline{0}1118222.h1
5'-most EST
Method
                   BLASTN
                   g3341671
NCBI GI
BLAST score
                   42
                   3.0e-14
E value
Match length
                   122
                   84
% identity
                   Arabidopsis thaliana chromosome II BAC F16B22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   3213
                   2237 1.R1040
Contig ID
                   uC-gmrominsoy093g12b1
5'-most EST
                   BLASTX
Method
                   g1171577
NCBI GI
BLAST score
                   745
E value
                   3.0e-79
Match length
                   173
                   82
% identity
                   (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
Seq. No.
Contig ID
                   2238 1.R1040
5'-most EST
                   jC-gmf102220114g03a1
Seq. No.
Contig ID
                   2245 1.R1040
5'-most EST
                   LIB3028-046-Q1-B1-G11
Method
                   BLASTX
NCBI GI
                   q4455337
BLAST score
                   290
E value
                   8.0e-26
Match length
                   213
% identity
                   (AL035525) pectinesterase-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3216
                   2247 1.R1040
Contig ID
                   LIB3106-021-Q1-K1-C9
5'-most EST
Method
                   BLASTX
                   g478409
NCBI GI
BLAST score
                   491
                   2.0e-73
E value
                   256
Match length
% identity
                   peroxidase (EC 1.11.1.7), cationic - adzuki bean
NCBI Description
                   >gi 218328 dbj BAA01950_ (D11337) peroxidase [Vigna
                   angularis]
Seq. No.
                   3217
                   2249 1.R1040
Contig ID
5'-most EST
                   wrg7\overline{0}0789411.h2
```

3218

Seq. No.

```
Contig ID
                   2250 1.R1040
                   pmv700894288.h1
5'-most EST
                   BLASTX
Method
                   g3164115
NCBI GI
BLAST score
                   231
                   1.0e-18
E value
Match length
                   133
% identity
                   37
                   (AJ224145) major latex-like protein [Rubus idaeus]
NCBI Description
                   3219
Seq. No.
Contig ID
                   2251 1.R1040
                   LIB3028-046-Q1-B1-G6
5'-most EST
Seq. No.
                   3220
Contig ID
                   2253 1.R1040
                   smc7\overline{0}0748727.h1
5'-most EST
Method
                   BLASTX
                   g2154609
NCBI GI
BLAST score
                   390
                   1.0e-37
E value
Match length
                   136
% identity
                   51
                   (D63509) endoxyloglucan transferase related protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1_
                   (AC007069) endoxyloglucan transferase [Arabidopsis
                   thaliana]
                   3221
Seq. No.
                   2254 1.R1040
Contig ID
                   LIB3051-045-Q1-K1-C5
5'-most EST
                   BLASTX
Method
                   q1019946
NCBI GI
BLAST score
                   852
                   2.0e-91
E value
                   210
Match length
                   77
% identity
NCBI Description
                   (U37060) ascorbate peroxidase [Gossypium hirsutum]
Seq. No.
                   3222
                   2254 2.R1040
Contig ID
                   leu701157531.h1
5'-most EST
                   BLASTX
Method
                   g1019946
NCBI GI
BLAST score
                   531
                   5.0e-54
E value
                   159
Match length
                   73
% identity
                   (U37060) ascorbate peroxidase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   3223
                   2256 1.R1040
Contig ID
5'-most EST
                   LIB3093-027-Q1-K1-A3
                   BLASTX
Method
```

g4204313

532 3.0e-54

NCBI GI BLAST score

E value

5'-most EST

```
Match length
                  118
                  85
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  3224
Seq. No.
Contig ID
                  2256 2.R1040
                  hyd700727331.h1
5'-most EST
Method
                  BLASTX
                  g4204313
NCBI GI
BLAST score
                  372
                  1.0e-35
E value
                  83
Match length
                  84
% identity
                   (AC003027) lcl_prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  3225
Seq. No.
                  2257 1.R1040
Contig ID
                  ssr700556995.h1
5'-most EST
                  BLASTX
Method
                  g3548808
NCBI GI
BLAST score
                  493
                  2.0e-49
E value
                  297
Match length
                  45
% identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                  3226
Seq. No.
                  2258 1.R1040
Contig ID
                  jC-qmle01810093f07d1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q20721
BLAST score
                  150
                  1.0e-78
E value
                  290
Match length
                  90
% identity
                  Pea mRNA for ferredoxin-NADP+ reductase
NCBI Description
Seq. No.
                  3227
                  2258 2.R1040
Contig ID
                  LIB3049-003-Q1-E1-F4
5'-most EST
Method.
                  BLASTX
NCBI GI
                  g1351408
BLAST score
                  1781
                  0.0e+00
E value
                  467
Match length
                  79
% identity
                  VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                  >gi_1076563_pir__S51117 cystein proteinase - sweet orange
                  >gi 633185_emb_CAA87720_ (Z47793) cystein proteinase (by
                  similarity) [Citrus sinensis] >gi_1588548_prf__2208463A
                  vascular processing protease [Citrus sinensis]
                  3228
Seq. No.
                  2258 3.R1040
Contig ID
```

uC-qmflminsoy010h10b1

```
Method
                   BLASTN
NCBI GI
                   g2511696
BLAST score
                   743
                   0.0e + 00
E value
                   1412
Match length
                   89
% identity
                   Phaseolus vulgaris Moldavian encoding asparagine-specific
NCBI Description
                   endopeptidase precursor (clone cp6b)
                   3229
Seq. No.
                   2258 4.R1040
Contig ID
5'-most EST
                   jC-gmle01810009h12d1
Method
                   BLASTN
NCBI GI
                   g551130
BLAST score
                   437
                   0.0e+00
E value
Match length
                   877
% identity
                   Vicia faba ferredoxin NADP+ reductase precursor (fnr) mRNA,
NCBI Description
                   complete cds
                   3230 4
Seq. No.
Contig ID
                   2258 5.R1040
                   fde7\overline{0}0871556.h1
5'-most EST
Method
                   BLASTN
                   g2511696
NCBI GI
                   715
BLAST score
E value
                   0.0e+00
Match length
                   1488
                   88
% identity
                   Phaseolus vulgaris Moldavian encoding asparagine-specific
NCBI Description
                   endopeptidase precursor (clone cp6b)
Seq. No.
                   3231
                   2259 1.R1040
Contig ID
                   ssr700554396.hl
5'-most EST
                   BLASTX
Method
                   q4539003
NCBI GI
BLAST score
                   203
                   2.0e-15
E value
Match length
                   81
% identity
                   (AL049481) putative protein [Arabidopsis thaliana]
NCBI Description
                   3232
Seq. No.
                   2260 1.R1040
Contig ID
                   rlr700898755.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4544432
                   227
BLAST score
                   1.0e-18
E value
Match length
                   93
                   55
% identity
                   (AC006955) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana]
```

3233

Seq. No.

```
Contig ID
                   2261 1.R1040
5'-most EST
                   LIB3049-053-Q1-E1-E3
Seq. No.
                   3234
                   2262 1.R1040
Contig ID
                   uC-gmronoir068e07b1
5'-most EST
                   3235
Seq. No.
                   2262 2.R1040
Contig ID
                   LIB3170-078-Q1-K1-A7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4049344
                   158
BLAST score
                   3.0e-10
E value
Match length
                   214
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   3236
Seq. No.
                   2262 3.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy089e10b1
Seq. No.
                   3237
                   2264 1.R1040
Contig ID
                   LIB3138-074-P1-N1-D5
5'-most EST
                   3238
Seq. No.
Contig ID
                   2268 1.R1040
5'-most EST
                   jC-gmst02400072c10a1
Method
                   BLASTX
                   g3776005
NCBI GI
                   663
BLAST score
                   1.0e-69
E value
Match length
                   156
                   87
% identity
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   3239
Seq. No.
Contig ID
                   2268 2.R1040
5'-most EST
                   LIB3050-002-Q1-E1-H10
Method
                   BLASTX
NCBI GI
                   q3776005
BLAST score
                   444
E value
                   3.0e-44
                   94
Match length
                   93
% identity
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   3240
Seq. No.
Contig ID
                   2269 1.R1040
5'-most EST
                   LIB3109-011-Q1-K1-E11
                   BLASTN
Method
                   q1666229
NCBI GI
BLAST score
                   327
E value
                   0.0e + 00
                   655
Match length
                   87
% identity
```

....

5'-most EST

```
NCBI Description Pisum sativum actin (PEAc9) mRNA, complete cds
                   >qi 1724138 gb U81047 PSU81047 Pisum sativum actin (PEAc9)
                   mRNA, complete cds
                   3241
Seq. No.
                   2269 2.R1040
Contig ID
                   jC-qmst02400043b09a1
5'-most EST
                   BLASTN
Method
                   g1666229
NCBI GI
BLAST score
                   358
                   0.0e+00
E value
Match length
                   719
                   89
% identity
                   Pisum sativum actin (PEAc9) mRNA, complete cds
NCBI Description
                   >gi_1724138_gb_U81047_PSU81047 Pisum sativum actin (PEAc9)
                   mRNA, complete cds
                   3242
Seq. No.
                   2269 3.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0986316.h1
Method
                   BLASTN
NCBI GI
                   g940812
BLAST score
                   167
                   1.0e-88
E value
Match length
                   394
% identity
                   86
NCBI Description P.sativum mRNA for actin protein
                   3243
Seq. No.
                   2269 4.R1040
Contig ID
                   wvk700683029.hl
5'-most EST
                   BLASTN
Method
                   g3860316
NCBI GI
BLAST score
                   192
                   1.0e-103
E value
Match length
                   465
                   88
% identity
NCBI Description
                  Cicer arietinum mRNA for actin, partial
                   3244
Seq. No.
                   2269 5.R1040
Contig ID
5'-most EST
                   zhf700963064.h1
Method
                   BLASTN
NCBI GI
                   g18317
BLAST score
                   113
E value
                   7.0e-57
Match length
                   197
                   89
% identity
                  D.carota RNA for actin gene Acl
NCBI Description
                   3245
Seq. No.
                   2270 1.R1040
Contig ID
5'-most EST
                   rca700997077.h1
                   3246
Seq. No.
                   2270 2.R1040
Contig ID
```

LIB3074-036-Q1-K1-F11

```
Method
                   BLASTX
                   g1881585
NCBI GI
BLAST score
                   330
                   2.0e-30
E value
                   145
Match length
                   52
% identity
                   (U72489) remorin [Solanum tuberosum]
NCBI Description
                   3247
Seq. No.
                   2271 1.R1040
Contig ID
                   fC-gmro700848271a1
5'-most EST
Method
                   BLASTX
                   q1905785
NCBI GI
BLAST score
                   895
E value
                   2.0e-96
Match length
                   347
                   60
% identity
                   (Y10685) G/HBF-1 [Glycine max]
NCBI Description
Seq. No.
                   3248
                   2271 2.R1040
Contig ID
                   uC-gmflminsoy020d04b1
5'-most EST
Method
                   BLASTX
                   g1905785
NCBI GI
BLAST score
                   154
                   2.0e-15
E value
Match length
                   69
% identity
                   75
                   (Y10685) G/HBF-1 [Glycine max]
NCBI Description
                   3249
Seq. No.
                   2272 1.R1040
Contig ID
5'-most EST
                   fde700870883.h1
                   3250
Seq. No.
                   2277 1.R1040
Contig ID
                   LIB3093-058-Q1-K1-E12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3075488
BLAST score
                   1240
                   1.0e-137
E value
Match length
                   286
                   82
% identity
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                   3251
Seq. No.
                   2277 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400014b12d1
Method
                   BLASTN
                   g3075487
NCBI GI
BLAST score
                   74
E value
                   5.0e-33
                   180
Match length
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
```

mRNA, complete cds

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NCBI Description

```
Seq. No.
                   3252
                   2277 3.R1040
Contig ID
5'-most EST
                   LIB3138-062-Q1-N1-G10
Method
                   BLASTX
                   q2827649
NCBI GI
BLAST score
                   156
                   3.0e-10
E value
Match length
                   46
% identity
                   61
                   (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2277 4.R1040
Contig ID
                   LIB3065-008-Q1-N1-A8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3075488
BLAST score
                   486
E value
                   8.0e-49
Match length
                   119
% identity
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   3254
                   2277 5.R1040
Contig ID
                   LIB3093-019-Q1-K2-H3
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3075487
BLAST score
                   58
E value
                   7.0e-24
Match length
                   86
% identity
                   92
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
                   3255
Seq. No.
                   2278 1.R1040
Contig ID
                   LIB3107-053-Q1-K1-E8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244970
BLAST score
                   2257
E value
                   0.0e + 00
Match length
                   585
% identity
                   69
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >qi 2326365 emb CAA74765 (Y14423) putative cell wall
                   protein [Arabidopsis thaliana]
                   3256
Seq. No.
                   2280 1.R1040
Contig ID
                   ssr700556839.hl
5'-most EST
                   BLASTX
Method
                   q1710807
NCBI GI
BLAST score
                   2464
                   0.0e + 00
E value
                   584
Match length
% identity
                   86
```

RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

```
KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390 (U21105) alphacpn60 [Pisum sativum]
```

```
3257
Seq. No.
                   2280 2.R1040
Contig ID
                   LIB3093-027-Q1-K1-D2
5'-most EST
Method
                   BLASTN
                   g3790440
NCBI GI
                   256
BLAST score
                   1.0e-142
E value
                   367
Match length
% identity
                   92
                   Canavalia lineata chaperonin 60 alpha subunit mRNA, nuclear
NCBI Description
                   gene encoding chloroplast protein, complete cds
Seq. No.
                   3258
                   2280 4.R1040
Contig ID
                   epx7\overline{0}1109229.h1
5'-most EST
                   BLASTN
Method
                   q3790440
NCBI GI
BLAST score
                   84
                   2.0e-39
E value
Match length
                   272
                   83
% identity
                   Canavalia lineata chaperonin 60 alpha subunit mRNA, nuclear
NCBI Description
                   gene encoding chloroplast protein, complete cds
Seq. No.
                   3259
Contig ID
                   2280 5.R1040
                   LIB3051-052-Q1-K1-A10
5'-most EST
                   BLASTN
Method
                   q3790440
NCBI GI
                   52
BLAST score
E value
                   2.0e-20
                   152 -
Match length
% identity
                   Canavalia lineata chaperonin 60 alpha subunit mRNA, nuclear
NCBI Description
                   gene encoding chloroplast protein, complete cds
Seq. No.
                   3260
Contig ID
                   2281 1.R1040
                   wrq7\overline{0}0791180.h1
5'-most EST
                   BLASTX
Method
                   q2136011
NCBI GI
                   228
BLAST score
                   2.0e-18
E value
                   84
Match length
% identity
                   protein DS 1, 24K - human >gi_1045059_emb_CAA57387_
NCBI Description
                   (X81788) ICT1 protein [Homo sapiens]
                   >gi_4557657_ref_NP_001536.1_pICT1_ immature colon carcinoma
                   transcript
```

Contig ID 2284\_1.R1040 5'-most EST fC-gmro700835781b1

Method BLASTX

5'-most EST

```
NCBI GI
                  g3482919
BLAST score
                  900
                  4.0e-97
E value
Match length
                  241
% identity
                  71
                  (AC003970) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3262
                  2290 1.R1040
Contig ID
                  g5605900
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2253442
BLAST score
                  270
                  3.0e-23
E value
Match length
                  78
% identity
                  56
                  (AF007784) LTCOR11 [Lavatera thuringiaca]
NCBI Description
                  3263
Seq. No.
                  2290 2.R1040
Contig ID
                  LIB3028-023-Q1-B1-A9
5'-most EST
Seq. No.
                  3264
                  2290 3.R1040
Contig ID
                  jex700904808.h1
5'-most EST
                  3265
Seq. No.
Contig ID
                  2290 4.R1040
5'-most EST
                  crh700851666.hl
                  BLASTX
Method
                  q2253442
NCBI GI
                  191
BLAST score
                   1.0e-14
E value
Match length
                   46
                   63
% identity
                   (AF007784) LTCOR11 [Lavatera thuringiaca]
NCBI Description
                   3266
Seq. No.
                   2291 1.R1040
Contig ID
                  LIB3049-008-Q1-E1-H2
5'-most EST
Method
                   BLASTX
                   q3298548
NCBI GI
                   340
BLAST score
                   6.0e-32
E value
                   138
Match length
% identity
                   (AC004681) putative spliceosomal protein [Arabidopsis
NCBI Description
                   thaliana]
                   3267
Seq. No.
                   2292 1.R1040
Contig ID
                   LIB3051-011-Q1-E1-G12
5'-most EST
Seq. No.
                   3268
                   2292 2.R1040
Contig ID
```

LIB3170-085-Q1-K1-D6

```
3269
Seq. No.
Contig ID
                   2293 1.R1040
                   g5175583
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2078350
                   799
BLAST score
                   3.0e-85
E value
Match length
                   192
                   83
% identity
NCBI Description
                   (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   3270
Contig ID
                   2293 2.R1040
                   LIB3139-031-P1-N1-G9
5'-most EST
                   BLASTX
Method
                   g2078350
NCBI GI
BLAST score
                   1457
E value
                   1.0e-162
Match length
                   384
% identity
                   75
                   (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                   3271
Seq. No.
Contig ID
                   2293 4.R1040
                   uC-gmrominsoy026g11b1
5'-most EST
                   BLASTX
Method
                   q2078350
NCBI GI
BLAST score
                   321
E value
                   1.0e-29
Match length
                   71
                   83
% identity
                   (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                   3272
Seq. No.
Contig ID
                   2294 1.R1040
5'-most EST
                   LIB3028-009-Q1-B1-G4
                   BLASTX
Method
NCBI GI
                   q1935019
BLAST score
                   438
E value
                   4.0e-43
Match length
                   161
% identity
                   (293774) sucrose transport protein [Vicia faba]
NCBI Description
Seq. No.
                   3273
                   2294 2.R1040
Contig ID
                   smc7\overline{0}0749544.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1935019
BLAST score
                   473
E value
                   2.0e-47
Match length
                   112
% identity
                   78
                   (Z93774) sucrose transport protein [Vicia faba]
NCBI Description
Seq. No.
                   3274
```

2294 3.R1040

Contig ID

. .

BLAST score

10 mm

415

```
5'-most EST
                   LIB3093-015-Q1-K1-G9
Seq. No.
                   3275
                   2296 1.R1040
Contig ID
                   kl1701214421.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245135
BLAST score
                   581
                   7.0e-60
E value
Match length
                   156
% identity
                   70
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3276
Contig ID
                   2297 1.R1040
5'-most EST
                   LIB3107-025-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4433048
BLAST score
                   592
                   6.0e-61
E value
Match length
                   147
% identity
                   79
                   (D26578) DNA-binding protein [Daucus carota]
NCBI Description
                   3277
Seq. No.
                   2297 2.R1040
Contig ID
                   uC-gmflminsoy064a03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4433048
                   592
BLAST score
                   7.0e-61
E value
                   154
Match length
                   78
% identity
                   (D26578) DNA-binding protein [Daucus carota]
NCBI Description
                   3278
Seq. No.
                   2297 5.R1040
Contig ID
5'-most EST
                   zsg701125668.hl
                   3279
Seq. No.
                   2298 1.R1040
Contig ID
                   uC-gmropic094g04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827143
                   937
BLAST score
                   1.0e-101
E value
                   195
Match length
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   3280
Seq. No.
                   2298 2.R1040
Contig ID
5'-most EST
                   q429\overline{2}031
                   BLASTX
Method
                   g2827143
NCBI GI
```

• 5

```
1.0e-40
E value
Match length
                   79
                   92
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   3281
Seq. No.
Contig ID
                   2298 3.R1040
                   dpv701097183.h1
5'-most EST
                   BLASTX
Method
                   g2827143
NCBI GI
BLAST score
                   2504
E value
                   0.0e + 00
Match length
                   522
                   89
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   3282
                   2305 1.R1040
Contig ID
                  pxt700946213.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4185513
BLAST score
                   589
                   1.0e-60
E value
Match length
                   130
                   85
% identity
NCBI Description
                   (AF102823) actin depolymerizing factor 5 [Arabidopsis
                   thaliana] >gi 4185517 (AF102825) actin depolymerizing
                   factor 5 [Arabidopsis thaliana]
                   3283
Seq. No.
                   2305 2.R1040
Contig ID
5'-most EST
                   LIB3107-025-Q1-K1-C12
Method
                   BLASTX
NCBI GI
                   g4185513
BLAST score
                   613
                   1.0e-63
E value
Match length
                   143
% identity
                   (AF102823) actin depolymerizing factor 5 [Arabidopsis
NCBI Description
                   thaliana] >gi_4185517 (AF102825) actin depolymerizing
                   factor 5 [Arabidopsis thaliana]
                   3284
Seq. No.
                   2306_1.R1040
Contig ID
                   LIB3051-042-Q1-K1-H9
5'-most EST
Method
                   BLASTX
                   g2262195
NCBI GI
BLAST score
                   323
                   1.0e-29
E value
                   150
Match length
% identity
                   42
                   (U64820) josephin MJD1 [Homo sapiens]
NCBI Description
Seq. No.
                   3285
```

2306 3.R1040

Contig ID

Match length

454

```
5'-most EST
                   LIB3051-104-Q1-K1-G1
                   BLASTX
Method
NCBI GI
                   g1781299
BLAST score
                   397
                   2.0e-38
E value
Match length
                   151
% identity
                   57
                   (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                   tabacum]
                   3286
Seq. No.
                   2306 4.R1040
Contig ID
                   g5687810
5'-most EST
Method
                   BLASTX
                   g1781299
NCBI GI
BLAST score
                   272
                   8.0e-28
E value
Match length
                   110
% identity
                   66
                   (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                   3287
Seq. No.
                   2307 1.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0980603.h1
                   3288
Seq. No.
Contig ID
                   2309 2.R1040
5'-most EST
                   uC-gmrominsoy074e05b1
                   3289
Seq. No.
                   2310 1.R1040
Contig ID
                   jex700908408.h1
5'-most EST
                   3290
Seq. No.
                   2310 2.R1040
Contig ID
5'-most EST
                   k117\overline{0}1202645.h1
                   3291
Seq. No.
                   2311 1.R1040
Contig ID
                   uC-gmflminsoy061a11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2511693
BLAST score
                   2060
                   0.0e+00
E value
Match length
                   458
% identity
                   83
                   (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
                   3292
Seq. No.
Contig ID
                   2311 2.R1040
5'-most EST
                   taw700658011.hl
                   BLASTN
Method
NCBI GI
                   g2511692
BLAST score
                   168
                   3.0e-89
E value
```

```
% identity
                   90
NCBI Description
                   Phaseolus vulgaris Moldavian encoding cysteine proteinase
                   precursor (clone cp71)
Seq. No.
                   3293
                   2311 3.R1040
Contig ID
                   zhf700958286.h1
5'-most EST
Method
                   BLASTN
                   q2511692
NCBI GI
BLAST score
                   70
                   4.0e-31
E value -
                                                                     . .
                   209
Match length
% identity
                   86
                   Phaseolus vulgaris Moldavian encoding cysteine proteinase
NCBI Description
                   precursor (clone cp71)
Seq. No.
                   3294
                   2311 5.R1040
Contig ID
5'-most EST
                   xpa7\overline{0}0793534.h1
Method
                   BLASTN
                   g2511692
NCBI GI
                   55
BLAST score
                   4.0e-22
E value
Match length
                   170
                   86
% identity
                   Phaseolus vulgaris Moldavian encoding cysteine proteinase
NCBI Description
                   precursor (clone cp71)
Seq. No.
                   3295
Contig ID
                   2312 1.R1040
                   dpv701103305.hl
5'-most EST
                   BLASTX
Method
                   a1350720
NCBI GI
BLAST score
                   452
E value
                   1.0e-44
                   111
Match length
                   76
% identity
                   60S RIBOSOMAL PROTEIN L32
NCBI Description
Seq. No.
Contig ID
                   2312 2.R1040
5'-most EST
                   LIB3028-045-Q1-B1-H12
                   BLASTX
Method
NCBI GI
                   q1350720
BLAST score
                   452
E value
                   6.0e-45
Match length
                   111
                   76
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L32
Seq. No.
                   3297
Contig ID
                   2312 3.R1040
5'-most EST
                   LIB3040-060-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   q1350720
BLAST score
                   438
E value
                   3.0e-43
```

5'-most EST

Method

```
94
Match length
% identity
                  60S RIBOSOMAL PROTEIN L32
NCBI Description
Seq. No.
                  3298
                  2312 4.R1040
Contig ID
                  LIB3073-013-Q1-K1-C6
5'-most EST
Method
                  BLASTX
                  q132886
NCBI GI
BLAST score
                  246
                  1.0e-20
E value
                  130
Match length
% identity
                  43
                  60S RIBOSOMAL PROTEIN L32 >gi 71335_pir R5HU32 ribosomal
NCBI Description
                  protein L32 - human >gi 71336_pir__R5MS32 ribosomal protein
                  L32 - mouse >gi_71337_pir__R5RT32 ribosomal protein L32 -
                  rat >qi 36132 emb CAA27048 (X03342) rpL32 (aa 1-135) [Homo
                  sapiens >qi 57117 emb CAA29777 (X06483) ribosomal protein
                  L32 [Rattus norvegicus] >gi 200781 (K02060) ribosomal
                  protein L32-3A [Mus musculus] >gi_226004_prf__1405339A
                  ribosomal protein L32 [Rattus norvegicus]
                  >qi 4506635 ref NP 000985.1 pRPL32 ribosomal protein L32
Seq. No.
                  2312 5.R1040
Contig ID
                  LIB3106-086-Q1-K1-H6
5'-most EST
Method
                  BLASTX
                  q132886
NCBI GI
BLAST score
                  185
E value
                  6.0e-14
                  54
Match length
% identity
                  60S RIBOSOMAL PROTEIN L32 >gi 71335 pir R5HU32 ribosomal
NCBI Description
                  protein L32 - human >gi_71336 pir__R5MS32 ribosomal protein
                  L32 - mouse >gi 71337 pir R5RT32 ribosomal protein L32 -
                  rat >gi 36132 emb CAA27048 (X03342) rpL32 (aa 1-135) [Homo
                  sapiens] >gi_57117_emb_CAA29777_ (X06483) ribosomal protein
                  L32 [Rattus norvegicus] >gi 200781 (K02060) ribosomal
                  protein L32-3A [Mus musculus] >gi 226004 prf__1405339A
                  ribosomal protein L32 [Rattus norvegicus]
                  >qi 4506635 ref NP 000985.1 pRPL32 ribosomal protein L32
Seq. No.
                  3300
Contig ID
                  2313 1.R1040
5'-most EST
                  LIB3049-045-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q3608485
BLAST score
                  1089
E value
                  1.0e-119
Match length
                  223
% identity
                  (AF088915) proteasome beta subunit [Petunia x hybrida]
NCBI Description
Seq. No.
                  3301
                  2313 2.R1040
Contig ID
```

zzp700835212.h1

BLASTX

5'-most EST

```
g3608485
NCBI GI
BLAST score
                   455
                   2.0e-45
E value
Match length
                   92
% identity
                   (AF088915) proteasome beta subunit [Petunia x hybrida]
NCBI Description
Seq. No.
                   2315 1.R1040
Contiq ID
5'-most EST
                   q4292157
                   BLASTX
Method
                   q2347088
NCBI GI
BLAST score
                   417
                   2.0e-40
E value
                   117
Match length
% identity
NCBI Description
                   (U72765) non-specific lipid transfer protein PvLTP-24
                   [Phaseolus vulgaris]
Seq. No.
                   2315 2.R1040
Contig ID
5'-most EST
                   q5753304
                   BLASTN
Method
NCBI GI
                   g4490324
BLAST score
                   40
                   5.0e-13
E value
Match length
                   88
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
                   (ESSA project)
                   3304
Seq. No.
Contig ID
                   2315 3.R1040
5'-most EST
                   q5126391:
Method
                   BLASTX
NCBI GI
                   g4490331
BLAST score
                   520
                   1.0e-52
E value
Match length
                   139
% identity
                   70
NCBI Description
                   (AL035656) hypothetical protein [Arabidopsis thaliana]
                   3305
Seq. No.
                   2316 1.R1040
Contig ID
                   1eu7\overline{0}1157155.h1
5'-most EST
Method
                   BLASTX
                   g2160182
NCBI GI
BLAST score
                   206
                   9.0e-16
E value
Match length
                   155
                   37
% identity
                   (AC000132) ESTs gb ATTS1236, gb T43334, gb N97019, gb AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
                   3306
Seq. No.
                   2316 2.R1040
Contig ID
```

LIB3170-012-Q1-J1-A10

E value

```
3307
Seq. No.
Contig ID
                   2316 3.R1040
                   LIB3039-012-Q1-E1-C9
5'-most EST
                   3308
Seq. No.
                   2317 1.R1040
Contig ID
                   uC-gmropic007e02b1
5'-most EST
Method
                   BLASTX
                   g4309738
NCBI GI
BLAST score
                   820
                   1.0e-87
E value
                   297
Match length
                   58
% identity
                   (AC006439) putative tubby protein [Arabidopsis thaliana]
NCBI Description
                   3309
Seq. No.
                   2317 2.R1040
Contig ID
                   vwf700673985.hl
5'-most EST
Method
                   BLASTX
                   g4309738
NCBI GI
                   505
BLAST score ~
E value
                   5.0e-51
Match length
                   145
                   66
% identity
                   (AC006439) putative tubby protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3310
                   2321 1.R1040
Contig ID
5'-most EST
                   LIB3028-046-Q1-B1-A11
Method
                   BLASTX
NCBI GI
                   g1263160
BLAST score
                   360
                   6.0e-34
E value
                   251
Match length
                   12
% identity
                   (X89226) leucine-rich repeat/receptor protein kinase [Oryza
NCBI Description
                  sativa]
                   3311
Seq. No.
                   2322 1.R1040
Contig ID
                   asn7\overline{0}1130506.h1
5'-most EST
Method
                   BLASTN
                   g1370195
NCBI GI
                   308
BLAST score
                   1.0e-172
E value
Match length
                   412
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB8D
                   3312
Seq. No.
                   2322 2.R1040
Contig ID
5'-most EST
                   sat701004249.h1
Method
                   BLASTN
NCBI GI
                   q1370195
BLAST score
                   256
```

1.0e-142

```
Match length
                   497
% identity
                   89
                   L.japonicus mRNA for small GTP-binding protein, RAB8D
NCBI Description
Seq. No.
                   3313
Contig ID
                   2322 3.R1040
5'-most EST
                   LIB3087-002-Q1-K1-F6
Method
                   BLASTN
NCBI GI
                   q1370197
BLAST score
                   294
                   1.0e-164
E value
Match length
                   402
                   93
% identity
                   L.japonicus mRNA for small GTP-binding protein, RAB8E
NCBI Description
Seq. No.
                   2322 4.R1040
Contig ID
5'-most EST
                   fC-qmse700751577a1
Method
                   BLASTN
NCBI GI
                   q1370195
BLAST score
                   210
E value
                   1.0e-114.
Match length
                   302
% identity
                   92
                   L.japonicus mRNA for small GTP-binding protein, RAB8D
NCBI Description
                   3315
Seq. No.
Contig ID
                   2323 1.R1040
5'-most EST
                   LIB3092-061-Q1-K1-G5
Method
                   BLASTX
                   g2495091
NCBI GI
BLAST score
                   362
                   7.0e-34
E value
Match length
                   175
                   42
% identity
                   GRPE PROTEIN >gi_1075599_pir__PC2235 GrpE protein -
NCBI Description
                   Synechococcus sp. (PCC 7942) (fragment)
                   >gi_507817_dbj_BAA05902_ (D28550) heat shock protein GrpE
                   homolog [Synechococcus sp.]
                   3316
Seq. No.
Contig ID
                   2326 1.R1040
                   jC-qmst02400073c02a1
5'-most EST
                   BLASTX
Method
                   q3005599
NCBI GI
BLAST score
                   223
                   4.0e-18
E value
                   168
Match length
% identity
                   28
                   (AF052432) katanin p80 subunit [Homo sapiens]
NCBI Description
                   3317
Seq. No.
                   2326 2.R1040
Contig ID
5'-most EST
                   crh700853505.hl
                   BLASTX
Method
                   g940288
NCBI GI
```

BLAST score

. . . . . . . . .

5'-most EST

```
1.0e-82
E value
                  223
Match length
                   68
% identity
                   (L43510) protein localized in the nucleoli of pea nuclei;
NCBI Description
                  ORF; putative [Pisum sativum]
                   3318
Seq. No.
                   2328_1.R1040
Contig ID
                   g5677260
5'-most EST
                  BLASTX
Method
                   g2244910
NCBI GI
BLAST score
                   316
                   6.0e-29
E value
                   105
Match length
                   50
% identity
                   (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   3319
Seq. No.
                   2329 1.R1040
Contig ID
                   LIB3028-045-Q1-B1-F2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2832695
                   181
BLAST score
                   3.0e-13
E value
                   62
Match length
                   58
% identity
                  (AL021713) putative protein [Arabidopsis thaliana]
NCBI Description
                   3320
Seq. No.
                   2330 1.R1040
Contig ID
                   k117\overline{0}1202518.h1
5'-most EST
                   BLASTX
Method
                   g1518855
NCBI GI
                   211
BLAST score
                   2.0e-16
E value
                   72
Match length
                   61
% identity
                   (U65960) HASPP28 [Homo sapiens]
NCBI Description
                   3321
Seq. No.
                   2330 2.R1040
Contig ID
                   LIB3109-027-Q1-K1-E1
5'-most EST
                   BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   48
Match length
                   65
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   3322
Seq. No.
                   2330 4.R1040
Contig ID
5'-most EST
                   LIB3051-024-Q1-K1-H6
                   3323
Seq. No.
                   2330 5.R1040
Contig ID
```

LIB3040-015-Q1-E1-A2

```
Seq. No.
                       3324
    Contig ID
                       2330 7.R1040
                       gsv701055923.hl
    5'-most EST
    Seq. No.
                       3325
    Contiq ID
                       2333 1.R1040
                       ssr700559590.hl
    5'-most EST
    Method
                       BLASTX
    NCBI GI
                       g4469011
    BLAST score
                       881
👵 E value
                       6.0e-95
                       238
    Match length
    % identity
    NCBI Description
                       (AL035602) carbohydrate kinase-like protein [Arabidopsis
                       thaliana]
    Seq. No.
                       3326
                       2333 2.R1040
    Contig ID
    5'-most EST
                       LIB3106-097-Q1-K1-F11
    Method
                       BLASTX
    NCBI GI
                       g4469011
   BLAST score
                       223
                      5.0e-18
    E value
    Match length
                       68
    % identity
                       (AL035602) carbohydrate kinase-like protein [Arabidopsis
    NCBI Description
                       thaliana]
    Seq. No.
                       3327
                       2334 1.R1040
    Contig ID
                       ncj7\overline{0}0985896.h1
    5'-most EST
   Method
                       BLASTX
    NCBI GI
                       q4455284
    BLAST score
                       617
                       4.0e-64
    E value
   Match length
                       163
    % identity
    NCBI Description
                       (AL035527) beta-glucosidase-like protein [Arabidopsis
                       thaliana]
    Seq. No.
                       3328
                       2334 2.R1040
    Contig ID
                       LIB3028-041-Q1-B1-F2
    5'-most EST
   Method
                       BLASTX
                       q4455284
    NCBI GI
    BLAST score
                       395
                       2.0e-38
    E value
                       109
   Match length
    % identity
    NCBI Description
                       (AL035527) beta-glucosidase-like protein [Arabidopsis
                       thaliana]
                       3329
    Seq. No.
                       2339_1.R1040 <sup>-</sup>
   Contig ID
                       LIB3055-005-Q1-N1-C11
    5'-most EST
```

BLASTX

Method

% identity

87

```
NCBI GI
                  q1710840
BLAST score
                  2261
                  0.0e+00
E value
Match length
                   480
% identity
                  89
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57)
                  >gi 441217 dbj BAA03709 (D16138) S-adenosyl-L-homocystein
                  hydrolase [Nicotiana sylvestris] >gi 1857024 dbj BAA08142
                   (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana
                  tabacum] >gi 2588781 dbj BAA23164_ (D49804)
                  S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]
Seq. No.
                  2339 3.R1040
Contig ID
5'-most EST
                  zhf700951722.h1
Method
                  BLASTN
                  g170772
NCBI GI
BLAST score
                  176
                  4.0e-94
E value
                  296
Match length
% identity
                  Triticum aestivum S-adenosyl-L-homocysteine hydrolase
NCBI Description
                   (SH6.2) mRNA, complete cds
Seq. No.
                  2339 4.R1040
Contig ID
5'-most EST
                  sat701008057.hl
Method
                  BLASTN
NCBI GI
                  q535583
BLAST score
                  110
                  6.0e-55
E value
                  206
Match length
% identity
                  Medicago sativa adenosylhomocysteinase mRNA, complete cds
NCBI Description
Seq. No.
                  3332
                  2339 5.R1040
Contig ID
5'-most EST
                  k117\overline{0}1209855.h1
Method
                  BLASTN
NCBI GI
                  g2244747
BLAST score
                  60
E value
                  4.0e-25
Match length
                  124
                  88
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  3333
Contig ID
                  2339 6.R1040
5'-most EST
                  LIB3139-004-P1-N1-H3
Method
                  BLASTN
NCBI GI
                  g535583
BLAST score
                  85
E value
                  7.0e-40
Match length
                  216
```

```
NCBI Description
                  Medicago sativa adenosylhomocysteinase mRNA, complete cds
Seq. No.
                   3334
Contig ID
                   2339 9.R1040
                   txt700735356.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g170772
BLAST score .
                   74
E value
                   1.0e-33
Match length
                   102
                   93
% identity
                   Triticum aestivum S-adenosyl-L-homocysteine hydrolase
NCBI Description
                   (SH6.2) mRNA, complete cds
Seq. No.
                   3335
Contig ID
                   2341 1.R1040
                   seb700649714.hl
5'-most EST
Seq. No.
                   3336
                   2341 2.R1040
Contig ID
5'-most EST
                   txt700734826.hl
Seq. No.
                   3337
                   2342 1.R1040
Contig ID
                                                                    . . .
                   k117\overline{0}1213196.h1
5'-most EST
Method
                  BLASTX
                   g2780365
NCBI GI
BLAST score
                   229
                   8.0e-19
E value
                   90
Match length
                   52
% identity
                   (AB007693) Elongin C [Drosophila melanogaster]
NCBI Description
Seq. No.
                   3338
                   2343 1.R1040
Contig ID
                  LIB3170-082-Q1-K1-G9
5'-most EST
Method
                   BLASTX
                   g1172874
NCBI GI
BLAST score
                   721
                   5.0e-76
E value
Match length
                   291
                   57
% identity
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                  >gi_479589_pir__S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi 391608 dbj BAA01546 (D10703) rd22
                   [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
                   [Arabidopsis thaliana]
                   3339
Seq. No.
Contig ID
                   2343 3.R1040
                  LIB3170-082-Q1-J1-G9
5'-most EST
                  BLASTX
Method
                   g1172874
NCBI GI
BLAST score
                   300
                   3.0e-27
E value
                  70
Match length
```

% identity

```
DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                  >gi 479589_pir__S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi 391608_dbj_BAA01546_ (D10703) rd22
                  [Arabidopsis thaliana] >gi 447134 prf 1913421A rd22 gene
                   [Arabidopsis thaliana]
                  3340
Seq. No.
                  2344 1.R1040
Contig ID
                  fua701038156.hl
5'-most EST
                  BLASTX
Method
                  g3894158
NCBI GI
                  420
BLAST score
                  7.0e-41
E value
Match length
                  198
                  43
% identity
                  (ACO05312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                  thaliana]
                  3341
Seq. No.
                  2346 1.R1040
Contig ID
                  jC-gmf102220054g02a1
5'-most EST
                  3342
Seq. No.
                  2348 1.R1040
Contig ID
                  LIB3167-010-P1-K1-F5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1321941
BLAST score
                  938
                  1.0e-101
E value
                  330
Match length
                  59
% identity
                  (Z48564) dihydrolipoamide dehydrogenase [Synechocystis
NCBI Description
                  PCC6803]
                  3343
Seq. No.
                  2349 1.R1040
Contig ID
5'-most EST
                  LIB3028-037-Q1-B1-G11
                  3344
Seq. No.
                  2352 1.R1040
Contig ID
                  uC-gmflminsoy043b08b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q871505
                  452
BLAST score
                  0.0e+00
E value
                  612
Match length
                  94
% identity
NCBI Description
                  P.sativum mRNA for small GTP-binding protein (clone pGTP11)
                  3345
Seq. No.
                  2352 2.R1040
Contig ID
5'-most EST
                  LIB3049-012-Q1-E1-B1
                  BLASTN
Method
                  q871507
NCBI GI
BLAST score
                  474
```

0.0e + 00

808

E value Match length

NCBI Description

thaliana]

13.00

```
% identity
                   90
                   P.sativum mRNA for small GTP-binding protein (clone pGTP13)
NCBI Description
Seq. No.
                   3346
                   2352 4.R1040
Contig ID
                   asn701139218.hl
5'-most EST
                   BLASTN
Method
                   g871507
NCBI GI
                   218
BLAST score
                   1.0e-119
E value
                   302
Match length
                   93
% identity
                   P.sativum mRNA for small GTP-binding protein (clone pGTP13)
NCBI Description
                   3347
Seq. No.
                   2353 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400072a07a1
Method
                   BLASTX
                   q4415908
NCBI GI
BLAST score
                   542
                   4.0e-69
E value
Match length
                   271
% identity
                   60
                   (AC006282) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3348
Seq. No.
Contig ID
                   2354 1.R1040
                   k117\overline{0}1214239.h1
5'-most EST
Seq. No.
                   3349
                   2356 1.R1040
Contiq ID
5'-most EST
                   LIB3028-045-Q1-B1-E6
                   3350
Seq. No.
                   2357 1.R1040
Contig ID
5'-most EST
                   k11701206565.hl
Seq. No.
                   3351
                   2357 2.R1040
Contig ID
5'-most EST
                   LIB3138-122-Q1-N1-D7
                   3352
Seq. No.
Contig ID
                   2357 3.R1040
                   LIB3028-045-Q1-B1-E7
5'-most EST
                   3353
Seq. No.
                   2358_1.R1040
Contig ID
5'-most EST
                   LIB3050-018-Q1-E1-B10
                   BLASTX
Method
NCBI GI
                   g4510363
BLAST score
                   556
E value
                   7.0e-57
Match length
                   143
% identity
                   73
```

(AC007017) putative DNA-binding protein [Arabidopsis

```
Seq. No.
                   3354
                   2358 2.R1040
Contig ID
5'-most EST
                  LIB3028-045-Q1-B1-E8
Method
                  BLASTX
                  g4510363
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
                  72
Match length
                  82
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   3355
Seq. No.
                   2364 1.R1040
Contig ID
                  LIB3028-010-Q1-B1-E4
5'-most EST
Method
                  BLASTX
                  q3687240
NCBI GI
BLAST score
                   154
                   4.0e-10
E value
                   40
Match length
% identity
                   65
                   (AC005169) extensin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3356
                   2365 1.R1040
Contig ID
                   jC-gmf102220082f04d1
5'-most EST
Method
                   BLASTX
NCBI GI
                  q4510383
BLAST score
                   569
                   3.0e-73
E value
                  253
Match length
                   63
% identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3357
Seq. No.
                   2368 1.R1040
Contig ID
                   LIB3028-045-Q1-B1-C7
5'-most EST
                   BLASTX
Method
NCBI GI
                  g3063458
BLAST score
                   215
E value
                   2.0e-17
                  80 -
Match length
                   51
% identity
                   (AC003981) F22013.20 [Arabidopsis thaliana]
NCBI Description
                   3358
Seq. No.
                   2370 1.R1040
Contig ID
5'-most EST
                  LIB3073-010-Q1-K1-C5
                  BLASTX
Method .
                  g4097547
NCBI GI
BLAST score
                   259
                   3.0e-22
E value
                  110
Match length
% identity
                  (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
```

...

3359

Seq. No.

5'-most EST

∹ .

```
Contig ID
                   2370 2.R1040
                   leu7\overline{0}1145557.h1
5'-most EST
Method
                   BLASTX
                   g4097547
NCBI GI
                   219
BLAST score
                   1.0e-17
E value
Match length
                   118
                   27
% identity
                   (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
                   3360
Seq. No.
Contig ID
                   2370 4.R1040
                   leu7\overline{0}1151209.h1
5'-most EST
Seq. No.
                   3361
Contig ID
                   2370 5.R1040
                   jex700906674.h1
5'-most EST
Seq. No.
                   3362
                   2371 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir008g01b1
Seq. No.
                   3363
                   2372 1.R1040 -
Contig ID
                   jC-gmf102220125f01a1
5'-most EST
                   3364
Seq. No.
Contig ID
                   2379 1.R1040
5'-most EST
                   jC-gmf102220097e06a1
Method
                   BLASTX
                   g3036810
NCBI GI
BLAST score
                   372
                   4.0e-35
E value
Match length
                   104
% identity
                   67
                   (AL022373) putative Myc-type transcription factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   3365
Contig ID
                   2379 2.R1040
                   LIB3109-009-Q1-K1-G5
5'-most EST
                   BLASTX
Method
                   q3036810
NCBI GI
BLAST score
                   171
                   2.0e-12
E value
Match length
                   48
                   67
% identity
                   (AL022373) putative Myc-type transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   3366
Seq. No.
                   2379 3.R1040
Contig ID
                   hrw701060875.hl
5'-most EST
Seq. No.
                   3367
                   2381 1.R1040
Contig ID
```

uC-gmropic097c12b1

```
Method
                   BLASTX
NCBI GI
                   g4544443
BLAST score
                   1076
                   1.0e-117
E value
Match length
                   317
                   68
% identity
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   3368
Seq. No.
Contig ID
                   2381 2.R1040
                   uC-gmropic039b05b1
5'-most EST
                   BLASTX
Method
                   g4544443
NCBI GI
BLAST score
                   365
                   9.0e-35
E value
Match length
                   111
% identity
                   70
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   3369
                                                                     . : ; . . .
Seq. No.
Contig ID
                   2381 3.R1040
5'-most EST
                   LIB3051-053-Q1-K2-B11
Method
                   BLASTX
NCBI GI
                   g4544443
BLAST score
                   385
E value
                   4.0e-37
Match length
                   141
% identity
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   3370
                   2381 4.R1040
Contig ID
                   LIB3106-061-Q1-K1-H10
5'-most EST
                   3371
Seq. No.
Contig ID
                   2382 1.R1040
                   leu7\overline{0}1147626.h1
5'-most EST
                   3372
Seq. No.
                   2384 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy080g10b1
Method
                   BLASTN
NCBI GI
                   g3821780
                   35
BLAST score
                   4.0e-10
E value
                   36
Match length
                   60
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   3373
Seq. No.
                   2388 1.R1040
Contig ID
                   awf700836736.hl
5'-most EST
```

BLASTX

q3522938

Method NCBI GI

```
BLAST score
                   379
                   1.0e-35
E value
Match length
                   352
% identity
                   30
                   (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3374
                   2388 2.R1040
Contiq ID
                   jC-qmle01810071h10a1
5'-most EST
                   3375
Seq. No.
Contig ID
                   2388 3.R1040
5'-most EST
                   uC-gmrominsoy202c09b1
Seq. No.
                   337.6
Contig ID
                   2390 1.R1040
5'-most EST
                   zzp700830963.hl
Method
                   BLASTN
NCBI GI
                   g2980757
BLAST score
                   51
E value
                   1.0e-19
Match length
                   229
% identity
                   87
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
NCBI Description
                   (ESSAII project)
                   3377
Seq. No.
Contig ID
                   2392 1.R1040
                   bth700843551.h1
5'-most EST
                   3378
Seq. No.
                   2394 1.R1040
Contig ID
                   LIB3039-005-Q1-E1-E2
5'-most EST
Method
                   BLASTX
                   g100196
NCBI GI
                   1174
BLAST score
                   1.0e-129
E value
                   249
Match length
% identity
                   86
                   chlorophyll a/b-binding protein (cab-11) - tomato
NCBI Description
                   3379
Seq. No.
                   2396 1.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0983176.h1
Method
                   BLASTX
NCBI GI
                   g549060
                   1088
BLAST score
                   1.0e-136
E value
Match length
                   363
                   69
% identity
                   T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
NCBI Description
                   >gi_631656_pir__S43058 CCTeta protein eta chain - mouse
                   >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of
                   the chaperonin containing TCP-1 (CCT) [Mus musculus]
```

Seq. No. 3380

Contig ID 2397\_1.R1040

```
leu701150938.h1
5'-most EST
                   3381
Seq. No.
                   2397 2.R1040
Contig ID
                   k117\overline{0}1203629.h2
5'-most EST
                   BLASTN
Method
                   g3046847
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   104
Match length
                   84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                  K11J9, complete sequence [Arabidopsis thaliana]
                   3382
Seq. No.
                   2397 3.R1040
Contig ID
5'-most EST
                   eep700868680.hl
Method
                   BLASTN
                   g3046847
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   104
                   84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                   K11J9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   3383
Contig ID
                   2400 1.R1040
                  LIB3051-054-Q1-K2-B11
5'-most EST
                   BLASTX
Method
                   g416564
NCBI GI
BLAST score
                   631
E value
                   9.0e-66
                   203
Match length
                   64
% identity
                  ABCISIC ACID-INDUCIBLE PROTEIN KINASE
NCBI Description
                   >gi_422013_pir__A46408 abscisic acid-inducible
                   serine/threonine protein kinase homolog - wheat (fragment)
                   >gi 170664 (M94726) protein kinase [Triticum aestivum]
                   3384
Seq. No.
                   2403 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy045d06b1
Method
                   BLASTN
                   g3449327
NCBI GI
                   35
BLAST score
E value
                   2.0e-09
Match length
                   168
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCA23, complete sequence [Arabidopsis thaliana]
                   3385
Seq. No.
Contig ID
                   2403 2.R1040
                   jC-gmst02400007d06a1
5'-most EST
```

Seq. No.

Contig ID 5'-most EST

```
Contig ID
                   2403 3.R1040
                   uC-gmrominsoy091c02b1
5'-most EST
                   3387
Seq. No.
                   2403 5.R1040
Contig ID
                   jC-gmst02400041e01a1
5'-most EST
                   3388
Seq. No.
                   2404 1.R1040
Contig ID
                   eep700865952.hl
5'-most EST
Seq. No.
                   3389
                   2404 2.R1040
Contig ID
                   uC-gmflminsoy056c06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827661
BLAST score
                   468
                                                       √. . ·
                   2.0e-46
E value
                   230
Match length
% identity
                   43
                   (AL021637) hyuC-like protein [Arabidopsis thaliana]
NCBI Description
                   3390
Seq. No.
                   2404 3.R1040
Contig ID
                   LIB3\overline{0}73-018-Q1-K1-E12
5'-most EST
                   3391
Seq. No.
Contig ID
                   2404 4.R1040
                   LIB3051-095-Q1-K1-F9
5'-most EST
                   BLASTN
Method
                   q20740
NCBI GI
                   49
BLAST score
                   3.0e-18
E value
                   187
Match length
                   86
% identity
                   Pisum sativum mRNA for P protein, a part of glycine
NCBI Description
                   cleavage complex
                   3392
Seq. No.
                   2404 5.R1040
Contig ID
                   zhf700962751.h1
5'-most EST
                   3393
Seq. No.
                   2405 1.R1040
Contig ID
                   vzy7\overline{0}0753858.h1
5'-most EST
                   BLASTX
Method
                   g1256259
NCBI GI
BLAST score
                   742
                   1.0e-78
E value
Match length
                   184
                   77
% identity
                   (U50900) voltage-dependent anion channel protein [Spinacia
NCBI Description
                   oleracea]
                   3394
Seq. No.
                   2406 1.R1040
```

LIB3139-083-P1-N1-F2

```
BLASTX
Method
                   g3193292
NCBI GI
BLAST score
                   1576
E value
                   1.0e-176
Match length
                   371
                   84
% identity
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
                   3395
Seq. No.
                   2407 1.R1040
Contig ID
5'-most EST
                  LIB3028-045-Q1-B1-A1
                  BLASTX
Method
NCBI GI
                   q4539351
BLAST score
                   345
                   1.0e-32
E value
                   139
Match length
                   47
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   3396
Seq. No.
                  2410 1.R1040
Contig ID
5'-most EST
                  LIB3028-044-Q1-B1-E3
Method
                  BLASTX
NCBI GI
                  q115833
BLAST score
                  1118
E value
                  1.0e-122
Match length
                  259
                  81
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein CablOA - tomato >gi 170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                   3397
Seq. No.
Contig ID
                  2410 2.R1040
5'-most EST
                  gsv701045116.hl
                  BLASTX
Method
NCBI GI
                  q115833
BLAST score
                  1142
E value
                  1.0e-125
Match length
                  256
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein CablOA - tomato >gi_170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
Seq. No.
                  3398
Contig ID
                  2413 1.R1040
                  LIB3055-005-Q1-N1-H2
5'-most EST
Method
                  BLASTX
                  q3068705
NCBI GI
BLAST score
                  612
                  3.0e-63
E value
Match length
                  245
```

```
% identity
                  51
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                  3399
Seq. No.
                  2413 2.R1040
Contig ID
                  fC-qmro700845160a3
5'-most EST
Method
                  BLASTX
                  g1617200
NCBI GI
BLAST score
                  798
                  6.0e-85
E value
Match length
                  161
                  89
% identity
                  (Y08607) Shaggy-like kinase 6 [Nicotiana tabacum]
NCBI Description
                  3400
Seq. No.
                  2413 3.R1040
Contig ID
                  jC-gmle01810025b09d1
5'-most EST
                  3401
Seq. No.
                  2413 4.R1040
Contig ID
                  fC-gmse700669136r4
5'-most EST
Method
                  BLASTX
                  g2598603
NCBI GI
BLAST score
                  173
                  3.0e-12
E value
                  37
Match length
                  86
% identity
                  (AJ002315) shaggy-like kinase 59 [Nicotiana tabacum]
NCBI Description
                  3402
Seq. No.
                  2414 1.R1040
Contig ID
                  LIB3039-010-Q1-E1-C7
5'-most EST
                  BLASTX
Method
                  g1086252
NCBI GI
                  482
BLAST score
                  2.0e-48
E value
                  142
Match length
                  59
% identity
                  sucrose cleavage protein - Potato >gi_707001_bbs_157931
NCBI Description
                  (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                  tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                  [Solanum tuberosum]
                  3403
Seq. No.
                  2414 2.R1040
Contig ID
                  LIB3092-037-Q1-K1-A2
5'-most EST
                  BLASTX
Method
                  g1086252
NCBI GI
                  209
BLAST score
                  1.0e-16
E value
Match length
                  74
% identity
                  sucrose cleavage protein - Potato >gi_707001_bbs_157931
NCBI Description
                   (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                  tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
```

[Solanum tuberosum]

NCBI GI

```
Seq. No.
                   3404
Contig ID
                   2414 3.R1040
5'-most EST
                   LIB3051-104-Q1-K1-D6
Method
                   BLASTX
                   g1086252
NCBI GI
BLAST score
                   271
E value
                   8.0e-24
                   95
Match length
                   52
% identity
                   sucrose cleavage protein - Potato >gi 707001 bbs 157931
NCBI Description
                   (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                   tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                   [Solanum tuberosum]
                   3405
Seq. No.
Contig ID
                   2418 1.R1040
                   LIB3028-044-Q1-B1-F3
5'-most EST
                   3406
Seq. No.
                   2420 1.R1040
Contig ID
5'-most EST
                   LIB3028-044-Q1-B1-F5
Method
                   BLASTX
NCBI GI
                   g1931654
BLAST score
                   159
                   9.0e-11
E value
Match length
                   64
                   50
% identity
NCBI Description
                   (U95973) BRCA1-associated RING domain protein isolog
                   [Arabidopsis thaliana]
                   3407
Seq. No.
                   2421 1.R1040
Contig ID
                   LIB3138-034-Q1-N1-C3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4220531
BLAST score
                   254
                   1.0e-21
E value
Match length
                   129
% identity
                   43
                   (AL035356) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   3408
Seq. No.
                   2421 2.R1040
Contig ID
5'-most EST
                   k117\overline{0}1214230.h1
Method
                   BLASTX
                   g4220531
NCBI GI
BLAST score
                   177
                   1.0e-12
E value
Match length
                   88
% identity
NCBI Description
                   (AL035356) hypothetical protein [Arabidopsis thaliana]
                   3409
Seq. No.
                   2422 1.R1040
Contig ID
                   LIB3040-039-Q1-E1-F10
5'-most EST
                   BLASTX
Method
```

g131390

BLAST score 1010 E value 1.0e-110 Match length 243 % identity 79 OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >qi 280396 pir JS0771 photosystem II oxygen-evolving complex protein 2 precursor - garden pea >qi 20617 emb CAA33557 (X15552) precursor polypeptide (AA -73 to 186) [Pisum satīvum] >gi 344006 dbj BAA02553 (D13296) precursor for 23-kDa protein of photosystem II [Pisum sativum] 3410 Seq. No. Contig ID 2422 2.R1040 5'-most EST LIB3167-050-P1-K1-F8 Method BLASTN NCBI GI q4185595 BLAST score 254 E value 1.0e-140 Match length 728 % identity NCBI Description Pisum sativum mRNA for precursor for 23-kDa protein of photosystem II, complete cds Seq. No. 3411 2422 3.R1040 Contig ID 5'-most EST LIB3106-095-Q1-K1-F3 Method BLASTX NCBI GI g131390 BLAST score 474 1.0e-47 E value 128 Match length % identity 73 OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 280396 pir JS0771 photosystem II oxygen-evolving complex protein 2 precursor - garden pea >gi\_20617\_emb\_CAA33557\_ (X15552) precursor polypeptide (AA -73 to 186) [Pisum satīvum] >gi 344006 dbj BAA02553 (D13296) precursor for 23-kDa protein of photosystem II [Pisum sativum] 3412 Seq. No. 2422 4.R1040 Contig ID 5'-most EST LIB3049-042-Q1-E1-C9 BLASTX Method g131393 NCBI GI

BLAST score 304 9.0e-30 E value Match length 100

% identity OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD NCBI Description SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)

>gi\_100360\_pir\_\_S15005 photosystem II oxygen-evolving complex protein 2 - common tobacco

>gi 19911 emb CAA39039.1 (X55354) photosystem II 23kDa

## polypeptide [Nicotiana tabacum]

```
Seq. No.
                   3413
Contig ID
                   2423 1.R1040
5'-most EST
                   uC-gmflminsoy089a10b1
Method
                   BLASTX
NCBI GI
                   q1402912
BLAST score
                   646
E value
                   2.0e-67
Match length
                   169
% identity
                   76
NCBI Description
                   (X98317) peroxidase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   2423 2.R1040
5'-most EST
                   jC-qmf102220062h05a1
Method
                   BLASTX
NCBI GI
                   q1402912
BLAST score
                   216
E value
                   1.0e-26
Match length
                   88
% identity
NCBI Description
                   (X98317) peroxidase [Arabidopsis thaliana]
                   3415
Seq. No.
Contig ID
                   2423 3.R1040
5'-most EST
                   LIB3028-001-Q1-B1-H7
Method
                   BLASTX
NCBI GI
                   g1403138
BLAST score
                   705
                   5.0e-74
E value
Match length
                   180
% identity
                   72
                   (X98190) peroxidase ATP2a [Arabidopsis thaliana]
NCBI Description
                   >gi 4371288 gb AAD18146 (AC006260) putative peroxidase
                  ATP2a [Arabidopsis thaliana]
                   3416
Seq. No.
Contig ID
                   2423 4.R1040
5'-most EST
                   LIB3028-004-Q1-B1-H7
Method
                   BLASTX
NCBI GI
                   q1402912
BLAST score
                   146
                   4.0e-09
E value
                   33
Match length
% identity
                   (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
                   3417
Seq. No.
                   2426_1.R1040
Contig ID
                   uC-gmropic033g08b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g20899
BLAST score
                   261
E value
                   1.0e-144
                   509
Match length
                   89
% identity
```

```
NCBI Description
                    Pea mRNA for Cu/Zn superoxide dismutase II (SOD9)
 Seq. No.
                    3418
                    2428 1.R1040
 Contig ID
 5'-most EST
                    wvk700683015.hl
                    BLASTX
 Method
 NCBI GI
                    q2499614
 BLAST score
                    1423
                    1.0e-158
 E value
 Match length
                    302
 % identity
                    88
                    MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)
 NCBI Description
                    >gi_481830_pir__S39559 mitogen-activated protein kinase 3
                    homolog ntf3 - common tobacco >gi 406751 emb CAA49592
                    (X69971) NTF3 [Nicotiana tabacum]
 Seq. No.
                    3419
 Contig ID
                    2428 2.R1040
                    LIB3049-045-Q1-E1-H6
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2499612
BLAST score
                   ·1·87
                    2.0e-18
 E value
                    55
 Match length
                    89
 % identity
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (PMEK1)
 NCBI Description
                    >gi 1076650 pir S52989 mitogen-activated,
                    extracelluar-regulated protein kinase 1 (EC 2.7.1.-) -
                    garden petunia >gi 603871 emb CAA58466 (X83440) MAP/ERK
                    kinase 1 [Petunia x hybrida]
                    3420
 Seq. No.
                    2429 1.R1040
 Contig ID
                    LIB3106-056-Q1-K1-H1
 5'-most EST
                    3421
 Seq. No.
                    2429 2.R1040
 Contig ID
 5'-most EST
                    g5688463
 Method
                    BLASTX
 NCBI GI
                    g1582580
 BLAST score
                    1759
                    0.0e + 00
 E value
                    364
 Match length
 % identity
                    caffeic acid O-methyltransferase [Stylosanthes humilis]
 NCBI Description
                    3422
 Seq. No.
                    2429 3.R1040
 Contig ID
                    LIB3139-024-P1-N1-A2
 5'-most EST
                    BLASTN
 Method
                    g4468045
 NCBI GI
 BLAST score
                    76
 E value
                    1.0e-34
 Match length
                    156
                    87
 % identity
```

NCBI Description V.planifolia mRNA for methyltransferase

BLAST score

1981

```
Seq. No.
                   3423
                   2429 5.R1040
Contig ID
5'-most EST
                   ssr700554583.hl
Method
                   BLASTN
NCBI GI
                   g258157
BLAST score
                   53
E value
                   7.0e-21
Match length
                   81
                   91
% identity
                   psbD=reaction center protein D2 {5'region} [peas,
NCBI Description
                   Chloroplast, 90 nt]
                   3424
Seq. No.
                   2431 1.R1040
Contig ID
5'-most EST
                   zhf700961150.hl
Method
                   BLASTX
NCBI GI
                   q2829898
BLAST score
                   285
E value
                   2.0e-25
Match length
                   89
% identity
                   61
                  (AC002311) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3425
                   2432 1.R1040
Contig ID
                   LIB3028-044-Q1-B1-C2
5'-most EST
Seq. No.
                   3426
Contig ID
                   2433 1.R1040
                   LIB3028-040-Q1-B1-E11
5'-most EST
Method
                   BLASTX
                   g2642153
NCBI GI
BLAST score
                   141
                   1.0e-08
E value
                   89
Match length
% identity
                   (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 2795810 (AC003674) unknown protein [Arabidopsis
                   thaliana]
                   3427
Seq. No.
                   2436 1.R1040
Contig ID
                   LIB3052-011-Q1-N1-A2
5'-most EST
                   BLASTX
Method
                   q2982465
NCBI GI
BLAST score
                   496
                   9.0e-50
E value
                   203
Match length
                   50
% identity
                   (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   3428
Seq. No.
                   2440 1.R1040
Contig ID
5'-most EST
                   gsf700698384.hl
Method
                   BLASTX
NCBI GI
                   q510876
```

```
E value
                    0.0e + 00
                    449
 Match length
 % identity
                    84
                    (X80051) NADP dependent malic enzyme [Phaseolus vulgaris]
 NCBI Description
 Seq. No.
                    3429
 Contig ID
                    2440 2.R1040
                    eep7\overline{0}0869552.h1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g1561774
 BLAST score
                    733
 E value
                    7.0e-78
 Match length
                    188
 % identity
                    81
 NCBI Description
                    (U67426) malate dehydrogenase [Vitis vinifera]
 Seq. No.
                    3430
 Contig ID
                    2440 5.R1040
 5'-most EST
                    kl1701206630.hl
 Method
                    BLASTX
 NCBI GI.
                    q1708924
 BLAST score
                    254
                    6.0e-22
 E value
 Match length
                    86
 % identity
                    85
                    MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
 NCBI Description
                    MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate
                    dehydrogenase (NADP+) [Vitis vinifera]
 Seq. No.
                    3431
                    2440 6.R1040
 Contig ID
                    crh700854758.hl
 5'-most EST
 Seq. No.
                    3432
                    2442 1.R1040
 Contig ID
 5'-most EST
                    g4293373
 Method
                    BLASTX
 NCBI GI
                    g585264
 BLAST score
                    374
 E value
                    1.0e-35
 Match length
                    185
 % identity
                    HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (HGPRT)
 NCBI Description
                    (HGPRTASE) >gi_2127112_pir__S66098 hypoxanthine-guanine phosphoribosyltransferase - Bacillus subtilis
                    >gi_467457_dbj_BAA05303_ (D26185) hypoxanthine-guanine
                    phosphoribosyltransferase [Bacillus subtilis]
                    >gi_2632335_emb_CAB11844_ (Z99104) hypoxanthine-guanine
                    phosphoribosyltransferase [Bacillus subtilis]
                    3433
 Seq. No.
                    2443 1.R1040
 Contig ID
                    gsv701049235.hl
 5'-most EST
 Method
                    BLASTX
                    q1903364
 NCBI GI
 BLAST score
                    97
                    1.0e-08
 E value
```

```
Match length
                   112
                   34
% identity
                   (AC000104) EST gb T45093 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                  3434
Seq. No.
                  2443 2.R1040
Contig ID
                  LIB3170-062-Q1-J1-H8
5'-most EST
                  3435
Seq. No.
                  2444 ·1.R1040
Contig ID
5'-most EST
                  uC-gmropic005h11b1
Method
                  BLASTX
NCBI GI
                  q1352088
BLAST score
                  1834
E value
                  0.0e + 00
Match length
                   466
% identity
                  73
                  CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi 624676
NCBI Description
                   (U19481) citrate synthase precursor [Citrus maxima]
Seq. No.
                  3436
                   2444 2.R1040
Contig ID
                  vwf700674464.h1
5'-most EST
Method
                  BLASTX
                  g3493367
NCBI GI
                  181
BLAST score
E value
                  2.0e-13
Match length
                  53
% identity
                   (AB017159) citrate synthase [Daucus carota]
NCBI Description
                  3437
Seq. No.
                  2447 1.R1040
Contig ID
                  jC-gmro02910051g10a1
5'-most EST
                  BLASTX
Method
                  g2118017
NCBI GI
BLAST score
                  639
                  8.0e-67
E value
Match length
                  131
% identity
                  81
NCBI Description
                  non-S-RNase (EC 3.1.-.-) - Japanese pear
                  >gi 1526417_dbj_BAA08475_ (D49529) ribonuclease [Pyrus
                  pyrifolia]
                  3438
Seq. No.
                  2448 1.R1040
Contig ID
                  LIB3167-004-P1-K1-D7
5'-most EST
Method
                  BLASTX
                  g399082
NCBI GI
BLAST score
                  676
E value
                  6.0e-71
                  248
Match length
                  60
% identity
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_322713_pir__S28171 H+-transporting ATP synthase (EC
                  3.6.1.34) delta chain, chloroplast - garden pea >gi 169045
```

Method

BLASTX

: -

## (M94558) ATP synthase delta subunit [Pisum sativum]

```
3439
Seq. No.
                   2448 2.R1040
Contig ID
5'-most EST
                   LIB3138-032-Q1-N1-D4
                   3440
Seq. No.
                   2448 3.R1040
Contig ID
                   rlr700899859.hl
5'-most EST
                   BLASTX
Method
                   g399082
NCBI GI
BLAST score
                   157
                   2.0e-10
E value
Match length
                   116
                   36
% identity
                   ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_322713_pir__S28171 H+-transporting ATP synthase (EC
                   3.6.1.34) delta chain, chloroplast - garden pea >gi_169045
                   (M94558) ATP synthase delta subunit [Pisum sativum]
                   3441
Seq. No.
                   2450 1.R1040
Contig ID
                   LIB3049-038-Q1-E1-B10
5'-most EST
                   BLASTX
Method
                   g643469
NCBI GI
                   798
BLAST score
E value
                   4.0e-85
Match length
                   252
% identity
                   62
                   (U19886) unknown [Lycopersicon esculentum]
NCBI Description
                   3442
Seq. No.
                   2450 2.R1040
Contig ID
                   LIB3106-037-Q1-K1-H6
5'-most EST
                   BLASTX
Method
                   g3158376
NCBI GI
BLAST score
                   298
E value
                   7.0e-27
                   114
Match length
                   56
% identity
                   (AF035385) unknown [Arabidopsis thaliana]
NCBI Description
                   3443
Seq. No.
                   2450 3.R1040
Contig ID
5'-most EST
                   LIB3170-031-Q1-J1-A6
                   BLASTX
Method
NCBI GI
                   g643469
BLAST score
                   323
E value
                   8.0e-30
Match length
                   82
                   71
% identity
                   (U19886) unknown [Lycopersicon esculentum]
NCBI Description
                   3444
Seq. No.
                   2450 4.R1040
Contig ID
                   gsv701045693.hl
5'-most EST
```

```
g3434973
NCBI GI
                   251
BLAST score
                   5.0e-21
E value
                   66
Match length
                   73
% identity
                   (AB008106) ethylene responsive element binding factor 4
NCBI Description
                   [Arabidopsis thaliana]
                   3445
Seq. No.
                   2450_5.R1040
Contig ID
                   wrg700790552.h2
5'-most EST'
                   BLASTN
Method
                   g4099920
NCBI GI
BLAST score
                   63
                   2.0e-26
E value
                   143
Match length
                   90
% identity
                   Stylosanthes hamata EREBP-3 homolog mRNA, complete cds
NCBI Description
                   3446
Seq. No.
Contig ID
                   2450 6.R1040
5'-most EST
                   LIB3170-031-Q1-K1-A12
                   BLASTX
Method
                   g643469
NCBI GI
BLAST score
                   264
                   1.0e-22
E value
Match length
                   71
% identity
                   72
                   (U19886) unknown [Lycopersicon esculentum]
NCBI Description
                   3447
Seq. No.
                   2450 10.R1040
Contig ID
                   jC-gmst02400057b12d1
5'-most EST
                   3448
Seq. No.
                   2450 11.R1040
Contig ID
5'-most EST
                   jC-gmle01810042e11a1
Method
                   BLASTX
                   g4099921
NCBI GI
BLAST score
                   287
                   1.0e-25
E value
                   108
Match length
% identity
                   54
                   (U91982) EREBP-3 homolog [Stylosanthes hamata]
NCBI Description
                   3449
Seq. No.
                   2450 12.R1040
Contig ID
5'-most EST
                   epx7\overline{0}1107465.h1
                   3450
Seq. No.
                   2450 14.R1040
Contig ID
                   dpv7\overline{0}1101450.h1
5'-most EST
Method
                   BLASTN
                   g3434972
NCBI GI
                   57
BLAST score
                   2.0e-23
E value
                   101
Match length
```

E value

```
89
% identity
                   Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive
NCBI Description
                   element binding factor 4, complete cds
                   3451
Seq. No.
                   2453 1.R1040
Contig ID
                   LIB3030-006-Q1-B1-D8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4105097
BLAST score
                   281
E value
                   4.0e-41
Match length
                   110
% identity
                   (AF043255) MADS box protein 26 [Cucumis sativus]
NCBI Description
Seq. No.
                   3452
Contig ID
                   2454 1.R1040
                   LIB3109-010-Q1-K1-E1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2570047
BLAST score
                   339
E value ;
                   5.0e-31
Match length
                   164
                   43
% identity
                   (Y09234) MSTK2S kinase-like protein [Mus musculus]
NCBI Description
Seq. No.
                   3453
Contig ID
                   2457 1.R1040
                   LIB3030-008-Q1-B1-E2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3386614
BLAST score
                   415
                   1.0e-40
E value
Match length
                   115
% identity
                   40
NCBI Description
                   (AC004665) putative transcription factor SF3 [Arabidopsis
                   thaliana]
                   3454
Seq. No.
                   2458 1.R1040
Contig ID
5'-most EST
                   LIB3028-044-Q1-B1-B11
Method
                   BLASTX
NCBI GI
                   q3123059
BLAST score
                   185
E value
                   5.0e-13
Match length
                   180
% identity
                   31
NCBI Description
                   HYPOTHETICAL PROTEIN KIAA0253 >gi_1665773_dbj_BAA13383_
                   (D87442) KIAA0253 [Homo sapiens]
                   3455
Seq. No.
                   2459 1.R1040
Contig ID
5'-most EST
                   LIB3028-043-01-B1-H5
Method
                   BLASTX
NCBI GI
                   g2264373
BLAST score
                   335
```

4.0e-31

```
169
Match length
                   43
% identity
                   (AC002354) putative NAM/no apical meristem protein
NCBI Description
                   [Arabidopsis thaliana]
                   3456
Seq. No.
                   2461_1.R1040
Contig ID
                  jC-gmle01810068f07a1
5'-most EST
                  BLASTX
Method
                  g1749474
NCBI GI
BLAST score
                  151
                   2.0e-09
E value
                  96
Match length
                   40
% identity
                   (D89133) similar to Saccharomyces cerevisiae Lph16p,
NCBI Description
                  GENBANK Accession Number U43503 [Schizosaccharomyces pombe]
                   3457
Seq. No.
                  2462 1.R1040
Contig ID
5'-most EST
                  leu701151985.hl
Method
                  BLASTX
                  g3747111
NCBI GI
BLAST score
                   627
                   3.0e-65
E value
Match length
                   211
% identity
                   (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   3458
Seq. No.
                   2462 2.R1040
Contig ID
5'-most EST
                   epx701105770.h1
Method
                   BLASTN
NCBI GI
                   g11565
BLAST score
                   308
                                            E value
                   1.0e-173
Match length
                   316
% identity
                   99
                   Soybean chloroplast psb A gene coding for photosystem II
NCBI Description
                   thylakoid membrane protein
                   3459
Seq. No.
Contig ID
                   2465 1.R1040
                   bth700845088.h1
5'-most EST
Method
                   BLASTX
                   g2792297
NCBI GI
                   334
BLAST score
E. value
                   8.0e-31
Match length
                   66
% identity
                   83
                   (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                   3460
Seq. No.
Contig ID
                   2465 2.R1040
                   LIB3093-015-Q1-K1-A3
5'-most EST
                   BLASTX
Method
                   g2792297.
NCBI GI
```

BLAST score

```
5.0e-31
E value
                   66
Match length
                   83
% identity
                   (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                   3461
Seq. No.
                   2465 3.R1040
Contig ID
                   LIB3107-060-Q1-K1-G3
5'-most EST
                   BLASTX
Method
                   g2792297
NCBI GI
                   342
BLAST score
                   8.0e-32
E value
Match length
                   66
                   86
% identity
                   (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                   3462
Seq. No.
                   2466 1.R1040
Contig ID
                   jsh7\overline{0}1067168.h1
5'-most EST
                   BLASTX
Method
                   g4572679
NCBI GI
BLAST score
                   322
                   2.0e-29
E value
                   69
Match length
                   87
% identity
                   (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                   motif [Arabidopsis thaliana]
                   3463
Seq. No.
                   2466 2.R1040
Contig ID
                   LIB3051-005-Q1-E1-D11
5'-most EST
                   BLASTX
Method
                   g4572679
NCBI GI
                   406
BLAST score
                   2.0e-39
E value
                   104
Match length
                   76
% identity
                   (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                   motif [Arabidopsis thaliana]
                   3464
Seq. No.
                   2466 3.R1040
Contig ID
5'-most EST
                   jC-gmf102220115e04a1
                   3465
Seq. No.
                   2466_4.R1040
Contig ID
                   jC-gmst02400026d01a1
5'-most EST
                   BLASTX
Method
                   g4572679
NCBI GI
BLAST score
                   278
                   1.0e-24
E value
                    60
Match length
                   87
% identity
                    (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                   motif [Arabidopsis thaliana]
```

Seq. No.

```
2466 5.R1040
Contig ID
                  LIB3106-040-Q1-K1-B2
5'-most EST
                  3467
Seq. No.
                  2467 1.R1040
Contig ID
                  LIB3109-028-Q1-K1-F3
5'-most EST
                  BLASTX
Method
                  g3128228
NCBI GI
BLAST score
                  871
                  9.0e-94
E value
                  178
Match length
                  90
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
Seq. No.
                  3468
                  2467 2.R1040
Contig ID
                  LIB3028-043-Q1-B1-G5
5'-most EST
Method
                  BLASTX
                  g3128228
NCBI GI
BLAST score
                  601
                  1.0e-62
E value
                  123
Match length
                  91
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
                  3469
Seq. No.
                  2469 1.R1040
Contig ID
5'-most EST
                  leu701146773.hl
                  BLASTX
Method
NCBI GI
                  g4220524
                  185
BLAST score
                  2.0e-13
E value
Match length
                  68
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  3470
Seq. No.
                  2469 2.R1040
Contig ID
5'-most EST
                  kl1701203514.h2
                  3471
Seq. No.
                  2469 3.R1040
Contig ID
5'-most EST
                  pxt700942179.h1
                  3472
Seq. No.
Contig ID
                  2472 1.R1040
                  LIB3028-043-Q1-B1-H1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4538897
BLAST score
                  461
E value
                  4.0e-46
Match length
                  134
```

% identity

```
(ALO49482) AX110P-like protein [Arabidopsis thaliana]
NCBI Description
                                            'n
Seq. No.
                   3473
                   2474_1.R1040
Contig ID
5'-most EST
                   LIB3028-020-Q1-B1-G11
                   3474
Seq. No.
                   2474 3.R1040
Contig ID
                   jC-gmst02400036d12d2
5'-most EST
                   3475
Seq. No.
                   2477 1.R1040
Contig ID
5'-most EST
                  LIB3170-053-Q1-K1-A2
Method
                   BLASTN
                   g1142620
NCBI GI
BLAST score
                   296
E value
                   1.0e-165
                   1181
Match length
                   86
% identity
                   Phaseolus vulgaris phaseolin G-box binding protein PG2
NCBI Description
                   (PG2) mRNA, partial cds
                   3476
Seq. No.
                   2477 2.R1040
Contig ID
                  uC-gmropic075f09b1
5'-most EST
Method
                  BLASTN
NCBI GI
                   g1142620
BLAST score
                   208
                   1.0e-113
E value
                   390
Match length
                   88
% identity
                   Phaseolus vulgaris phaseolin G-box binding protein PG2
NCBI Description
                   (PG2) mRNA, partial cds
                   3477
Seq. No.
                   2478 1.R1040
Contig ID
5'-most EST
                  LIB3051-112-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   g3522945
BLAST score
                   223
E value
                   3.0e-18
Match length
                   130
% identity
                   34
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   3478
Seq. No.
                   2480_1.R1040
Contig ID
                   fC-gmro700866825a3
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3461814
BLAST score
                  1410
E value
                   1.0e-156
Match length
                   397
% identity
                   (AC004138) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

BLAST score

204

```
2480 2.R1040
Contig ID
                  uC-gmrominsoy308c02b1
5'-most EST
                  3480
Seq. No.
                  2481 1.R1040
Contig ID
                  jex700906745.hl
5'-most EST
Method
                  BLASTX
                  g4490318
NCBI GI
BLAST score
                  1704
                  0.0e + 00
E value
Match length
                  382
% identity
                  85
                   (AL035678) 2-dehydro-3-deoxyphosphoheptonate aldolase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  3481
Contig ID
                  2481 2.R1040
5'-most EST
                  LIB3029-012-Q1-B1-B5
Method
                  BLASTX
                  g99743
NCBI GI
BLAST score
                  741
E value
                  1.0e-78
Match length
                  156
                  92
% identity
NCBI Description
                  2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2
                  - Arabidopsis thaliana
                  3482
Seq. No.
Contig ID
                  2485 1.R1040
                  LIB3049-055-Q1-E1-G3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4321188
BLAST score
                  337
E value
                  3.0e-31
Match length
                  146
% identity
NCBI Description
                   (AF021807) low molecular weight heat-shock protein [Corylus
                  avellana]
                  3483
Seq. No.
                  2485 2.R1040
Contig ID
5'-most EST
                  LIB3053-002-Q1-B1-E1
Method
                  BLASTX
NCBI GI
                  g4321188
BLAST score
                  310
                  3.0e-28
E value
Match length
                  94
% identity
NCBI Description
                   (AF021807) low molecular weight heat-shock protein [Corylus
                  avellana]
                  3484
Seq. No.
Contig ID
                  2486 1.R1040
5'-most EST
                  rca701001119.h1
Method
                  BLASTX
NCBI GI
                  q732003
```

÷.,

```
E value
                  7.0e-16
                   153
Match length
                   35
% identity
                   OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
NCBI Description
                   >gi 2125977 pir I84534 outer membrane lipoprotein -
                   Escherichia coli >gi 536993 (U14003) ORF f177 [Escherichia
                   coli] >gi 717134 (U21726) lipocalin precursor [Escherichia
                   coli] >gi_1790592 (AE000487) outer membrane lipoprotein
                   (lipocalin) [Escherichia coli]
                   3485
Seq. No.
                   2487 1.R1040
Contig ID
                   gsv701056217.hl
5'-most EST
Method
                   BLASTX
                   g4454475
NCBI GI
BLAST score
                   231
                   4.0e-19
E value
Match length
                   67
% identity
                   63
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3486
Seq. No.
Contig ID
                   2488 1.R1040
                   LIB3138-082-P1-N1-D4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4220481
BLAST score
                   418
E value
                   3.0e-43
Match length
                   160
% identity
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3487
Seq. No.
Contig ID
                   2488 2.R1040
                   uC-gmrominsoy093c03b1
5'-most EST
                   BLASTX
Method
                   g4508082
NCBI GI
BLAST score
                   363
                   2.0e-34
E value
Match length
                   71
                   90
% identity
                   (AC005882) Putative RNA polymerase II subunit Rpb10
NCBI Description
                   [Arabidopsis thaliana]
                   3488
Seq. No.
                   2488 3.R1040
Contig ID
                   zhf7\overline{0}0962530.h1
5'-most EST
                   BLASTX
Method
                   g4508082
NCBI GI
BLAST score
                   361
                   3.0e-34
E value
Match length
                   71
                   92
% identity
                   (AC005882) Putative RNA polymerase II subunit Rpb10
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No.

•

5'-most EST

```
2488 4.R1040
Contig ID
5'-most EST
                   jC-gmro02800038a07d1
                   3490
Seq. No.
Contig ID
                   2488 6.R1040
                   eep700865123.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4220481
BLAST score
                   242
E value
                   2.0e-20
                   85
Match length
                   55
% identity
NCBI Description
                   (AC006069) unknown protein [Arabidopsis thaliana]
                   3491
Seq. No.
                   2488 8.R1040
Contig ID
                   pcp700992848.hl
5'-most EST
                   3492
Seq. No.
                   2489 1.R1040
Contig ID
5'-most EST
                   LIB3170-007-Q1-K1-E9
                   3493
Seq. No.
                   2490 1.R1040
Contig ID
5'-most EST
                   LIB3028-043-Q1-B1-F7
Method
                   BLASTX
                   g1353018
NCBI GI
BLAST score
                   196
                   2.0e-14
E value
Match length
                   157
                   31
% identity
                  HYPOTHETICAL 34.4 KD PROTEIN IN IDS2-MPI2 INTERGENIC REGION
NCBI Description
                   >gi_1077841_pir__S55168 hypothetical protein YJL145w -
                   yeast (Saccharomyces cerevisiae) >gi_854552_emb_CAA60810_
                   (X87371) ORF10 [Saccharomyces cerevisiae]
                   >gi_1015557_emb_CAA89440_ (Z49420) ORF YJL145w
                   [Saccharomyces cerevisiae]
                   3494
Seq. No.
Contig ID
                   2491 1.R1040
5'-most EST
                   uC-gmrominsoy119a01b1
Method
                   BLASTX
NCBI GI
                   g1684851
BLAST score
                   326
E value
                   3.0e-30
Match length
                   117
                   62
% identity
                   (U77935) DnaJ-like protein [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   3495
                   2492 1.R1040
Contig ID
5'-most EST
                   gsv7\overline{0}1055713.h1
                   3496
Seq. No.
                   2492 2.R1040
Contig ID
```

LIB3106-072-P1-K1-B6

NCBI Description

```
Seq. No.
                   3497
Contig ID
                   2492 3.R1040
5'-most EST
                   LIB3109-027-Q1-K1-F8
                   3498
Seq. No.
                   2494 1.R1040
Contig ID
                   LIB3170-005-Q1-K1-F3
5'-most EST
Method
                   BLASTX
                   g119958
NCBI GI
BLAST score
                   459
                   2.0e-45
E value
Match length
                   152
                   59
% identity
NCBI Description
                   FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)
                   ferredoxin [Zea mays] >gi 1864001 dbj_BAA19251_ (AB001387)
                   Fd III [Zea mays] >gi 444686 prf 1907324C
                   ferredoxin:ISOTYPE=III [Zea mays]
                   3499
Seq. No.
                   2494 2.R1040
Contig ID
                   zhf700964962.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4115534
BLAST score
                   481
                   5.0e-48
E value
Match length
                   226
                   41
% identity
NCBI Description
                   (AB012114) UDP-qlycose:flavonoid glycosyltransferase [Vigna
                   3500
Seq. No.
                   2497 1.R1040
Contig ID
5'-most EST
                   jsh7\overline{0}1064037.h1
                   3501
Seq. No.
                   2498 1.R1040
Contig ID
                   leu7\overline{0}1153865.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4415930
                   207
BLAST score
                   3.0e-16
E value
                   66
Match length
                   58
% identity
                   (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4559389 qb AAD23049.1 AC006526 14 (AC006526) unknown
                   protein [Arabidopsis thaliana]
                   3502
Seq. No.
Contig ID
                   2498 2.R1040
5'-most EST
                   LIB3049-032-Q1-E1-E1
Method
                   BLASTX
NCBI GI
                   g4415930
                   225
BLAST score
                   1.0e-18
E value
                   69
Match length
% identity
                   (AC006418) unknown protein [Arabidopsis thaliana]
```

Match length

% identity

74

43

```
>gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown
protein [Arabidopsis thaliana]
```

```
3503
Seq. No.
                  2501 1.R1040
Contig ID
5'-most EST
                  LIB3028-043-Q1-B1-D7
Method
                  BLASTX
                   g4006922
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
Match length
                  35
                  77
% identity
                   (299708) cytochrome P450 like protein [Arabidopsis
NCBI Description
                  thaliana]
                  3504
Seq. No.
Contig ID
                  2503 1.R1040
                  uC-gmrominsoy135g07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2462826
BLAST score
                  759
E value
                  1.0e-109
Match length
                  477
% identity
                  45
                   (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
                  3505
Seq. No.
Contig ID
                  2503 2.R1040
                  zhf700956794.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2462826
BLAST score.
                  240
                   3.0e-20
E value
                  99
Match length
                   45
% identity
                   (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3506
                  2504 1.R1040
Contig ID
5'-most EST
                  LIB3039-018-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  g3241945
BLAST score
                  438
E value
                  4.0e-43
Match length
                  146
% identity
                   (AC004625) unknown protein [Arabidopsis thaliana]
NCBI Description
                  3507
Seq. No.
Contig ID
                  2505_1.R1040
5'-most EST
                  uC-gmflminsoy053h03b1
                  BLASTX
Method
NCBI GI
                  g2935523
BLAST score
                  142
E value
                  1.0e-08
```

5'-most EST

```
NCBI Description (AF049066) 21 kD protein precursor [Pinus radiata]
Seq. No.
                   3508
                   2505 2.R1040
Contig ID
                   LIB3028-043-Q1-B1-E10
5'-most EST
Method
                   BLASTX
                   g112717
NCBI GI
                   235
BLAST score
                   2.0e-19
E value
                   128
Match length
                   40
% identity
                   21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi_82050 pir S10911
NCBI Description
                   hypothetical protein precursor - carrot
                   >gi 18312 emb CAA36642 (X52395) precursor polypeptide (AA
                   -22 to 171) [Daucus carota]
                   3509
Seq. No.
Contig ID
                   2508 1.R1040
                   zhf700963215.hl
5'-most EST
Method
                   BLASTX
                   g2252871
NCBI GI
BLAST score
                   162·
E value
                   2.0e-23
                   134
Match length
                   48
% identity
                   (AF013294) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3510
                   2510 1.R1040
Contig ID
                   LIB3170-036-Q1-K2-A6
5'-most EST
                   BLASTX
Method
                   q2895866
NCBI GI
                   399
BLAST score
                   1.0e-38
E value
                   154
Match length
% identity
NCBI Description
                   (AF045770) methylmalonate semi-aldehyde dehydrogenase
                   [Oryza sativa]
Seq. No.
                   3511
Contig ID
                   2510 2.R1040
                   LIB3\overline{0}92-048-Q1-K1-F8
5'-most EST
                   3512
Seq. No.
Contig ID
                   2511 1.R1040
                   LIB3\overline{1}38-006-Q1-N1-C7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2529683
BLAST score
                   426
E value
                   9.0e-42
                   186
Match length
% identity
                   (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3513
Seq. No.
                   2512 1.R1040
Contiq ID
```

LIB3049-046-Q1-E1-H9

Method

BLASTX

```
3514
Seq. No.
                   2513 1.R1040
Contig ID
                   uC-gmropic010e09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g728882
                   808
BLAST score
                   2.0e-86
E value
                   178
Match length
% identity
                   87
                   ADP-RIBOSYLATION FACTOR 3 >gi 541846 pir S41938
NCBI Description
                   ADP-ribosylation factor 3 - Arabidopsis thaliana
                   >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3
                   [Arabidopsis thaliana]
                   3515
Seq. No.
Contig ID
                   2513 2.R1040
5'-most EST
                   leu7\overline{0}1145405.h1
                   BLASTN
Method
                   q453190
NCBI GI
BLAST score
                   95
E value
                   8.0e-46
                   191
Match length
                   87
% identity
                   A.thaliana mRNA for ADP-ribosylation factor
NCBI Description
                   3516
Seq. No.
                   2517 1.R1040
Contig ID
                   rca701001442.hl
5'-most EST
                   BLASTX
Method
                   g4521322
NCBI GI
BLAST score
                   391
E value
                   1.0e-63
                   279
Match length
                   50
% identity
                   (U11790) mitotic centromere-associated kinesin [Cricetulus
NCBI Description
                   griseus]
                   3517
Seq. No.
                   2518 1.R1040
Contig ID
                   LIB3028-043-Q1-B1-B8
5'-most EST
                   BLASTX
Method
                   g4490317
NCBI GI
BLAST score
                   239
E value
                   4.0e-20
Match length
                   131
                   39
% identity
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
                   3518
Seq. No.
                   2519 1.R1040
Contig ID
5'-most EST
                   leu701153841.h1
Seq. No.
                   3519
                   2523 1.R1040
Contig ID
5'-most EST.
                   ssr7\overline{0}0556872.h1
```

NCBI GI

```
g3123515
NCBI GI
                   599
BLAST score
                   3.0e-62
E value
                   126
Match length
                   90
% identity
                   (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
NCBI Description
                   3520
Seq. No.
                   2525_1.R1040
Contig ID
5'-most EST
                   ncj700979085.hl
Method
                   BLASTX
                   g3193292
NCBI GI
BLAST score
                   502
                   7.0e-51
E value
                   159
Match length
                   58
% identity
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
                   3521
Seq. No.
                   2526_1.R1040
Contig ID
5'-most EST
                   pcp700992672.hl
                   3522
Seq. No.
                   2526 2.R1040
Contig ID
5'-most EST
                   LIB3094-099-Q1-K1-G5
                   3523
Seq. No.
Contig ID
                   2527 1.R1040
5'-most EST
                   wrq700789265.h2
Method
                   BLASTX
                   g2367392
NCBI GI
BLAST score
                   358
E value
                   1.0e-33
Match length
                   330
% identity
                   29
                   (U82513) random slug cDNA25 protein [Dictyostelium
NCBI Description
                   discoideum]
                   3524
Seq. No.
                   2527 2.R1040
Contig ID
                   uC-gmflminsoy011a04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2367392
BLAST score
                   288
E value
                   1.0e-25
Match length
                   170
% identity
NCBI Description
                   (U82513) random slug cDNA25 protein [Dictyostelium
                  discoideum]
Seq. No.
                   3525
Contig ID
                   2528 1.R1040
5'-most EST
                   q4296284
Method
                  BLASTN
```

q3820639

E value

```
BLAST score
                   281
                   1.0e-156
E value
Match length
                   782
% identity
                   84
                   C.arietinum mRNA for cysteine proteinase
NCBI Description
Seq. No.
                   3526
                   2528 2.R1040
Contig ID
                   LIB3\overline{0}93-045-Q1-K1-B2
5'-most EST
Method
                   BLASTN
                   g3820639
NCBI GI
BLAST score
                   101
                   5.0e-49
E value
                   312
Match length
% identity
                   86
                   C.arietinum mRNA for cysteine proteinase
NCBI Description
Seq. No.
                   3527
                   2528 3.R1040
Contig ID
                   LIB3092-058-Q1-K1-B11
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3820639
BLAST score
                   203
                   1.0e-110
E value
Match length
                   632
% identity
                   84
                   C.arietinum mRNA for cysteine proteinase
NCBI Description
Seq. No.
                   3528
                   2528 4.R1040
Contig ID
                   q5510260
5'-most EST
                   BLASTN
Method
                   g3820639
NCBI GI
BLAST score
                   169
                   6.0e-90
E value
                   404
Match length
                   86
% identity
                   C.arietinum mRNA for cysteine proteinase
NCBI Description
                   3529
Seq. No.
                   2528 5.R1040
Contig ID
                   jC-gmf102220070g10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1134882
                   226
BLAST score
                   2.0e-18
E value
                   94
Match length
                   49
% identity
                   (Z68291) cysteine protease [Pisum sativum]
NCBI Description
                   3530
Seq. No.
                   2529 1.R1040
Contig ID
                   LIB3107-062-Q1-K1-D8
5'-most EST
                   BLASTN
Method
                   g1370145
NCBI GI
BLAST score
                   386
```

0.0e + 00

Contig ID

```
Match length
                   797
% identity
                   88
                   L.japonicus mRNA for small GTP-binding protein, RAB11C
NCBI Description
                   3531
Seq. No.
                   2529 2.R1040
Contig ID
                   LIB3107-060-Q1-K1-A7
5'-most EST
                   BLASTN
Method
                   g1370145
NCBI GI
BLAST score
                   175
E value
                   1.0e-93
Match length
                   267
                   91
% identity
                   L.japonicus mRNA for small GTP-binding protein, RAB11C
NCBI Description
                   3532
Seq. No.
                   2530 1.R1040
Contig ID
                   LIB3170-052-Q1-J1-B11
5'-most EST
                   3533
Seq. No.
                   2532 1.R1040
Contig ID
                   LIB3028-043-Q1-B1-A11
5'-most EST
                   3534
Seq. No.
                   2534_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910016c11d1
Method
                   BLASTX
NCBI GI
                   g2462825
BLAST score
                   468
                   3.0e-46
E value
                   180
Match length
                   62
% identity
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                   3535
Seq. No.
                   2534 2.R1040
Contig ID
5'-most EST
                   g5606849
Seq. No.
                   3536
                   2534 3.R1040
Contig ID
5'-most EST
                   jC-gmro02910002g10a1
Seq. No.
                   3537
                   2534 4.R1040
Contig ID
5'-most EST
                   asn7\overline{0}1135234.h1
Method
                   BLASTX
NCBI GI
                   g2462825
BLAST score
                   450
E value
                   1.0e-44
                   100
Match length
% identity
                   89
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                   3538
Seq. No.
```

2534 5.R1040

```
5'-most EST
                   dpv701101840.h1
Method
                   BLASTX
NCBI GI
                   g2462825
                   404
BLAST score
                   4.0e-39
E value
Match length
                   88
% identity
                   89
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                   3539
Seq. No.
Contig ID
                   2534 6.R1040
                   zsg7\overline{0}1124648.h1
5'-most EST
Seq. No.
                   3540
Contig ID
                   2534 7.R1040
                   LIB3028-021-Q1-B1-A6
5'-most EST
                   3541
Seq. No.
                   2536 1.R1040
Contig ID
                   rlr700901294.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3241945
BLAST score
                   376
                   6.0e-36
E value
Match length
                   156
% identity
                   48
NCBI Description
                   (AC004625) unknown protein [Arabidopsis thaliana]
Seq. No.
                   3542
                   2539 1.R1040
Contig ID
                   uC-qmflminsoy064d02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2960364
BLAST score
                   1321
                   1.0e-146
E value
Match length
                   332
% identity
NCBI Description
                   (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
                   subsp. trichocarpa]
                   3543
Seq. No.
                   2539 2.R1040
Contig ID
                   jC-gmro02910026a02a1
5'-most EST
Method
                   BLASTX
                   g2960364
NCBI GI
                   291
BLAST score
                   3.0e-26
E value
                   71
Match length
% identity
NCBI Description
                   (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
                   subsp. trichocarpa]
                   3544
Seq. No.
Contig ID
                   2539 3.R1040
5'-most EST
                   LIB3050-008-Q1-E1-G8
```

BLASTX

Method

5'-most EST

```
g2058311
NCBI GI
                   466
BLAST score
E value
                   1.0e-46
Match length
                   116
% identity
                   76
                   (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
NCBI Description
                   3545
Seq. No.
                   2539 4.R1040
Contig ID
5'-most EST
                   jsh7\overline{0}1068331.h1
                   BLASTX
Method
NCBI GI
                   g2960364
BLAST score
                   400
                   5.0e-39
E value
                   100
Match length
                   75
% identity
                   (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
NCBI Description
                   subsp. trichocarpa]
                   3546
Seq. No.
Contig ID
                   2539 5.R1040
                   pmv700889373.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2960364
BLAST score
                   451
                   8.0e-45
E value
Match length
                   115
                   75
% identity
                   (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
NCBI Description
                   subsp. trichocarpa]
                   3547
Seq. No.
                   2539 7.R1040
Contig ID
                   jC-gmst02400030a10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2058311
BLAST score
                   190
E value
                   2.0e-29
Match length
                   92
                   72
% identity
                   (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]
NCBI Description
                   3548
Seq. No.
                   2540 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220068c05a1
Method
                   BLASTX
NCBI GI
                   g633890
BLAST score
                   406
E value
                   1.0e-39
Match length
                   127
                   62
% identity
NCBI Description
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                   vulgare]
Seq. No.
                   3549
Contig ID
                   2541 1.R1040
```

jC-gmf102220091e04a1

```
Method
                  BLASTX
NCBI GI
                  q128592
BLAST score
                  425
                  8.0e-42
E value
Match length
                  126
                  63
% identity
                  POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                  >gi_82190_pir__S22495 pollen-specific protein precursor -
                  common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
                  specific protein [Nicotiana tabacum]
```

Seq. No. 3550

Contig ID 2544\_1.R1040 5'-most EST ujr700646514.h1

Seq. No. 3551

Contig ID 2544\_4.R1040 5'-most EST hrw701063009.h1

Seq. No. 3552

Contig ID 2545\_1.R1040 5'-most EST sat701014436.h1

Method BLASTX
NCBI GI g2160156
BLAST score 606
E value 1.0e-62
Match length 214

% identity 56

NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA

synthetase (gb\_Z73100). [Arabidopsis thaliana]

Seq. No. 3553

Contig ID 2547\_1.R1040

5'-most EST LIB3107-061-Q1-K1-H1

Seq. No. 3554

Contig ID 2547\_2.R1040 5'-most EST pcp700995149.h1

Seq. No. 3555

Contig ID 2548 1.R1040

5'-most EST uC-gmropic074b05b1

Method BLASTX
NCBI GI g2506277
BLAST score 2497
E value 0.0e+00
Match length 543
% identity 93

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60

KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi\_806808

(U21139) chaperonin precursor [Pisum sativum]

Seq. No. 3556

Contig ID 2548 2.R1040

5'-most EST LIB3106-005-Q1-K1-F7

Method BLASTN NCBI GI g2746720

BLAST score

117

```
128
BLAST score
                   2.0e-65
E value
                   308
Match length
                  85
% identity
                  Capsicum annuum histone H4 mRNA, complete cds
NCBI Description
                  3557
Seq. No.
Contig ID
                  2548_3.R1040
                  LIB3040-055-Q1-E1-H12
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2746720
                  115
BLAST score
                  9.0e-58
E value
                  299
Match length
                  85
% identity
                  Capsicum annuum histone H4 mRNA, complete cds
NCBI Description
Seq. No.
                  3558
                  2548 4.R1040
Contig ID
5'-most EST
                  LIB3170-002-Q1-K1-D3
Method
                  BLASTN
NCBI GI
                  g2746720
                  133
BLAST score
                  2.0e-68
E value
                  309
Match length
                  86
% identity
                  Capsicum annuum histone H4 mRNA, complete cds
NCBI Description
                  3559
Seq. No.
                  2548 5.R1040
Contig ID
                  LIB3040-013-Q1-E1-E12
5'-most EST
                  BLASTN
Method
                  g2351070
NCBI GI
BLAST score
                  106
                   4.0e-52
E value
                  294
Match length
                  84
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTH12, complete sequence [Arabidopsis thaliana]
                  3560
Seq. No.
                  2548 6.R1040
Contig ID
5'-most EST
                  LIB3106-105-Q1-K1-E10
                  BLASTN
Method
NCBI GI
                  g2746720
BLAST score
                  112
E value
                   6.0e-56
Match length
                  308
                  84
% identity
NCBI Description
                  Capsicum annuum histone H4 mRNA, complete cds
                  3561
Seq. No.
Contig ID
                  2548 7.R1040
                  LIB3106-005-Q1-K2-F7
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2746720
```

5.0e-59 E value Match length 309 84 % identity Capsicum annuum histone H4 mRNA, complete cds NCBI Description 3562 Seq. No. 2548 8.R1040 Contig ID zhf700957937.h1 5'-most EST BLASTN Method NCBI GI g2746720 121 BLAST score 10 2.0e-61 E value Match length 309 85 % identity Capsicum annuum histone H4 mRNA, complete cds NCBI Description 3563 Seq. No. 2550 1.R1040 Contig ID LIB3106-069-P1-K1-A5 5'-most EST 3564 Seq. No. Contig ID 2555 1.R1040  $LIB3\overline{0}39-039-Q1-E1-H5$ 5'-most EST BLASTX Method NCBI GI g3075394 2205 BLAST score E value 0.0e + 00532 Match length 79 % identity (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead protein [Arabidopsis thaliana] 3565 Seq. No. 2555 2.R1040 Contig ID 5'-most EST  $leu7\overline{0}1146601.h1$ Method BLASTX g3075394 NCBI GI BLAST score 414 1.0e-40 E value Match length 97 % identity (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead protein [Arabidopsis thaliana] 3566 Seq. No. Contig ID 2556 1.R1040 LIB3028-042-Q1-B1-D6 5'-most EST

Method BLASTX
NCBI GI g3894172
BLAST score 811
E value 2.0e-86
Match length 319
% identity 48

NCBI Description (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Match length

92

```
3567
Seq. No.
                   2556 2.R1040
Contig ID
                   LIB3109-037-Q1-K1-E4
5'-most EST
                   BLASTN
Method
                   g2656025
NCBI GI
                   42
BLAST score
                   3.0e-14
E value
                   58
Match length
                   93
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCD7
                   3568
Seq. No.
                   2556 3.R1040
Contig ID
5'-most EST
                   kmv700737795.h1
                   BLASTX
Method
NCBI GI
                   g3894172
                   171
BLAST score
                   3.0e-12
E value
                   56
Match length
% identity
                   (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   3569
Seq. No.
                   2556 5.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy121d12b1
Method
                   BLASTN
                   g2656025
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   51
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCD7
                   3570
Seq. No.
Contig ID
                   2556 6.R1040
                   LIB3109-018-Q1-K1-H8
5'-most EST
Method
                   BLASTX
                   g3482924
NCBI GI
BLAST score
                   191
                   6.0e-24
E value
                   117
Match length
                   53
% identity
                   (AC003970) Highly similar to cinnamyl alcohol
NCBI Description
                   dehydrogenase, gi_1143445 [Arabidopsis thaliana]
Seq. No.
                   3571
                   2556 7.R1040
Contig ID
5'-most EST
                   ssr700560974.hl
Method
                   BLASTX
                   g3482925
NCBI GI
                   125
BLAST score
                   2.0e-13
E value
```

```
51
% identity
NCBI Description
                   (AC003970) Highly similar to cinnamyl alcohol
                   dehydrogenase, gi_1143445 [Arabidopsis thaliana]
Seq. No.
                   3572
                   2556 8.R1040
Contig ID
                   jC-gmle01810036c11d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3894172
BLAST score
                   161
E value
                   4.0e-11
Match length
                   67
% identity
                   49
                   (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   3573
Seq. No.
                   2557 1.R1040
Contig ID
5'-most EST
                   epx7\overline{0}1108487.h1
                   3574
Seq. No.
                   2558_1.R1040
Contig ID
                   jC-gmle01810089g08a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4220477
BLAST score
                   191
E value
                   3.0e-14
Match length
                   91
                   53
% identity
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3575
Seq. No.
Contig ID
                   2558 2.R1040
                   fde700874755.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4220477
BLAST score
                   180
E value
                   5.0e-13
                   89
Match length
                   51
% identity
NCBI Description
                   (AC006069) unknown protein [Arabidopsis thaliana]
                   3576
Seq. No.
                   2560 1.R1040
Contig ID
                   LIB3\overline{0}28-042-Q1-B1-E1
5'-most EST
                   3577
Seq. No.
Contig ID
                   2562 1.R1040
5'-most EST
                   smw700646136.hl
                   3578
Seq. No.
Contig ID
                   2566 1.R1040
5'-most EST
                   jC-gmle01810067e05a1
Method
                   BLASTX
                   g2129578
NCBI GI
BLAST score
                   330
```

1.0e-30

E value

133 Match length % identity 54 dTDP-glucose 4-6-dehydratases homolog - Arabidopsis NCBI Description thaliana >gi\_928932\_emb\_CAA89205\_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene [Arabidopsis thaliana] 3579 Seq. No. Contig ID 2566\_2.R1040 . 5'-most EST jC-gmro02910030d09a1 Method BLASTX NCBI GI g3522929 BLAST score 901 1.0e-114 E value Match length 299 76 % identity (AC002535) putative dTDP-glucose 4-6-dehydratase NCBI Description [Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] Seq. No. 3580 2566 3.R1040 Contig ID 5'-most EST LIB3051-019-Q1-E1-G5 Method BLASTX NCBI GI g2129578 BLAST score 217 E value 2.0e-17 112 Match length 46 % identity dTDP-glucose 4-6-dehydratases homolog - Arabidopsis NCBI Description thaliana >gi\_928932\_emb\_CAA89205\_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi\_1585435\_prf\_\_2124427B diamide resistance gene [Arabidopsis thaliana] Seq. No. 3581 Contig ID 2567 1.R1040 xzy700966701.hl 5'-most EST Method BLASTX NCBI GI q1743354 BLAST score 2238 E value 0.0e+00Match length 502 82 % identity NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] 3582 Seq. No. 2567 2.R1040 Contig ID

Contig ID 2567\_2.R1040 5'-most EST pmv700890220.h1

Method BLASTX
NCBI GI g1421730
BLAST score 406
E value 2.0e-39
Match length 111
% identity 69

NCBI Description (U43082) RF2 [Zea mays]

NCBI GI

```
3583
Seq. No.
                   2567 3.R1040
Contig ID
5'-most EST
                   jC-qmro02800029f04d1
                   BLASTX
Method
                   q1743354
NCBI GI
BLAST score
                   353
                   1.0e-33
E value
Match length
                   71
% identity
NCBI Description
                   (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
                   3584
Seq. No.
Contig ID
                   2567 5.R1040
5'-most EST
                   zsg7\overline{0}1126328.h1
Method `
                   BLASTX
NCBI GI
                   q1421730
BLAST score
                   418
E value
                   5.0e-41
Match length
                   86
% identity
                   88
NCBI Description
                   (U43082) RF2 [Zea mays]
                   3585
Seq. No.
Contig ID
                   2569 1.R1040
5'-most EST
                   LIB3028-042-Q1-B1-E8
Method
                   BLASTX
NCBI GI
                   q2459445
BLAST score
                   218
                   1.0e-17
E value
Match length
                   96
% identity
                   26
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
                   3586
Seq. No.
Contig ID
                   2570 1.R1040
5'-most EST
                   dpv7\overline{0}1101023.h1
Method
                   BLASTX
NCBI GI
                   a2959767
BLAST score
                   1002
E value
                   1.0e-109
Match length
                   261
% identity
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                   3587
                   2572 1.R1040
Contig ID
5'-most EST
                   LIB3028-042-Q1-B1-B7
Seq. No.
                   3588
                   2574 1.R1040
Contig ID
5'-most EST
                   LIB3028-042-Q1-B1-C1
Method
                   BLASTX
```

g4490330

Contig ID

```
1167
BLAST score
                   1.0e-128
E value
Match length
                   257
                   79
% identity
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   3589
Seq. No.
                   2574 2.R1040
Contig ID
5'-most EST
                   crh700856225.h1
Method
                  BLASTX
NCBI GI
                   g4490330
BLAST score
                  1033
                   1.0e-113
E value
Match length
                   220
% identity
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  3590
Seq. No.
                  2577 1.R1040
Contig ID
5'-most EST
                  LIB3051-084-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2129918
BLAST score
                  915
                  1.0e-101
E value
Match length
                  405
% identity
                  54
                  BPF-1 protein - parsley >gi_396197_emb_CAA48413_ (X68337)
NCBI Description
                  BPF-1 [Petroselinum crispum] >gi 441310 emb CAA44518
                   (X62653) BPF-1 [Petroselinum crispum]
                  3591
Seq. No.
                  2578 1.R1040
Contig ID
                  leu701144328.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3334667
BLAST score
                  405
E value
                  3.0e-39
                  214
Match length
                  40
% identity
NCBI Description
                   (Y10493) putative cytochrome P450 [Glycine max]
                  3592
Seq. No.
Contig ID
                  2579 1.R1040
5'-most EST
                  LIB3170-048-Q1-J1-H6
Method
                  BLASTX
NCBI GI
                  g3355480
BLAST score
                  159
E value
                  1.0e-10
Match length
                  65
% identity
NCBI Description
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
                  thaliana]
                  3593
Seq. No.
```

75- . .

2580 1.R1040

```
5'-most EST
                   jC-gmro02910072d02a1
                   BLASTX
Method
                   g3859659
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
Match length
                   53
                   51
% identity
                   (AL031394) putative potassium transporter AtKT5p (AtKT5)
NCBI Description
                   [Arabidopsis thaliana]
                   3594
Seq. No.
Contig ID
                   2582 1.R1040
                   gsv7\overline{0}1050196.h1
5'-most EST
                   BLASTX
Method
                   g4539008
NCBI GI
BLAST score
                   522
                   3.0e-53
E value
                   165
Match length
                   65
% identity
                   (AL049481) lipase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3595
Contig ID
                   2583 1.R1040
5'-most EST
                   hyd700731246.h1
Method
                   BLASTX
NCBI GI
                   g2194119
BLAST score
                   633
                   5.0e-66
E value
Match length
                   237
% identity
                   (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                   3596
Seq. No.
                   2584_1.R1040
Contig ID
                   LIB3092-028-Q1-K1-F1
5'-most EST
                   BLASTX
Method
                   g4455313
NCBI GI
BLAST score
                   304
E value
                   3.0e-27
Match length
                   276
                   29
% identity
                   (AL035528) fatty acid elongase-like protein (cer2-like)
NCBI Description
                   [Arabidopsis thaliana]
                   3597
Seq. No.
                   2584 2.R1040
Contig ID
5'-most EST
                   LIB3028-042-Q1-B1-D11
                   3598
Seq. No.
Contig ID
                   2585_1.R1040
                   LIB3040-033-Q1-E1-F7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3367591
BLAST score
                   393
                   5.0e-38
E value
Match length
                   124
% identity
                   57
```

```
4.
                   (ALO31135) putative protein [Arabidopsis thaliana]
NCBI Description
                   3599
Seq. No.
                   2588 1.R1040
Contig ID
                   jC-gmle01810020g09a1
5'-most EST
                   BLASTX
Method
                   q4263711
NCBI GI
BLAST score
                   647
                   1.0e-67
E value
                   170
Match length
% identity
                   71
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   3600
Seq. No.
                   2588 2.R1040
Contig ID
5'-most EST
                   uC-gmropic020e10b1
Method
                   BLASTX
                   q4263711
NCBI GI
                   332
BLAST score
                   8.0e-31
E value
Match length
                   82
                   73
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   3601
Seq. No.
Contig ID
                   2588 3.R1040
                   LIB3167-002-Q1-K1-A12
5'-most EST
                   BLASTX
Method
                   q4263711
NCBI GI
BLAST score
                   282
E value
                   3.0e-25
                   67
Match length
                   75
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   3602
Seq. No.
                   2588 4.R1040
Contig ID
                   jC-gmro02800038g09a1
5'-most EST
                   3603
Seq. No.
                   2589 1.R1040
Contig ID
                   LIB3138-093-Q1-N1-F1
5'-most EST
                   BLASTX
Method
                   g4539359
NCBI GI
BLAST score
                   272
                   2.0e-23
E value
Match length
                   168
                   36
% identity
                   (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
                   3604
Seq. No.
```

2589 2.R1040

 $leu7\overline{0}1152776.h1$ 

Contig ID

5'-most EST

```
3605
Seq. No.
Contig ID
                  2593 1.R1040
                  uC-gmronoir044b03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2129613
BLAST score
                  529
                  1.0e-83
E value
Match length
                  342
                  48
% identity
NCBI Description
                  homeotic protein BEL1 - Arabidopsis thaliana >gi 1122533
                   (U39944) BELL1 [Arabidopsis thaliana]
Seq. No.
                  3606
Contig ID
                  2593 2.R1040
5'-most EST
                  fde700873280.hl
Seq. No.
                  3607
                  2594 1.R1040
Contig ID
5'-most EST
                  fua701038018.h1
                  BLASTX
Method
                  g3128228
NCBI GI
BLAST score
                  514
                  6.0e-52
E value
Match length
                  178
% identity
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
Seq. No.
                  3608
Contig ID
                  2595 1.R1040
5'-most EST
                  LIB3028-042-Q1-B1-A7
Method
                  BLASTX
NCBI GI
                  q4455340
BLAST score
                  420
E value
                  3.0e-41
Match length
                  138
% identity
NCBI Description
                  (AL035522) putative protein [Arabidopsis thaliana]
Seq. No.
                  3609
                  2597 1.R1040
Contig ID
                  LIB3028-042-Q1-B1-A9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2832605
BLAST score
                  175
                  2.0e-12
E value
Match length
                  78
                  51
% identity
NCBI Description
                  (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                  3610
                  2598 1.R1040
Contig ID
                  ncj700980293.hl
5'-most EST
Method
                  BLASTN
                  g1370199
NCBI GI
```

391

BLAST score

```
E value
                   0.0e+00
Match length
                   611
                   91
% .identity
                   L. japonicus mRNA for small GTP-binding protein, RAC1
NCBI Description
                   3611
Seq. No.
                   2598 2.R1040
Contig ID
5'-most EST
                   g4286070
                   BLASTN
Method
                   g1370199
NCBI GI
BLAST score
                   196
                                                                    • .
                   1.0e-106
E value
Match length
                   276
                   93
% identity
                   L.japonicus mRNA for small GTP-binding protein, RAC1
NCBI Description
                   3612
Seq. No.
                   2599 1.R1040
Contig ID
5'-most EST
                   q4395750
                   BLASTX
Method
                   g3882309
NCBI GI
BLAST score
                   310
                   3.0e-28
E value
Match length
                   186
                   34
% identity
                   (AB018337) KIAA0794 protein [Homo sapiens]
NCBI Description
Seq. No.
                   3613
                   2609 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400027h09a1
Method
                   BLASTN
NCBI GI
                   q684941
BLAST score
                   352
                   0.0e+00
E value
                   716
Match length
                   87
% identity
                   Medicago sativa S-adenosyl-L-methionine:trans-caffeoyl-CoA
NCBI Description
                   3-O-methyltransferase (CCOMT) mRNA, complete cds
                   3614
Seq. No.
                   2609 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400031b03d1
Method
                   BLASTN
NCBI GI
                   g857577
BLAST score
                   141
                   3.0e-73
E value
Match length
                   313
% identity
                   Populus tremuloides caffeoyl-CoA 3-O-methyltransferase
NCBI Description
                   mRNA, complete cds
                   3615
Seq. No.
Contig ID
                   2609 3.R1040
                   fua7\overline{0}1042628.h1
5'-most EST
                   BLASTN
Method
                   g2465011
NCBI GI
```

....

96

BLAST score

```
E value
                   2.0e-46
Match length
                   212
% identity
                   89
                   Fragaria vesca mRNA for putative caffeoyl-CoA
NCBI Description
                   3-0-methyltransferase, partial
                   3616
Seq. No.
                   2609 6.R1040
Contig ID
                   fde700873805.hl
5'-most EST
Method
                   BLASTN
NCBI GI 🖰
                   g3550589
BLAST score
                   36
                   6.0e-11
E value
Match length
                   119
% identity
                   89
NCBI Description
                   Populus trichocarpa CCoAOMT2 gene, exon 1 to exon
Seq. No.
                   3617
                   2610 1.R1040
Contig ID
                  LIB3139-071-P1-N1-G5
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4538929
BLAST score
                  271
                   9.0e-24
E value
                  76
Match length
                   42
% identity
                   (AL049483) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  3618
Seq. No.
                   2613 1.R1040
Contig ID
5'-most EST
                  uC-qmrominsoy280g07b1
Method
                  BLASTX
NCBI GI
                  g3046700
BLAST score
                   674
                  1.0e-70
E value
Match length:
                  249
% identity
NCBI Description
                   (AJ005261) cytidine deaminase [Arabidopsis thaliana]
                  >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
                   [Arabidopsis thaliana] >gi 4191787 (AC005917) putative
                  cytidine deaminase [Arabidopsis thaliana]
                  3619
Seq. No.
                  2614_1.R1040
Contig ID
5'-most EST
                  LIB3028-041-Q1-B1-H3
Method
                  BLASTX
NCBI GI
                  g1076291
BLAST score
                  204
E value
                  4.0e-16
                  63
Match length
% identity
                  49
                  amino acid transporter AAT1 - Arabidopsis thaliana
NCBI Description
                  >gi_2911069_emb_CAA17531_ (AL021960) amino acid transport
                  protein AATI [Arabidopsis thaliana]
```

3620

Seq. No.

```
2616 1.R1040
Contig ID
5'-most EST
                   taw700655504.hl
Seq. No.
Contig ID
                   2620 1.R1040
5'-most EST
                   LIB3028-042-Q1-B1-A1
                   BLASTX
Method
NCBI GI
                   q2245068
BLAST score
                   545
E value
                   3.0e-55
Match length
                   133
% identity
                   (Z97342) serine protease homolog [Arabidopsis thaliana]
NCBI Description
                   3622
Seq. No.
Contig ID
                   2620 2.R1040
5'-most EST
                   fua701038204.h1
Seq. No.
                   3623
Contig ID
                   2620 3.R1040
5'-most EST
                   jC-gmst02400045e09a1
Seq. No.
                   3624
Contig ID
                   2620 6.R1040
5'-most EST
                   zhf700962164.h1
Method
                   BLASTX
NCBI GI
                   g2245068
BLAST score
                   152
E value
                   5.0e-10
Match length
                   39
% identity
                   69
                   (Z97342) serine protease homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3625
                   2621 1.R1040
Contig ID
                   uC-gmropic089d07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g303742
BLAST score
                   1049
E value
                   1.0e-114
Match length
                   217
% identity
                  (D12544) GTP-binding protein [Pisum sativum]
NCBI Description
                   >gi 738936 prf 2001457D GTP-binding protein [Pisum
                   sativum]
                   3626
Seq. No.
                   2622 1.R1040
Contig ID
5'-most EST
                   LIB3028-041-Q1-B1-E4
                   3627
Seq. No.
                   2623 1.R1040
Contig ID
                   LIB3053-004-Q1-N1-E3
5'-most EST
Method
                   BLASTX
                   g1076621
NCBI GI
BLAST score
                   432
```

2.0e-42

E value

```
Match length
                   140
% identity
                   56
                  cytochrome b5 - common tobacco >gi_296386_emb_CAA50575
NCBI Description
                   (X71441) cytochrome b5 [Nicotiana tabacum]
Seq. No.
                   3628
                   2624 1.R1040
Contig ID
                   kl1701204472.h2
5'-most EST
Method
                   BLASTX
                   g2760832
NCBI GI
BLAST score
                   480
E value
                   3.0e-48
                   154
Match length
% identity
NCBI Description
                   (AC003105) similar to barley ids-4 gene product
                   [Arabidopsis thaliana]
Seq. No.
                   3629
                   2624 2.R1040
Contig ID
5'-most EST
                   uC-qmronoir030b12b1
Method
                   BLASTX
NCBI GI
                   g2760832 ·
BLAST score
                   373
                   8.0e-36
E value
Match length
                   111
% identity
                   (AC003105) similar to barley ids-4 gene product
NCBI Description
                   [Arabidopsis thaliana]
                   3630
Seq. No.
                   2625 1.R1040
Contig ID
                   LIB3039-012-Q1-E1-B7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3643610
                   972
BLAST score
                   1.0e-105
E value
                   211
Match length
% identity
NCBI Description
                   (AC005395) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
                   3631
Seq. No.
                   2627 1.R1040
Contig ID
5'-most EST
                  LIB3093-038-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                   g4263711
                   1041
BLAST score
                   1.0e-113
E value
                   247
Match length
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   3632
Seq. No.
                   2627 2.R1040
Contig ID
5'-most EST
                  q5058533
```

BLASTX

Method

```
NCBI GI
                    g4106061
                   269
BLAST score
E value
                   2.0e-23
                   83
Match length
                    61
% identity
                    (AF053318) CCR4-associated factor 1 [Homo sapiens]
NCBI Description
Seq. No.
                    3633
                   2627 4.R1040
Contig ID
                   LIB3\overline{0}49-043-Q1-E1-B1
5'-most EST
Seq. No.
                    3634
                   2630 1.R1040
Contig ID
                   pmv700893795.h1
5'-most EST
Seq. No.
                    3635
                   2631 1.R1040
Contig ID
5'-most EST
                   uaw7\overline{0}0663361.h1
Seq. No.
                   3636
                   2632 1.R1040
Contig ID
5'-most EST
                   LIB3170-013-Q1-K1-H5
Seq. No.
                   3637
                   2632 2.R1040
Contig ID
                   LIB3074-009-Q1-E1-C5
5'-most EST
Seq. No.
                   3638
Contig ID
                   2633 1.R1040
                    zhf700953666.hl
5'-most EST
Seq. No.
                    3639
                    2634 1.R1040
Contig ID
5'-most EST
                    6HA - \overline{0}2 - Q1 - B1 - A12
                    3640
Seq. No.
                   2636 1.R1040
Contig ID
                   jC-gmst02400061f01a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4454452
BLAST score
                    936
                    1.0e-101
E value
Match length
                   278
% identity
NCBI Description
                    (AC006234) unknown protein [Arabidopsis thaliana]
                   3641
Seq. No.
                   2638 1.R1040
Contig ID
                   bnu700967569.h1
5'-most EST
Method
                   BLASTX
                   g2330797
NCBI GI
BLAST score
                   371
E value
                   6.0e-35
Match length
                   205
% identity
                   38
```

NCBI Description (Z98601) zinc finger protein [Schizosaccharomyces pombe]

Seq. No.

Contig ID

```
Seq. No.
                   3642
                   2639 1.R1040
Contig ID
                   ssr700558953.hl
5'-most EST
                   BLASTX
Method
                   q4468986
NCBI GI
                   321
BLAST score
                   2.0e-29
E value
                   187
Match length
                   38
% identity
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3643
                   2639 2.R1040
Contig ID
                   ncj7\overline{0}0981812.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4468986
                   170
BLAST score
E value
                   4.0e-12
                   93
Match length
% identity
                   40
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3644
                   2639 3.R1040
Contig ID
                   awf700839353.hl
5'-most EST
Method
                   BLASTX
                   g4468986
NCBI GI
BLAST score
                   186
E value
                   7.0e-14
                   102
Match length
                   41
% identity
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3645
                   2641 1.R1040
Contig ID
                   wvk700684348.hl
5'-most EST
Method
                   BLASTN
                   g602358
NCBI GI
BLAST score
                   344
                   0.0e + 00
E value
Match length
                   811
                   89
% identity
                   P.sativum mRNA for type II chlorophyll a/b binding protein
NCBI Description
                   3646
Seq. No.
                   2641 2.R1040
Contig ID
                   LIB3039-028-Q1-E1-G10
5'-most EST
                   BLASTN
Method
                   g602358
NCBI GI
BLAST score
                   260
                   1.0e-144
E value
Match length
                   723
% identity
                   86
                   P.sativum mRNA for type II chlorophyll a/b binding protein
NCBI Description
                   3647
```

. .

2643 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   LIB3138-048-Q1-N1-H4
Seq. No.
                   3648
                   2643 2.R1040
Contig ID
                   LIB3092-033-Q1-K1-G10
5'-most EST
                   BLASTX
Method
                   g2190540
NCBI GI
BLAST score
                   331
                   1.0e-30
E value
Match length
                   7.4
% identity
                   80
NCBI Description
                   (ACO01229) Similar to Arabidopsis TFL1 (gb_U77674).
                   [Arabidopsis thaliana]
Seq. No.
                   3649
Contig ID
                   2644 1.R1040
5'-most EST
                   LIB3039-012-Q1-E1-D3
Seq. No.
                   3650
Contig ID
                   2647 1.R1040
5'-most EST
                   LIB3109-020-Q1-K1-D10
                   BLASTN
Method
NCBI GI
                   g169980
BLAST score
                   138
E value
                   3.0e-71
Match length
                   447
                   87
% identity
NCBI Description
                   Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                   2651 1.R1040
Contig ID
                   seb700652937.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2982303
BLAST score
                   1236
                   1.0e-136
E value
Match length
                   267
% identity
                   (AF051236) hypothetical protein [Picea mariana]
NCBI Description
Seq. No.
                   3652
                   2653 1.R1040
Contig ID
                   LIB3093-042-Q1-K1-A6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2501337
BLAST score
                   500
                   1.0e-119
E value
Match length
                   414
% identity
                   52
                   AMINE OXIDASE PRECURSOR [COPPER-CONTAINING]
NCBI Description
                   >gi_2129875_pir__C44239 amine oxidase (copper-containing)
                   (EC 1.4.3.6) precursor - garden pea >gi_685198 (L39931)
                   copper amine oxidase [Pisum sativum]
                   3653
Seq. No.
```

2656 1.R1040

uC-gmrominsoy026h04b1

```
Method
                   BLASTX
NCBI GI
                   g2275196
BLAST score
                   1337
                   1.0e-148
E value
Match length
                   328
                   77
% identity
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   3654
Seq. No.
Contig ID
                   2658 1.R1040
                   LIB3049-031-Q1-E1-C9
5'-most EST
Method
                   BLASTX
                   g4559346
NCBI GI
BLAST score
                   400
E value
                   1.0e-38
Match length
                   176
% identity
                   (AC006585) early nodulin 16 [Arabidopsis thaliana]
NCBI Description
                   3655 ·
Seq. No.
                   2660 1.R1040
Contig ID
                   uxk700671869.h1
5'-most EST
Method
                   BLASTX
                   g2088652
NCBI GI
BLAST score
                   671
                   1.0e-70
E value
Match length
                   166
% identity
                   74
                   (AF002109) 26S proteasome regulatory subunit S12 isolog
NCBI Description
                   [Arabidopsis thaliana] >gi 2351376 (U54561) translation
                   initiation factor eIF2 p47 subunit homolog [Arabidopsis
                   thaliana]
                   3656
Seq. No.
                   2661 1.R1040
Contig ID
5'-most EST
                   g4292101
Method
                   BLASTX
NCBI GI
                   g4262149
BLAST score
                   607
E value
                   5.0e-63
                   151
Match length
                   73
% identity
NCBI Description
                   (AC005275) putative xyloglucan endotransglycosylase
                   [Arabidopsis thaliana]
                   3657
Seq. No.
                   2661 2.R1040
Contig ID
                   fC-qmle700554113a3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4262149
BLAST score
                   622
E value
                   8.0e-65
Match length
                   136
% identity
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
```

15.7

5'-most EST

```
3658
Seq. No.
Contig ID
                   2663 1.R1040
                   LIB3028-040-Q1-B1-H3
5'-most EST
                   3659
Seq. No.
                   2664 1.R1040
Contig ID
                   fde700874478.h1
5'-most EST
                   BLASTX
Method
                   g1922240
NCBI GI
                   143
BLAST score
E value
                   1.0e-08
                   28
Match length
% identity
                   (Y10083) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   3660
Seq. No.
Contig ID
                   2669 1.R1040
                   LIB3049-034-Q1-E1-F6
5'-most EST
Method
                   BLASTX
                   q4454263
NCBI GI
BLAST score
                   152
E value
                   2.0e-09
                   94
Match length
                   38
% identity
                   (Y18046) FGFR1 oncogene partner (FOP) [Homo sapiens]
NCBI Description
Seq. No.
                   3661
Contig ID
                   2669 2.R1040
                   vzy700755346.h1
5'-most EST
                   BLASTX
Method
                   g4454263
NCBI GI
                   153
BLAST score
                   5.0e-10
E value
                   94
Match length
% identity
                   (Y18046) FGFR1 oncogene partner (FOP) [Homo sapiens]
NCBI Description
Seq. No.
                   3662
                   2669 3.R1040
Contig ID
                   eep700864394.h1
5'-most EST
                   3663
Seq. No.
                   2672 1.R1040
Contig ID
                   uC-gmflminsoy029c04b1
5'-most EST
                   BLASTX
Method
                   g2578444
NCBI GI
                   275
BLAST score
                   1.0e-23
E value
                   89
Match length
                   61
% identity
NCBI Description
                   (X67427) ptxA [Pisum sativum]
                   3664
Seq. No.
                   2672 2.R1040
Contig ID
```

jC-qmst02400061d09d1

Match length

110

```
3665
Seq. No.
Contig ID
                   2672 3.R1040
                   LIB3028-041-Q1-B1-A4
5'-most EST
Method
                   BLASTN .
NCBI GI
                   q2578443
BLAST score
                   45
                   6.0e-16
E value
Match length
                   257
                   76
% identity
NCBI Description
                  Pisum sativum ptxA gene
                   3666
Seq. No.
Contig ID
                   2675 1.R1040
5'-most EST
                   uC-gmrominsoy298a12b1
Method
                   BLASTX
                   g3319340
NCBI GI
BLAST score
                   716
                   2.0e-75
E value
Match length
                   208
% identity
                   (AF077407) contains similarity to E. coli cation transport
NCBI Description
                  protein ChaC (GB:D90756) [Arabidopsis thaliana]
Seq. No.
                   2675 2.R1040
Contig ID.
                   leu7\overline{0}1148029.h1
5'-most EST
                   BLASTX
Method
                   g2827524
NCBI GI
BLAST score
                   615
E value
                   3.0e-68
                   212
Match length
% identity
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3668
                   2678 1.R1040
Contig ID
                   LIB3106-036-Q1-K1-D4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3874214
BLAST score
                   647
                   2.0e-67
E value
Match length
                   361
                   42
% identity
                   (283217) Similarity to Yeast E1-E2 ATPase YEL031W
NCBI Description
                   (SW:YED1 YEAST); cDNA EST EMBL:D27574 comes from this gene;
                   cDNA EST EMBL: D33757 comes from this gene; cDNA EST
                   EMBL: D34256 comes from this gene; cDNA EST EMBL: D37288
                   comes from
                   3669
Seq. No.
Contig ID
                   2679 1.R1040
5'-most EST
                   pcp700993216.hl
                   BLASTX
Method
NCBI GI
                   q3717946
BLAST score
                   257
                   7.0e-22
E value
```

```
% identity
                  50
                   (AJ005901) vag1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3670
                  2679 2.R1040
Contig ID
                  taw700654871.hl
5'-most EST
Method
                  BLASTX
                  q3492806
NCBI GI
BLAST score
                  678
                  6.0e-71
E value
Match length
                  289
% identity
                   (AJ225045) adventitious rooting related oxygenase [Malus
NCBI Description
                  domestica]
                  3671
Seq. No.
Contig ID
                  2681 1.R1040
5'-most EST
                  LIB3050-004-Q1-E1-A9
Method
                  BLASTX
NCBI GI
                  q2961372
BLAST score
                  1239
E value
                  1.0e-137
Match length
                  238
% identity
                  95
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                  thaliana] >gi 3036817 emb CAA18507 (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
Seq. No.
                  3672
                  2681 2.R1040
Contig ID
                  LIB3051-063-Q1-K1-G12
5'-most EST
Method
                  BLASTX
                  g2961372
NCBI GI
BLAST score
                  861
                  8.0e-93
E value
Match length
                  173
                  91
% identity
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                  thaliana] >gi 3036817 emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
                  3673
Seq. No.
                  2681 3.R1040
Contig ID
5'-most EST
                  LIB3170-034-Q1-K1-B9
Method
                  BLASTN
                  g2961370
NCBI GI
BLAST score
                  121
                  2.0e-61
E value
                  305
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13
NCBI Description
                   (ESSAII project)
                  3674
Seq. No.
Contig ID
                  2681 4.R1040
                  LIB3139-080-P1-N1-B12
5'-most EST
```

BLASTX

Method

```
NCBI GI
                  q2961372
BLAST score
                   416
                  7.0e-41
E value
Match length
                  132
                  71
% identity
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                  thaliana] >gi 3036817 emb CAA18507 (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
Seq. No.
                  2681 5.R1040
Contig ID
                  LIB3170-034-Q1-K1-C1
5'-most EST
Method
                  BLASTN
                  q4406805
NCBI GI
                  87
BLAST score
                   5.0e-41
E value
Match length
                   263
% identity
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   2681 6.R1040
Contig ID
5'-most EST
                   jC-gmro02910025d01a1
                   BLASTN
Method
                 - q4406805
NCBI GI
                  81
BLAST score
                   1.0e-37
E value
Match length
                   141
% identity
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
Contig ID
                   2681 7.R1040
5'-most EST
                   jsh7\overline{0}1067395.h1
                   BLASTX
Method
NCBI GI
                   q2961372
BLAST score
                   350
E value
                   2.0e-33
Match length
                   69
% identity
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                   thaliana] >gi 3036817 emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
                   3678
Seq. No.
                   2681 8.R1040
Contig ID
                   epx701109002.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2961372
BLAST score
                   359
E value
                   2.0e-34
Match length
                   74
                   91
% identity
                   (AL022141) putative ribosomal protein L8 (Arabidopsis
NCBI Description
                   thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
```

BLAST score

184

## protein L2 [Arabidopsis thaliana]

```
3679
Seq. No.
                   2683 1.R1040
Contig ID
                   jC-qmf102220091c10d1
5'-most EST
Seq. No.
                   3680
                   2686 1.R1040
Contig ID
                   txt700736173.hl
5'-most EST
Method
                   BLASTX
                   g3182981
NCBI GI
BLAST score
                   2770
E value
                   0.0e + 00
Match length
                   567
                   89
% identity
NCBI Description
                   CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj BAA13096
                   (D86494) diminuto [Pisum sativum]
                   3681
Seq. No.
Contig ID
                   2690 1.R1040
                                                                     . . . .
5'-most EST
                   crh700855489.hl
                   BLASTX
Method
NCBI GI
                   q3510538
BLAST score
                   403
                   4.0e-39
E value
Match length
                   125
                   60
% identity
NCBI Description
                   (U93167) expansin [Prunus armeniaca]
Seq. No.
                   3682
                   2693 1.R1040
Contig ID
                   LIB3028-040-Q1-B1-F5
5'-most EST
Seq. No.
                   3683
                   2693 2.R1040
Contig ID
                   LIB3055-011-Q1-N1-D11
5'-most EST
                   3684
Seq. No.
Contig ID
                   2694 1.R1040
5'-most EST
                   uC-gmropic011g06b1
Method
                   BLASTX
NCBI GI
                   g2351378
BLAST score
                   367
                   1.0e-34
E value
Match length
                   173
                   53
% identity
                   (U54558) translation initiation factor eIF3 p66 subunit
NCBI Description
                   [Homo sapiens] >gi 4200328_emb_CAA18440_ (AL022313)
                   EIF3-P66 [Homo sapiens]
                   >gi_4503523_ref_NP_003744.1_pEIF3S7_ UNKNOWN
                   3685
Seq. No.
                   2695 1.R1040
Contig ID
                   vzy7\overline{0}0752220.h1
5'-most EST
                   BLASTX
Method
                   q3402282
NCBI GI
```

Method

```
E value
                   2.0e-28
Match length
                   112
% identity
                   54
                   (AJ000997) proline-rich protein [Solanum tuberosum]
NCBI Description
                   3686
Seq. No.
                   2699 1.R1040
Contig ID
                  bth700845695.h1
5'-most EST
                   BLASTX
Method
                   g4512651
NCBI GI
BLAST score
                   1083
E value
                   1.0e-118
Match length
                   410
% identity
                   49
                   (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3687
                   2699 2.R1040
Contig ID
                   fC-qmf1700908904a1
5'-most EST
                   3688
Seq. No.
Contig ID
                   2699 3.R1040
                   jC-gmf102220063e05d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4512651
                   263
BLAST score
E value
                   1.0e-22
Match length
                   121
                   39
% identity
                   (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thalianal
                   3689
Seq. No.
                   2699 4.R1040
Contig ID
                   jC-gmf102220148b08a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4512651
BLAST score
                   203
                   7.0e-16
E value
                   111
Match length
                   35
% identity
                   (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thaliana]
                   3690
Seq. No.
                   2699 5.R1040
Contig ID
5'-most EST
                   pcp700990102.hl
                   3691
Seq. No.
                   2700_1.R1040
Contig ID
5'-most EST
                   LIB3028-040-Q1-B1-E5
                   3692
Seq. No.
                   2701 2.R1040
Contig ID
5'-most EST
                   LIB3028-040-Q1-B1-E6
                   BLASTX
```

```
NCBI GI
                   g4558548
BLAST score
                   188
                   6.0e-14
E value
Match length
                   55
% identity
                   64
                   (AC007138) putative RNaseP-associated protein [Arabidopsis
NCBI Description
                   thalianal
                   3693
Seq. No.
Contig ID
                   2701 3.R1040
5'-most EST
                   ejt700606219.hl
                   BLASTX
Method
NCBI GI
                   q4558548
BLAST score
                   314
                   2.0e-34
E value
                   152
Match length
% identity
                   48
                   (AC007138) putative RNaseP-associated protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3694
Contig ID
                   2703 1.R1040
5'-most EST
                   LIB3107-025-Q1-K1-A8
Seq. No.
                   3695
Contig ID
                   2704 1.R1040
5'-most EST
                   uC-gmropic062g06b1
                   BLASTX
Method
NCBI GI
                   q4103243
BLAST score
                   460
E value
                   1.0e-48
Match length
                   185
% identity
                   59
NCBI Description
                  (AF022368) BIPOSTO [Arabidopsis thaliana]
Seq. No.
                   3696
Contig ID
                   2706 1.R1040
5'-most EST
                   zhf700962987.h1
Method
                   BLASTX
NCBI GI
                   q4056489
BLAST score
                   429
E value
                   5.0e-42
Match length
                   222
% identity
NCBI Description
                   (AC005896) putative white protein [Arabidopsis thaliana]
Seq. No.
                   3697
                   2708 1.R1040
Contig ID
                   zpv700763310.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3873710
BLAST score
                   353
E value
                   5.0e-33
Match length
                  113
                   56
% identity
                  (Z73102) predicted using Genefinder; similar to Zinc
NCBI Description
```

finger, C2H2 type; cDNA EST EMBL:M89161 comes from this

```
gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

3698
2708_2.R1040
LIB3093-031-Q1-K1-B12
```

Method BLASTN
NCBI GI g4191760
BLAST score 54
E value 1.0e-21
Match length 134
% identity 85

Seq. No.

Contig ID 5'-most EST

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17F8,

complete sequence [Arabidopsis thaliana]

Seq. No. 3699 Contig ID 2709 1.R1040 5'-most EST q5057680 BLASTX Method NCBI GI q3033380 BLAST score 1159 E value 1.0e-127 Match length 285 % identity 76

NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis

thaliana]

Seq. No. 3700

Contig ID 2709\_2.R1040 5'-most EST gsv701045190.h1

Method BLASTX
NCBI GI g3033380
BLAST score 286
E value 1.0e-25
Match length 83
% identity 67

NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis

thaliana]

Seq. No. 3701

Contig ID 2709\_3.R1040 5'-most EST sat701008044.h1

Method BLASTX
NCBI GI g3033380
BLAST score 203
E value 5.0e-16
Match length 45
% identity 82

NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis

thaliana]

Seq. No. 3702

Contig ID 2709 4.R1040 5'-most EST zhf700961443.h1

Seq. No. 3703

```
Contig ID
                  2710 1.R1040
                  wvk700681157.h2
5'-most EST
Seq. No.
                  3704
                  2711 1.R1040
Contig ID
                  uC-qmflminsoy054f05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4101589
BLAST score
                  629
                  2.0e-65
E value
                  238
Match length
% identity
                  52
                  (AF005050) aspartyl aminopeptidase [Homo sapiens]
NCBI Description
Seq. No.
                  3705
Contig ID
                  2712 1.R1040
5'-most EST
                  LIB3093-044-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                  1864
E value
                  0.0e + 00
Match length
                  423
                  84
% identity
                  (ACO02292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                  3706
Seq. No.
Contig ID
                  2712 2.R1040
5'-most EST
                  zhf700959649.h1
Method
                  BLASTX
NCBI GI
                  q2462746
BLAST score
                  355
E value
                  9.0e-34
Match length
                  88
% identity
                  77
                  (ACO02292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
Seq. No.
                  3707
Contig ID
                  2712 4.R1040
5'-most EST
                  LIB3106-025-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                  150
E value
                  6.0e-10
Match length
                  37
% identity
                  81
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                  3708
Seq. No.
                  2712 6.R1040
Contig ID
5'-most EST
                  wrg700791527.hl
Method
                  BLASTX
                  q2462746
NCBI GI
BLAST score
                  253
                  5.0e-22
E value
```

BLAST score

353

```
Match length
                   60
% identity
                   78
NCBI Description
                    (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
                   thaliana]
                   3709
Seq. No.
Contig ID
                   2712 9.R1040
                   hyd7\overline{0}0730039.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2462746
BLAST score
                   167
E value
                   9.0e-12
Match length
                   43
% identity
                   77
NCBI Description
                   (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
                   thaliana]
Seq. No.
                   3710
Contig ID
                   2713 1.R1040
5'-most EST
                   zhf700965295.h1
Method
                   BLASTX
NCBI GI
                   g4006878
BLAST score
                   1192
E value
                   1.0e-131
Match length
                   312
% identity
                   (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3711
                   2716 1.R1040
Contig ID
                   leu701152981.hl
5'-most EST
Method
                   BLASTX
                   g4191774
NCBI GI
BLAST score
                   487
                   8.0e-49
E value
Match length
                   168
% identity
                   60
                   (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3712
                   2718 1.R1040
Contig ID
5'-most EST
                   LIB3028-001-Q1-B1-B3
Method
                   BLASTX
NCBI GI
                   q4580389
BLAST score
                   801
                   1.0e-85
E value
Match length
                   211
                   70
% identity
NCBI Description
                   (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                   3713
                   2719 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810005c04a1
Method
                   BLASTX
                   g1076685
NCBI GI
```

NCBI GI

```
. . <del>. . . . .</del>
E value
                   8.0e-33
Match length
                   149
                   39
% identity
                   SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_
NCBI Description
                   (D30038) SPF1 protein [Ipomoea batatas]
                   3714
Seq. No.
                   2719 2.R1040
Contig ID
                   LIB3139-045-P1-N1-E11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1076685
BLAST score
                   1414
                   1.0e-157
E value
Match length
                   524
% identity
                   57
                   SPF1 protein - sweet potato >gi 484261_dbj_BAA06278_
NCBI Description
                   (D30038) SPF1 protein [Ipomoea batatas]
                   3715
Seq. No.
                   2719 3.R1040
Contig ID
                   jC-gmro02910075a07a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1076685
BLAST score
                   468
                   1.0e-46
E value
                   232
Match length
                   35
% identity
NCBI Description
                   SPF1 protein - sweet potato >gi 484261_dbj_BAA06278_
                   (D30038) SPF1 protein [Ipomoea batatas]
                   3716
Seq. No.
                   2723 1.R1040
Contig ID
5'-most EST
                   gsv701045628.hl
Method
                   BLASTX
                   g1769887
NCBI GI
                   1541
BLAST score
                   1.0e-172
E value
Match length
                   408
                   72
% identity
NCBI Description
                   (X95736) amino acid permease 6 [Arabidopsis thaliana]
Seq. No.
                   3717
                   2723 2.R1040
Contig ID
                   LIB3106-018-Q1-K1-D1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1769887
BLAST score
                   443
                   9.0e-44
E value
Match length
                   143
% identity
                   (X95736) amino acid permease 6 [Arabidopsis thaliana]
NCBI Description
                   3718
Seq. No.
                   2726 1.R1040
Contig ID
                   sat701014367.hl
5'-most EST
                   BLASTX
Method
```

q4455159

```
214
BLAST score
E value
                   6.0e-17
                   61
Match length
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   3719
Seq. No.
Contig ID
                   2728 1.R1040
5'-most EST
                   LIB3049-015-Q1-E1-A2
                   BLASTX
Method
                   g2827710
NCBI GI
BLAST score
                   214
E value
                   3.0e-17
                   99
Match length
                   45
% identity
                   (AL021684) lysosomal Pro-X carboxypeptidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   3720
                   2732 1.R1040
Contig ID
5'-most EST
                   LIB3028-035-Q1-B1-F7
                   3721
Seq. No.
Contig ID
                   2733 1.R1040
                   LIB3109-014-Q1-K1-D2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3044214
BLAST score
                   1125
E value
                   1.0e-123
Match length
                   271
                   80
% identity
                   (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2733 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy189c09b1
Method
                   BLASTX
NCBI GI
                   g2245030
BLAST score
                   260
E value
                   4.0e-24
Match length
                   141
% identity
                   (Z97341) apetala2 domain TINY homolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3723
                   2736 1.R1040
Contig ID
                   pcp700995727.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3335359
BLAST score
                   1989
E value
                   0.0e+00
Match length
                   489
% identity
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

```
Contig ID
                   2736 3.R1040
5'-most EST
                  ujr700646525.hl
Method
                  BLASTX
                  q3335359
NCBI GI
BLAST score
                   238
                   3.0e-20
E value
Match length
                   62
% identity
                   73
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3725
Seq. No.
Contig ID
                  2741 1.R1040
                  uC-gmropic037d01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4006886
BLAST score
                   209
E value
                   1.0e-16
Match length
                  107
% identity
                   48
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                  3726
Seq. No.
Contig ID
                  2741 2.R1040
                  uC-gmropic075f05b1
5'-most EST
Method
                  BLASTX
                  g4006886
NCBI GI
                  169
BLAST score
E value
                  5.0e-12
Match length
                  72
                  51
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3727
                  2742 1.R1040
Contig ID
                  LIB3170-015-Q1-K1-C1
5'-most EST
                  BLASTX
Method
                  g3123230
NCBI GI
BLAST score
                  1359
E value
                  1.0e-150
Match length
                  657
                  42
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT
NCBI Description
                   (EIF-3 BETA) (EIF3 P116) (EIF3 P110) >gi_2558668 (U78525)
                  eukaryotic translation initiation factor [Homo sapiens]
                  3728
Seq. No.
                  2742 2.R1040
Contig ID
5'-most EST
                  gsv701045433.hl
                  3729
Seq. No.
                  2743 1.R1040
Contig ID
5'-most EST
                  LIB3028-039-Q1-B2-F8
                  3730
Seq. No.
                  2749 1.R1040
Contig ID
5'-most EST
                  LIB3039-028-Q1-E1-B11
Method
                  BLASTX
```

```
NCBI GI
                   g2262116
BLAST score
                   363
E value
                   2.0e-34
                   188
Match length
                   37
% identity
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   2749 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy061b01b1
Method
                   BLASTX
NCBI GI
                   g2262116
BLAST score
                   162
                   4.0e-11
E value
                   97
Match length
                   32
% identity
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                   3732
Seq. No.
                   2752 1.R1040
Contig ID
5'-most EST
                   awf700840376.h1
                   BLASTX
Method
                   g2529686
NCBI GI
BLAST score
                   283
E value
                   3.0e - 33
Match length
                   167
% identity
                   47
                   (AC002535) putative G-beta-repeat containing protein, 5'
NCBI Description
                   partial [Arabidopsis thaliana]
Seq. No.
                   3733
Contig ID
                   2753 1.R1040
5'-most EST
                   smw700646173.h1
                   BLASTX
Method
NCBI GI
                   q479406
BLAST score
                   1254
E value .
                   1.0e-138
Match length
                   253
                   92
% identity
                   chlorophyll a/b-binding protein - garden pea
NCBI Description
                   >gi 20671 emb_CAA49149 (X69215) chlorophyll a/b-binding
protein [Pisum sativum]
Seq. No.
                   3734
Contig ID
                   2753 2.R1040
5'-most EST
                   hyd700729030.h1
Seq. No.
                   3735
                   2754 1.R1040
Contig ID
5'-most EST
                   LIB3028-039-Q1-B1-A7
Method
                   BLASTX
NCBI GI
                   g3850818
BLAST score
                   781
                   3.0e-83
E value
Match length
                   190
% identity
                   (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
```

```
sativa]
                   3736
Seq. No.
                   2754 2.R1040
Contig ID
                   LIB3138-015-Q1-N2-H12
5'-most EST
Method
                   BLASTX
                   q3850819
NCBI GI
                   790
BLAST score
                   2.0e-84
E value
Match length
                   184
% identity
                   77
                   (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
Seq. No.
                   3737
Contig ID
                   2754 3.R1040
                   seb7\overline{0}0651223.h1
5'-most EST
Seq. No.
                   3738
                   2755 1.R1040
Contig ID
                   leu701149305.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3236248
BLAST score
                   1064
E value
                   1.0e-116
Match length
                   248
                   82
% identity
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   2755 2.R1040
                   zhf700953477.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3236248
BLAST score
                   324
E value
                   5.0e-30
Match length
                   95
% identity
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   3740
                   2756 1.R1040
Contig ID
                   LIB3106-090-Q1-K1-H6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q400578
BLAST score
                   269
                   2.0e-23
E value
                   109
Match length
                   46
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ)
                   >gi_346531_pir__S28240 NADH dehydrogenase (ubiquinone) (EC
```

Seq. No. 3741

Contig ID 2760 1.R1040

(X63215) NADH dehydrogenase [Bos taurus]

1.6.5.3) chain CI-18(IP) - bovine >gi 226 emb CAA44900\_

Method

BLASTN

```
5'-most EST
                   uC-gmrominsoy265a09b1
Method
                   BLASTX
NCBI GI
                   g2281115
BLAST score
                   2848
                   0.0e+00
E value
                   740
Match length
                   75
% identity
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                   thaliana]
                   3742
Seq. No.
                   2760 2.R1040
Contig ID
                   g4290426
5'-most EST
Method
                   BLASTX
                   g2281115
NCBI GI
BLAST score
                   407
                   2.0e-39
E value
Match length
                   111
                   73
% identity
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   3743
                   2760_3.R1040
Contig ID
                   uC-gmropic047g08b1
5'-most EST
Method
                   BLASTX
                   q2281115
NCBI GI
BLAST score
                   325
                   3.0e-30
E value
                   68
Match length
% identity
                   87
NCBI Description
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
                   thaliana]
Seq. No.
                   3744
Contig ID
                   2760 4.R1040
5'-most EST
                   LIB3138-095-Q1-N1-B3
                   3745
Seq. No.
                   2761 1.R1040
Contig ID
5'-most EST
                   LIB3039-040-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                   g473949
BLAST score
                   237
E value
                   6.0e-30
Match length
                   172
% identity
                   44
                  (D29958) KIAA0116 [Homo sapiens]
NCBI Description
                   3746
Seq. No.
                   2761 2.R1040
Contig ID
5'-most EST
                   eep7\overline{0}0868836.h1
                   3747
Seq. No.
Contig ID
                   2765_1.R1040
5'-most EST
                   jC-gmst02400077a08d1
```

```
NCBI GI
                  q1706955
BLAST score
                  81
                  1.0e-37
E value
Match length
                  157
% identity
                  88
                  Gossypium hirsutum cellulose synthase (celA1) mRNA,
NCBI Description
                  complete cds
                  3748
Seq. No.
                  2768 1.R1040
Contig ID
                  LIB3028-039-Q1-B1-F10
5'-most EST
Method
                  BLASTX
                  g2500036
NCBI GI
BLAST score
                  141
E value
                  1.0e-08
Match length
                  31
                  74
% identity
                  DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146)
NCBI Description
                  dihydroorotase [Arabidopsis thaliana]
                  >qi 3292818 emb CAA19808 (AL031018) dihydroorotase
                   [Arabidopsis thaliana]
Seq. No.
                  3749
                  2769 1.R1040
Contig ID
                  jC-gmf102220053a03a1
5'-most EST
Method
                  BLASTX
                  g2388689
NCBI GI
BLAST score
                  359
E value
                  1.0e-101
Match length
                  319
                   66
% identity
                   (AF016633) GH1 protein [Glycine max]
NCBI Description
                  3750
Seq. No.
                  2769 2.R1040
Contig ID
                   zhf700958581.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2388689
                  974
BLAST score
                  1.0e-105
E value
                  324
Match length
% identity
                   (AF016633) GH1 protein [Glycine max]
NCBI Description
                  3751
Seq. No.
                  2769_4.R1040
Contig ID
5'-most EST
                   jC-gmf102220065e10a1
Method
                  BLASTX
NCBI GI
                  q2388689
BLAST score
                  154
E value
                   4.0e-10
                  77
Match length
                   47
% identity
                   (AF016633) GH1 protein [Glycine max]
NCBI Description
                   3752
Seq. No.
```

2772\_1.R1040

Contig ID

E value

```
5'-most EST
                  zhf700960218.h1
Seq. No.
                  3753
Contig ID
                  2774 1.R1040
                  LIB3051-015-Q1-E1-C7
5'-most EST
Method
                  BLASTN
                  q3334755
NCBI GI
BLAST score
                  131
                  6.0e-67
E value
Match length
                  943
                  84
% identity
                  Medicago sativa mRNA for putative arginine/serine-rich
NCBI Description
                  splicing factor
                  3754
Seq. No.
                  2774 2.R1040
Contig ID
5'-most EST
                  LIB3106-093-Q1-K1-E8
Method
                  BLASTN
                  q3334755
NCBI GI
BLAST score
                  242
E value
                  1.0e-133
                  573
Match length
                  86
% identity
                  Medicago sativa mRNA for putative arginine/serine-rich
NCBI Description
                  splicing factor
Seq. No.
                  3755
Contig ID
                  2776 1.R1040
                  LIB3093-050-Q1-K1-D10
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4512624
BLAST score
                  1923
E value
                  0.0e+00
Match length
                  500
                  73
% identity
NCBI Description
                  (AC004793) Strong similarity to gi_3033401 F19I3.29
                  putative potassium transporter from Arabidopsis thaliana
                  BAC gb_AC004238
                  3756
Seq. No.
                  2779 1.R1040
Contig ID
5'-most EST
                  zhf700956246.h1
Method
                  BLASTX
NCBI GI
                  g2213610
BLAST score
                  278
                  2.0e-24
E value
Match length
                  158
% identity
NCBI Description
                  (AC000103) F21J9.4 [Arabidopsis thaliana]
Seq. No.
                  3757
Contig ID
                  2786 1.R1040
5'-most EST
                  LIB3073-017-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3355483
BLAST score
                  273
```

6.0e-24

NCBI Description

```
59
Match length
                   71
% identity
                   (AC004218) gibberellin-regulated protein (GASA5)-like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
Contig ID
                  2794 1.R1040
5'-most EST
                  LIB3028-039-Q1-B2-A2
Seq. No.
                                                            3
                  2794 2.R1040
Contig ID
5'-most EST
                  LIB3028-039-Q1-B1-A2
Method
                  BLASTX
                  g4063747
NCBI GI
BLAST score
                   491
                  2.0e-66
E value
Match length
                  248
% identity
                  (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3760
                  2799 1.R1040
Contig ID
                  LIB3170-046-Q1-J1-G2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  783
                  2.0e-83
E value
Match length
                  252
% identity
                  61
NCBI Description
                  (AJ223074) acid phosphatase [Glycine max]
Seq. No.
Contig ID
                  2801 1.R1040
5'-most EST
                  LIB3049-029-01-E1-A12
                  3762
Seq. No.
                  2801 3.R1040
Contig ID
5'-most EST
                   fde700871424.h1
Method
                  BLASTX
NCBI GI
                  q4454459
BLAST score
                  362
                  2.0e-34
E value
Match length
                  135
% identity
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
                  3763
Seq. No.
                  2801 4.R1040
Contig ID
                  pmv700893892.h1
5'-most EST
Method
                  BLASTX
                  g4454459
NCBI GI
BLAST score
                  228
                  8.0e-19
E value
                  77
Match length
                  58
% identity
```

(AC006234) unknown protein [Arabidopsis thaliana]

5'-most EST

```
3764
Seq. No.
                   2807 1.R1040
Contig ID
                  LIB3109-047-Q1-K1-D2
5'-most EST
                   BLASTN
Method
                   g4519195
NCBI GI
                   35
BLAST score
                   6.0e-10
E value
                   43
Match length
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MQC12, complete sequence
                   3765
Seq. No.
                   2809 1.R1040
Contig ID
                   LIB3056-006-Q1-N1-A4
5'-most EST
                   BLASTX
Method
                   g3367524
NCBI GI
BLAST score
                   403
                   6.0e-39
E value
Match length
                   193
                   56
% identity
                   (AC004392) F8K4.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3766
                   2809 2.R1040
Contig ID
                   LIB3051-009-Q1-E1-A10
5'-most EST
Seq. No.
                   3767
                   2810 1.R1040
Contig ID
                   wvk700681381.h2
5'-most EST
                   3768
Seq. No.
                   2811 1.R1040
Contig ID
                   LIB3028-039-Q1-B1-G12
5'-most EST
                   BLASTX
Method
                   g1766046
NCBI GI
                   738
BLAST score
                   2.0e-78
E value
Match length
                   153
% identity
                   (U81993) NAD+ dependent isocitrate dehydrogenase subunit 1
NCBI Description
                   [Arabidopsis thaliana]
                   3769
Seq. No.
                   2812 1.R1040
Contig ID
                   LIB3039-034-Q1-E1-D5
5'-most EST
                   BLASTX
Method
                   g3004565
NCBI GI
                   333
BLAST score
                   1.0e-30
E value
                   123
Match length
% identity
                   (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   3770
Seq. No.
                   2822 1.R1040
Contig ID
```

LIB3028-039-Q1-B1-D8

E value

```
Method
                   BLASTX
NCBI GI
                   g2651310
BLAST score
                   193
                   6.0e-26
E value
Match length
                   152
                   39
% identity
                   (ACO02336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
                   3771
Seq. No.
                   2825 1.R1040
Contig ID
5'-most EST
                   kl1701207614.h1
Method
                   BLASTX
                   g2827637
NCBI GI
BLAST score
                   370
E value
                   3.0e-35
Match length
                   107
% identity
                   63
                   (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                   3772
Seq. No.
                   2828 1.R1040
Contig ID
5'-most EST
                   gsv7\overline{0}1054363.h1
Seq. No.
                   3773
                   2828 2.R1040
Contig ID
                   LIB3072-017-Q1-E1-C2
5'-most EST
Seq. No.
                   3774
                   2829 1.R1040
Contig ID
                   jC-gmst02400018f02a1
5'-most EST
Method
                   BLASTX
                   q2244876
NCBI GI
BLAST score
                   1168
                   1.0e-128
E value
Match length
                   286
                   74
% identity
                   (Z97338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3775
                   2831 1.R1040
Contig ID
5'-most EST
                   leu701152319.hl
                   BLASTX
Method
NCBI GI
                   g2642443
BLAST score
                   826
                   2.0e-88
E value
Match length
                   371
% identity
                   (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3776
                   2832 1.R1040
Contig ID
5'-most EST
                   fC-gmle7000742258f1
                   BLASTX
Method
NCBI GI
                   q1706822
BLAST score
                   365
```

1.0e-34

Method

BLASTN

```
Match length
                   98
% identity
                   65
NCBI Description
                   FLAVONOL SYNTHASE (FLS) >gi 421946 pir S33510 flavonol
                   synthase - garden petunia >gi_311658_emb_CAA80264_ (Z22543)
                   flavonol synthase [Petunia x hybrida]
Seq. No.
                   3777
                   2832 2.R1040
Contig ID
5'-most EST
                   LIB3028-039-Q1-B1-A6
                   BLASTX
Method
NCBI GI
                   g1706822
BLAST score
                   934
                   1.0e-101
E value
                   265
Match length
% identity
                   65
                   FLAVONOL SYNTHASE (FLS) >gi_421946_pir__S33510 flavonol
NCBI Description
                   synthase - garden petunia >gi_311658_emb_CAA80264_ (Z22543)
                   flavonol synthase [Petunia x hybrida]
                   3778
Seq. No.
                   2837 1.R1040
Contig ID
5'-most EST
                   asn7\overline{0}1134785.h2
                   BLASTX
Method
NCBI GI
                   g3892051
                   1126
BLAST score
E value
                   1.0e-123
Match length
                   251
% identity
                   (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                   [Arabidopsis thaliana]
                   3779
Seq. No.
                   2840 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy035c05b1
Method
                   BLASTX
NCBI GI
                   g2924792
BLAST score
                   880
E value
                   1.0e-94
Match length
                   221
% identity
                   (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
NCBI Description
                   3780
Seq. No.
                   2841 1.R1040
Contig ID
5'-most EST
                   zhf700958558.h1
Method
                   BLASTX
NCBI GI
                   q3150411
BLAST score
                   1011
E value
                   1.0e-110
Match length
                   384
                   55
% identity
NCBI Description (AC004165) hookless1-like protein [Arabidopsis thaliana]
Seq. No.
                   2842 1.R1040
Contig ID
                   zzp7\overline{0}0831646.h1
5'-most EST
```

```
NCBI GI
                   g3176097 ·
BLAST score
                   346
E value
                   0.0e+00
                   937
Match length
                   84
% identity
                  Medicago truncatula mRNA for annexin
NCBI Description
                   3782
Seq. No.
                   2842 2.R1040
Contig ID
5'-most EST
                   rlr700900274.hl
                   BLASTN
Method
NCBI GI
                   q3176097
BLAST score
                   120
                   9.0e-61
E value
Match length
                   308
% identity
                   85
                  Medicago truncatula mRNA for annexin
NCBI Description
                   3783
Seq. No.
                   2844 1.R1040
Contig ID
                   k117\overline{0}1206547.h1
5!-most EST
Method
                   BLASTN
NCBI GI
                   g1370165
BLAST score
                   558
                   0.0e+00
E value
Match length
                  877
                   92
% identity
                  L.japonicus mRNA for small GTP-binding protein, RAB1C
NCBI Description
                   3784
Seq. No.
                  2844 3.R1040
Contig ID
5'-most EST
                  hrw7\overline{0}1058664.h1
Method
                  BLASTN
NCBI GI
                   g1370165
BLAST score
                  157
                   6.0e-83
E value
Match length
                  296
% identity
                   95
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1C
                   3785
Seq. No.
                   2846 1.R1040
Contig ID
5'-most EST
                   trc700564010.hl
                  BLASTX
Method
NCBI GI
                   g3551954
BLAST score
                   584
E value
                   5.0e-60
Match length
                  266
                   43
% identity
                   (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
Seq. No.
                   3786
                   2847 1.R1040
Contig ID
5'-most EST
                  xpa700796473.h1
```

Seq. No.

Contig ID

```
Contig ID
                   2848 1.R1040
                   kmv7\overline{0}0743979.h1
5'-most EST
Method
                   BLASTX
                   q2244866
NCBI GI
                   912
BLAST score
                   2.0e-98
E value
                   249
Match length
                   68
% identity
                   (297337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3788
                   2849 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800031c11a1
Method
                   BLASTX
NCBI GI
                   g2660670
BLAST score
                   1056
                   1.0e-115
E value
                   282
Match length
                   73
% identity
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   3789
Seq. No.
Contig ID
                   2851 1.R1040
                   LIB3056-008-Q1-N1-A11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2464865
BLAST score
                   1848
                   0.0e + 00
E value
Match length
                   516
% identity
                   66
                   (Z99707) pectinesterase like protein [Arabidopsis thaliana]
NCBI Description
                   3790
Seq. No.
Contig ID
                   2851 2.R1040
5'-most EST
                   LIB3107-059-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2464865
BLAST score
                   372
                   2.0e-35
E value
Match length
                   104
                   64
% identity
                   (Z99707) pectinesterase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3791
                   2851 3.R1040
Contig ID
                   gsv7\overline{0}1051641.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2464865
BLAST score
                   274
E value
                   2.0e-24
Match length
                   66
                   73
% identity
NCBI Description
                   (299707) pectinesterase like protein [Arabidopsis thaliana]
Seq. No.
                   2851 4.R1040
```

```
5'-most EST
                  leu701147408.h1
Method
                  BLASTX
NCBI GI
                  g2464865
BLAST score
                  210
                  8.0e-17
E value
                  55
Match length
                  69
% identity
                  (Z99707) pectinesterase like protein [Arabidopsis thaliana]
NCBI Description
                  3793
Seq. No.
                  2852 1.R1040
Contig ID
5'-most EST
                  LIB3051-059-Q1-K2-F11
                  BLASTX
Method
                  g3132479
NCBI GI
BLAST score
                  2193
                  0.0e+00
E value
                  572
Match length
                  54
% identity
                  (AC003096) multidrug resistance-associated protein, AtMRP2
NCBI Description
                  [Arabidopsis thaliana]
                  3794
Seq. No.
Contig ID
                  2852 2.R1040
5'-most EST
                  jC-qmf102220104d08d1
Seq. No.
                  2855 1.R1040
Contig ID
5'-most EST
                  dpv701098968.h1
Method
                  BLASTX
NCBI GI
                  g3250695
BLAST score
                  541
E value
                  8.0e-55
                  309
Match length
% identity
                  64
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
                  3796
Seq. No.
                  2855 2.R1040
Contig ID
5'-most EST
                  g4260400
                  BLASTX
Method
                  g3250695
NCBI GI
BLAST score
                  163
                  5.0e-11
E value
Match length
                  70
% identity
                  (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                  2857 1.R1040
5'-most EST
                  LIB3050-020-Q1-K1-F6
Method
                  BLASTN
                  g3204124
NCBI GI
BLAST score
                  105
E value
                  1.0e-51
                  260
Match length
                  85
% identity
NCBI Description Cicer arietinum mRNA for putative Pi starvation-induced
```

NCBI Description

```
3798
Seq. No.
                   2857 2.R1040
Contig ID
                   LIB3028-038-Q1-B1-D9
5'-most EST
                   3799
Seq. No.
                   2858 1.R1040
Contig ID
                   LIB3106-033-Q1-K1-E2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2558512
BLAST score
                   159
                   2.0e-10
E value
                   91
Match length
% identity
                   41
                   (AJ002020) proton pump interactor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3800
                   2861_1.R1040
Contig ID
5'-most EST
                   LIB3170-057-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   q2827536
BLAST score
                   302
E value
                   2.0e-26
Match length
                   162
% identity
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]
                   3801
Seq. No.
                   2861 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810093a10d1
                   3802
Seq. No.
Contig ID
                   2861 3.R1040
5'-most EST
                   jC-gmle01810030f03a2
                   3803
Seq. No.
Contig ID
                   2861 4.R1040
                   LIB3028-038-Q1-B1-E5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2827536
BLAST score
                   184
E value
                   2.0e-13
Match length
                   45
% identity
                   (AL021633) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3804
                   2864 1.R1040
Contig ID
                   r1r7\overline{0}0896672.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4263787
                   883
BLAST score
                   4.0e-95
E value
Match length
                   301
% identity
                   65
```

protein

(AC006068) unknown protein [Arabidopsis thaliana]

```
3805
Seq. No.
Contig ID
                   2864 2.R1040
                   LIB3049-010-Q1-E1-G3
5'-most EST
                   BLASTX
Method
                   q4263787
NCBI GI
                   292
BLAST score
                   4.0e-26
E value
                   75
Match length
                   76
% identity
                   (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3806
Seq. No.
                   2864 3.R1040
Contig ID
                   bth700846001.h1
5'-most EST
                   3807
Seq. No.
Contig ID
                   2865 1.R1040
5'-most EST
                   leu7\overline{0}1154015.h1
Seq. No.
                   3808
Contig ID
                   2869 1.R1040
5'-most EST
                   LIB3049-045-Q1-E1-D6
                   BLASTX
Method
NCBI GI
                   g3158476
BLAST score
                   1195
E value
                   1.0e-131
                   285
Match length
                   80
% identity
                   (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
Seq. No.
Contig ID
                   2871 1.R1040
5'-most EST
                   jC-gmf102220069d08a1
Seq. No.
                   3810
                   2873 1.R1040
Contig ID
                   leu701149165.h1
5'-most EST
Method
                   BLASTX
                   q1435021
NCBI GI
BLAST score
                   662
                   5.0e-69
E value
Match length
                   284
                   50
% identity
                   (D26575) DNA-binding protein [Daucus carota]
NCBI Description
                   3811
Seq. No.
                   2873 2.R1040
Contig ID
5'-most EST
                   uC-gmropic040b12b1
                   3812
Seq. No.
                   2873 4.R1040
Contig ID
                   LIB3139-005-P1-N1-A11
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1161574
BLAST score
                   35
```

3.0e-10

E value

```
51
Match length
% identity
                   92
                   L.esculentum mRNA for homeobox protein
NCBI Description
Seq. No.
                   3813
                   2878 1.R1040
Contig ID
5'-most EST
                   zhf700965057.h1
Method
                   BLASTX
NCBI GI
                   q3641868
BLAST score
                   320
E value
                   3.0e-29
Match length
                   108
% identity
                   60
                   (AJ011012) hypothetical protein [Cicer arietinum]
NCBI Description
                   3814
Seq. No.
Contig ID
                   2879 1.R1040
5'-most EST
                   LIB3106-104-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   q1854386
BLAST score
                   980
E value
                   1.0e-106
. Match length.
                   269
% identity
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                   vinifera]
                   3815
Seq. No.
Contiq ID
                   2879 2.R1040
5'-most EST
                   LIB3139-013-P1-N1-B8
Method
                   BLASTN
NCBI GI
                   q1854385
BLAST score
                   56
E value
                   1.0e-22
Match length
                   144
                   85
% identity
                   Vitis vinifera mRNA for soluble NSF attachment protein
NCBI Description
                   homologue, complete cds
Seq. No.
                   3816
Contig ID
                   2885 1.R1040
                   LIB3139-093-P1-N1-F2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2623295
BLAST score
                   457
                   2.0e-75
E value
                   219
Match length
% identity
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   3817
Seq. No.
                   2886 1.R1040
Contig ID
5'-most EST
                   LIB3109-037-Q1-K1-E6
                   BLASTX
Method
NCBI GI
                   q280401
BLAST score
                   1497
```

1.0e-167

E value

```
389
Match length
% identity
                   76
                   H+-transporting ATPase (EC 3.6.1.35) - curled-leaved
NCBI Description
                   tobacco >gi 170206 (M27888) H+-translocating ATPase
                   [Nicotiana plumbaginifolia]
                   3818
Seq. No.
Contig ID
                   2887 1.R1040
5'-most EST
                   epx701106441.hl
                   BLASTX
Method
NCBI GI
                   g4150963
BLAST score
                   565
E value
                   5.0e-58
                   169
Match length
                   60
% identity
                   (Y18620) DsPTP1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3819
Contig ID
                   2887 2.R1040
5'-most EST
                   asn7\overline{0}1141361.h1
                   3820
Seq. No.
                   2888 1.R1040
Contig ID
5'-most EST
                   jsh7\overline{0}1070307.h1
                   BLASTX
Method
NCBI GI
                   g4510373
BLAST score
                   628
                   3.0e-65
E value
Match length
                   191
% identity
NCBI Description
                   (AC007017) putative harpin-induced protein [Arabidopsis
                   thaliana]
                   3821
Seq. No.
Contig ID
                   2888 2.R1040
5'-most EST
                   jex700906012.h1
Method
                   BLASTX
                   g4510373
NCBI GI
BLAST score
                   293
E value
                   2.0e-26
Match length
                   88
% identity
NCBI Description
                   (AC007017) putative harpin-induced protein [Arabidopsis
                   thaliana]
Seq. No.
                   3822
Contig ID
                   2892 1.R1040
5'-most EST
                   LIB3028-038-Q1-B1-A6
Seq. No.
                   3823
Contig ID
                   2895 1.R1040
5'-most EST
                   pmv700894421.h1
Method
                   BLASTX
NCBI GI
                   g3702332
BLAST score
                   306
                   5.0e-63
E value
Match length
                   248
```

```
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   2895 2.R1040
5'-most EST
                   LIB3040-061-Q1-E11-E4
                  BLASTX
Method
NCBI GI
                   q4454032
BLAST score
                   257
                   3.0e-22
E value
Match length
                  89
                   56
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3825
Contig ID
                   2897 1.R1040
5'-most EST
                  LIB3051-040-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q2921823
BLAST score
                   327
E value
                   6.0e-30
Match length
                   144
% identity
                   55
                  (AF046934) shoot-forming PKSF1 [Paulownia kawakamii]
NCBI Description
Seq. No.
                   3826
Contig ID
                   2897 2.R1040
5'-most EST
                  LIB3028-038-Q1-B1-B5
Method
                  BLASTX
NCBI GI
                  g2246376
BLAST score
                  171
E value
                   4.0e-12
Match length
                   62
% identity
                   68
                  (Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3827
                  2898 1.R1040
Contig ID
5'-most EST
                   jex700905254.h1
Method
                  BLASTX
NCBI GI
                  q2961384
BLAST score
                   383
E value
                  1.0e-36
Match length
                  140
                  54
% identity
                  (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  3828
Seq. No.
                  2898 2.R1040
Contig ID
                  LIB3028-038-Q1-B1-B6
5'-most EST
Method
                  BLASTX
                  g2961384
NCBI GI
BLAST score
                  238
                  7.0e-20
E value
                  86
Match length
```

% identity

```
(AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  3829
Contig ID
                  2899 1.R1040
                  LIB3170-002-Q1-K1-A5
5'-most EST
                  BLASTN
Method
NCBI GI
                  q498907
BLAST score
                  170
                  2.0e-90
E value
Match length
                  382
                  88
% identity
                  Pisum sativum ribosomal protein L34 homolog (RPL34) mRNA,
NCBI Description
                  complete cds
                  3830
Seq. No.
                  2900 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy002d01b1
Method
                  BLASTX
NCBI GI
                  q1177320
BLAST score
                  487
                  1.0e-48
E value
Match length
                  176
% identity
                  53
                  (X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza
NCBI Description
                  sativa]
Seq. No.
                  3831
Contig ID
                  2900 3.R1040
                  LIB3051-048-Q1-K1-D5
5'-most EST
                  BLASTX
Method
                  g2270994
NCBI GI
BLAST score
                  121
E value
                  1.0e-13
                  57
Match length
% identity
                  63
                  (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
Seq. No.
                  3832
                  2901 1.R1040
Contig ID
                  LIB3093-022-Q1-K1-G7
5'-most EST
                  3833
Seq. No.
                  2901 2.R1040
Contig ID
                  LIB3049-006-Q1-E1-E10
5'-most EST
                  BLASTX
Method
                  g114420
NCBI GI
                  2306
BLAST score
                  0.0e+00
E value
                  513
Match length
                  89
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_100882_pir__S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >qi 22173 emb CAA38140 (X54233) ATPase F1 subunit protein
                  [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
```

mays]

```
3834
Seq. No.
Contig ID
                   2901 4.R1040
                   asn7\overline{0}1142701.h1
5'-most EST
                   BLASTN
Method
                   q2204063
NCBI GI
                   67
BLAST score
                   2.0e-29
E value
                   131
Match length
                   92
% identity
                   Pisum sativum mRNA for F1 ATPase, complete cds
NCBI Description
                   3835
Seq. No.
                   2901 5.R1040
Contig ID
                   zsq701119274.h1
5'-most EST
Method
                   BLASTN
                   g2204063
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   70
Match length
                   87
% identity
                   Pisum sativum mRNA for F1 ATPase, complete cds
NCBI Description
                   3836
Seq. No.
                   2906 1.R1040
Contig ID
                   fua701042256.hl.
5'-most EST
                   BLASTX.
Method
NCBI GI
                   q1688074
                   251
BLAST score
                   4.0e-21
E value
                   193
Match length
% identity
                   (U46570) tetratricopeptide repeat protein [Homo sapiens]
NCBI Description
                   >gi_4507711_ref_NP_003305.1_pTTC1_ tetratricopeptide repeat
                   domain
                   3837
Seq. No.
                   2906 2.R1040
Contig ID
                   hrw701059481.hl
5'-most EST
                   3838
Seq. No.
                   2909 1.R1040
Contig ID
5'-most EST
                   epx701108917.h1
                   BLASTX
Method
                   q1172494
NCBI GI
BLAST score
                   161
                   2.0e-10
E value
                   113
Match length
                   30
% identity
                   PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE (PHS)
NCBI Description
                   (4-ALPHA-HYDROXY-TETRAHYDROPTERIN DEHYDRATASE)
                   (PHENYLALANINE HYDROXYLASE-STIMULATING PROTEIN) (PCD)
                   >gi 476742 (M88627) phenylalanine hydroxylase [Pseudomonas
                   aeruginosa]
                   3839
Seq. No.
```

2909 3.R1040

Contig ID

```
5'-most EST
                  LIB3028-037-Q1-B1-H11
                  3840
Seq. No.
                  2910 1.R1040
Contig ID
5'-most EST
                  k117\overline{0}1211587.h1
Method
                  BLASTX
NCBI GI
                  g3183568
                  634
BLAST score
                  1.0e-65
E value
Match length
                  340
% identity
                  41
                  HYPOTHETICAL 45.1 KD PROTEIN IN CDD-MGLC INTERGENIC REGION
NCBI Description
                  3841
Seq. No.
                  2910 2.R1040
Contig ID
5'-most EST
                  trc700563552.h1
Seq. No.
                  3842
                  2912 1.R1040
Contig ID
                  LIB3049-051-Q1-E1-D8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3367593
BLAST score
                  512
E value
                  8.0e-52
                  125
Match length
                  78
% identity
NCBI Description
                  (AL031135) putative protein [Arabidopsis thaliana]
                  >gi 3805841_emb_CAA21461_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                  3843
Seq. No.
Contig ID
                  2912 2.R1040
                  LIB3109-035-Q1-K1-A5
5'-most EST
Method
                  BLASTX
                  g3367593
NCBI GI
BLAST score
                  195
E value
                  2.0e-22
Match length
                  81
                  73
% identity
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3805841 emb CAA21461 (AL031986) putative protein
                   [Arabidopsis thaliana]
                  3844
Seq. No.
                  2913 1.R1040
Contig ID
                  LIB3028-037-Q1-B1-H6
5'-most EST
Method
                  BLASTX
NCBI GI
                  a98837
BLAST score
                  177
E value
                  7.0e-13
Match length
                  106
                  36
% identity
                  enantiomer-selective amidase - Rhodococcus sp >gi 152052
NCBI Description
                   (M74531) enantiomerase-selective amidase [Rhodococcus sp.]
                  3845
Seq. No.
Contig ID
                  2914 1.R1040
```

NCBI GI

```
5'-most EST
                   epx701105154.h1
                   BLASTX
Method
                   g1209756
NCBI GI
BLAST score
                   173
                   1.0e-32
E value
Match length
                   119
% identity
                   68
                   (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
                   3846
Seq. No.
Contig ID
                   2914 2.R1040
5'-most EST
                   pxt700946327.h1
Method
                   BLASTX
NCBI GI
                   g1209756
BLAST score
                   177
E value
                   1.0e-12
Match length
                   134
% identity
                   49
                  (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
                   3847
Seq. No.
                   2915 1.R1040
Contig ID
5'-most EST
                   LIB3055-013-Q1-N1-G8
Method
                   BLASTX
NCBI GI
                   g2924507
BLAST score
                   809
                   2.0e-86
E value
Match length
                   178
% identity
                   83
                   (AL022023) cyclophilin - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   3848
Seq. No.
                   2918 1.R1040
Contig ID
5'-most EST
                  LIB3039-013-Q1-E1-H3
                   3849
Seq. No.
Contig ID
                  2918 2.R1040
5'-most EST
                  LIB3049-051-Q1-E1-H3
                   3850
Seq. No.
                   2919 1.R1040
Contig ID
5'-most EST
                   gsv701048547.h1
Method
                  BLASTX
NCBI GI
                  g3122703
BLAST score
                  586
E value
                  2.0e-60
Match length
                  138
                  84
% identity
                  60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
NCBI Description
                  protein L23a [Fritillaria agrestis]
Seq. No.
                  3851
Contig ID
                  2920_1.R1040
5'-most EST
                  jC-gmle01810053a11a1
Method
                  BLASTX
```

g1173198

```
BLAST score
                  731
                  2.0e-77
E value
Match length
                  151
                  95
% identity
                  40S RIBOSOMAL PROTEIN S13 >gi 480095 pir S36423 ribosomal
NCBI Description
                  protein S13.e - garden pea >gi 396639 emb CAA80974
                  (Z25509) ribosomal protein S13 [Pisum sativum]
                  3852
Seq. No.
                  2920 2.R1040
Contig ID
                  LIB3138-033-Q1-N1-B6
5!-most EST
Method
                  BLASTX
                  g3450842
NCBI GI
BLAST score
                  415
                  2.0e-40
E value
Match length
                  212
% identity
                  .45
NCBI Description
                  (AF080436) mitogen activated protein kinase kinase [Oryza
                  3853
Seq. No.
                  2920 3.R1040
Contig ID
5'-most EST
                  LIB3094-002-Q1-K1-A7
Method
                  BLASTX
                  g1173198
NCBI GI
BLAST score
                  723
                  2.0e-76
E value
Match length
                  151
% identity
                  93
                  40S RIBOSOMAL PROTEIN S13 >gi 480095 pir S36423 ribosomal
NCBI Description
                  protein S13.e - garden pea >gi 396639 emb CAA80974
                  (Z25509) ribosomal protein S13 [Pisum sativum]
Seq. No.
                  3854
                  2920 5.R1040
Contig ID
5'-most EST
                  2DC-01-Q1-E1-E7
Method
                  BLASTN
NCBI GI
                  g3193311
BLAST score
                  43
                  7.0e-15
E value
Match length
                  71
                  90
% identity
                  Arabidopsis thaliana BAC F6N15
NCBI Description
                  3855
Seq. No.
                  2920 8.R1040
Contig ID
                  taw700657103.h1
5'-most EST
                  3856
Seq. No.
Contig ID
                  2923 1.R1040
5'-most EST
                  ncj700976784.hl
Method
                  BLASTX
NCBI GI
                  g3046700
BLAST score
                  337
E value
                  1.0e-31
Match length
                  91
                  70
% identity
```

```
NCBI Description
                  (AJ005261) cytidine deaminase [Arabidopsis thaliana]
                  >gi 3093276 emb CAA06671 (AJ005687) cytidine deaminase
                   [Arabidopsis thaliana] >gi 4191787 (AC005917) putative
                  cytidine deaminase [Arabidopsis thaliana]
                  3857
Seq. No.
Contig ID
                  2926 1.R1040
                  kl1701204486.h2
5'-most EST
                  3858
Seq. No.
                  2926 2.R1040
Contig ID
5'-most EST
                  LIB3028-037-Q1-B1-G1
Seq. No.
                  3859
Contig ID
                  2929 1.R1040
5'-most EST
                  jC-gmf102220063f08a1
Method
                  BLASTX
NCBI GI
                  q3775993
BLAST score
                  1425
E value
                  0.0e + 00
Match length
                  424
% identity
NCBI Description
                  (AJ010460) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  3860
Contig ID
                  2929 2.R1040
5'-most EST
                  uC-gmrominsoy122f10b1
Seq. No.
                  3861
Contig ID
                  2929 3.R1040
5'-most EST
                  LIB3051-090-Q1-K1-F5
                  3862
Seq. No.
Contig ID
                  2929 4.R1040
5'-most EST
                  LIB3051-084-Q1-K1-C9
                  3863
Seq. No.
Contig ID
                  2930 1.R1040
5'-most EST
                  LIB3040-061-Q1-E1-A11
Method
                  BLASTN
NCBI GI
                  g20761
BLAST score
                  58
E value
                  2.0e-23
Match length
                  225
% identity
                  84
                 Pea mRNA for H1 histone
NCBI Description
Seq. No.
                  3864
                  2930 2.R1040
Contig ID
5'-most EST
                  LIB3049-056-Q1-E1-G12
```

Contig ID 2930\_2.R1
5'-most EST LIB3049-0
Method BLASTN
NCBI GI g20761
BLAST score 64
E value 6.0e-27

Match length 232 % identity 87

A STATE OF THE PARTY OF THE PAR

NCBI Description Pea mRNA for H1 histone

```
3865
Seq. No.
                   2930 4.R1040
Contig ID
5'-most EST
                  LIB3170-030-Q1-K1-H6
                   3866
Seq. No.
                  2931 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400055b09a1
                  BLASTX
Method
                  q1800147
NCBI GI
BLAST score
                  280
                  8.0e-25
E value
Match length
                  91
% identity
                   68
                   (U83655) membrane associated protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3867
                  2935 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400026e07a1
                  3868
Seq. No.
                  2939 1.R1040
Contig ID
                  leu701149477.h1
5'-most EST
Method
                  BLASTX
                  g4432835
NCBI GI
BLAST score
                  210
                  1.0e-16
E value
                  80
Match length
% identity
                  47
NCBI Description
                  (AC006283) unknown protein [Arabidopsis thaliana]
                  3869
Seq. No.
                  2939 2.R1040
Contig ID
5'-most EST
                  LIB3106-094-01-K1-D11
Method
                  BLASTX
NCBI GI
                  g4432835
BLAST score
                  249
                  3.0e-21
E value
Match length
                  95
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3870
Contig ID
                  2943 1.R1040
5'-most EST
                  LIB3028-037-Q1-B1-E4
Method
                  BLASTX
NCBI GI
                  g461498
BLAST score
                  874
E value
                  4.0e-94
Match length
                  221
% identity
                  73
NCBI Description
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                  (ALAAT-2) >qi 320619 pir S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
```

alanine aminotransferase [Panicum miliaceum]

5'-most EST

```
Seq. No.
                   3871
                   2945 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy099g11b1
                   3872
Seq. No.
                   2946 1.R1040
Contig ID
                   LIB3109-005-Q1-K1-C3
5'-most EST
Method
                   BLASTX
                   g2832686
NCBI GI
BLAST score
                   214
                   4.0e-17
E value
Match length
                   69
% identity
                   65
                   (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3873
Contig ID
                   2947 1.R1040
5'-most EST
                   uC-gmrominsoy263h01b1
Method
                   BLASTX
NCBI GI
                  g4063746
BLAST score
                   700
E value
                   2.0e-73
Match length
                  506
% identity
                   33
                   (AC005851) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   3874
Seq. No.
Contig ID
                   2947 2.R1040
5'-most EST
                   uC-gmrominsoy048a04b1
                   3875
Seq. No.
Contig ID
                   2947 3.R1040
5'-most EST
                   uC-gmrominsoy165e07b1
Method
                  BLASTX
NCBI GI
                  g4455155
BLAST score
                  350
E value
                   4.0e-33
Match length
                   115
% identity
                   65
                   (AL022023) EF-1 alpha - like protein (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                   3876
Seq. No.
                  2948 1.R1040
Contig ID
5'-most EST
                  pmv700893325.h1
                  3877
Seq. No.
                  2948 2.R1040
Contig ID
5'-most EST
                  jC-gmle01810052g12a1
                  3878
Seq. No.
                  2950 1.R1040
Contig ID
5'-most EST
                   zhf700963838.h1
                  3879
Seq. No.
Contig ID
                  2950 2.R1040
```

jC-qmle01810033d04a2

```
3880
Seq. No.
                   2950 3.R1040
Contig ID
                   jC-gmst02400050f12d1
5'-most EST
                   3881
Seq. No.
                   2950 5.R1040
Contig ID
                   jex700904169.hl
5'-most EST
                   BLASTN
Method
                   g312300
NCBI GI
BLAST score
                   36
                   2.0e-10
E value
Match length
                   52
                   92
% identity
                  G.max cDNA for glutamine synthetase (3' region)
NCBI Description
                   3882
Seq. No.
                   2950 6.R1040
Contig ID
                   LIB3051-109-Q1-K1-A2
5'-most EST
                   3883
Seq. No.
                   2951 1.R1040
Contig ID
5'-most EST
                   LIB3056-011-Q1-N1-C6
                   BLASTX
Method
NCBI GI
                   g3252856
BLAST score
                   2200
                   0:0e+00
E value
Match length
                   501
% identity
                   85
                   (AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   3884
                   2951 2.R1040
Contig ID
                   fC-gmse700654980f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4510342
BLAST score
                   516
E value
                   2.0e-52
Match length
                   133
% identity
                   73
                   (AC006921) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   3885
Seq. No.
                   2951 3.R1040
Contig ID
                   LIB3051-091-Q1-K1-E6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4510342
BLAST score
                   355
E value
                   1.0e-33
Match length
                   104
% identity
                   66
                   (AC006921) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No.

```
2952 1.R1040
Contig ID
                   LIB3170-006-Q1-J1-A6
5'-most EST
                   3887
Seq. No.
                   2953_1.R1040
Contig ID
                   uC-gmrominsoy169g02b1
5'-most EST
                   BLASTX
Method
                   g1304599
NCBI GI
BLAST score
                   231
                   5.0e-19
E value
                   178
Match length
                   32
% identity
                  (U41315) ZNF127-Xp [Homo sapiens]
NCBI Description
                   3888
Seq. No.
Contig ID
                   2954 1.R1040
                   uC-gmropic016e12b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3367523
BLAST score
                   419
                   5.0e-41
E value
Match length
                   121
                   63
% identity
                   (AC004392) ESTs gb_AA728658 and gb_N95943 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   3889
Seq. No.
Contig ID
                   2956 1.R1040
5'-most EST
                   LIB3028-037-Q1-B1-C3
Method
                   BLASTX
                   q1504008
NCBI GI
BLAST score
                   479
                   2.0e-95
E value
Match length
                   427
% identity
                   48
                   (D86967) Containing ATP/GTP-binding site motif A(P-loop):
NCBI Description
                   Similar to C.elegans protein(P1:CEC47E128); Similar to Mouse
                   alpha-mannosidase(P1:B54407) [Homo sapiens]
Seq. No.
                   3890
Contig ID
                   2960 1.R1040
                   seb7\overline{0}0651089.h1
5'-most EST
                   BLASTX
Method
                   q2244806
NCBI GI
BLAST score
                   415
                   1.0e-40
E value
Match length
                   158
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   3891
Seq. No.
                   2961 1.R1040
Contig ID
                   LIB3170-015-Q1-K1-F2
5'-most EST
                   BLASTX
Method
                   q3334333
NCBI GI
BLAST score
                   447
```

6.0e-61

E value

```
Match length
                  155
% identity
                  74
                  SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi 2660798 (AF034832)
NCBI Description
                  cytosolic copper/zinc superoxide dismutase
                   [Mesembryanthemum crystallinum]
                  3892
Seq. No.
Contig ID
                  2963 1.R1040
                  jC-qmf102220093c12a1
5'-most EST
                  BLASTX
Method
                  q2979547
NCBI GI
BLAST score
                  343
E value
                  5.0e-36
Match length
                  202
                  41
% identity
NCBI Description
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
                   [Arabidopsis thaliana]
Seq. No.
                  3893
                  2964 1.R1040
Contig ID
                  LIB3030-004-Q1-B1-D6
5'-most EST
                  3894
Seq. No.
Contig ID
                  2965 1.R1040
                  hyd700726944.h1
5'-most EST
Method
                  BLASTX
                  g2827715
NCBI GI
BLAST score
                  1946
E value
                  0.0e+00
Match length
                  482
% identity
                  71
                   (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  3895
                  2965 2.R1040
Contig ID
                  fC-gmle700870555g2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2827715
BLAST score
                  551
                  2.0e-56
E value
Match length
                  120
                  88
% identity
                   (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  3896
Contig ID
                  2966 1.R1040
5'-most EST
                  q5677385
Method
                  BLASTX
NCBI GI
                  g2654226
BLAST score
                  626
E value
                  3.0e-65
Match length
                  155
% identity
                  79
NCBI Description
                  (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis
                  thaliana]
```

Seq. No.

3905

```
3897
Seq. No.
                   2968 1.R1040
Contig ID
5'-most EST
                   zhf700963533.h1
                   BLASTX
Method
                   g4415912
NCBI GI
                   199 ,
BLAST score
E value
                   4.0e-15
                   86
Match length
% identity
                   (AC006282) putative protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3898
                   2969 1.R1040
Contig ID
                   LIB3\overline{0}92-057-Q1-K1-B8
5'-most EST
Seq. No.
                   3899
Contig ID
                   2969 2.R1040
5'-most EST
                   LIB3092-057-Q1-K1-B10
                   3900
Seq. No.
                   2969 3.R1040
Contig ID
                   LIB3051-035-Q1-K1-E9
5'-most EST
                   3901
Seq. No.
                   2971 1.R1040
Contig ID
                   LIB3028-037-Q1-B1-A5
5'-most EST
Seq. No.
                   3902
Contig ID
                   2973_1.R1040
                   jC-gmst02400056g01a1
5'-most EST
                   BLASTX
Method
                   g3413511
NCBI GI
                   1302
BLAST score
E value
                   1.0e-144
                   272
Match length
                   89
% identity
                   (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
                   oleracea]
                   3903
Seq. No.
Contig ID
                   2973 2.R1040
                   hyd7\overline{0}0730316.h1
5'-most EST
                   BLASTX
Method
                   q4220528
NCBI GI
BLAST score
                   1486
                   1.0e-165
E value
                   380
Match length
                   76
% identity
                   (AL035356) glucose-6-phosphate isomerase (Arabidopsis
NCBI Description
                   thaliana]
                   3904
Seq. No.
Contig ID
                   2974 1.R1040
5'-most EST
                   epx701105525.h1
```

 $\mathcal{A}_{\sum I_{j}}^{+}$ 

```
2975 1.R1040
Contig ID
                  LIB3039-027-Q1-E1-B4
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2583134
BLAST score
                   258
                   3.0e-22
E value
Match length
                   124
% identity
                   (AC002387) putative proline-rich protein [Arabidopsis
NCBI Description
                   thaliana]
                   3906
Seq. No.
                   2979 1.R1040
Contig ID
                  pxt700944651.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3582340
BLAST score
                   350
                   4.0e-33
E value
Match length
                   92
% identity
                   (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   3907
Seq. No.
Contig ID
                   2982 1.R1040
5'-most EST
                   q4307500
                   BLASTN
Method
NCBI GI
                   q2351065
BLAST score
                   34
E value
                   2.0e-09
Match length
                   164
                   84
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHF15, complete sequence [Arabidopsis thaliana]
                   3908
Seq. No.
                   2983 1.R1040
Contig ID
                   zhf700962539.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2582799
BLAST score
                   115
                   1.0e-57
E value
Match length
                   353
                   88
% identity
                  M.sativa mRNA for protein phosphatase 2C
NCBI Description
                   3909
Seq. No.
                   2983 2.R1040
Contig ID
                   dpv701103002.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2582800
BLAST score
                   809
                   2.0e-86
E value
Match length
                   209
% identity
                   (Y11607) protein phosphatase 2C [Medicago sativa]
NCBI Description
```

Seq. No.

```
2983 3.R1040
Contig ID
5'-most EST
                   uC-gmropic020b03b1
                   BLASTN
Method
                   q2582799
NCBI GI
BLAST score
                   194
                   1.0e-105
E value
Match length
                   417
% identity
                   88
NCBI Description M.sativa mRNA for protein phosphatase 2C
                   3911
Seq. No.
Contig ID
                   2983 4.R1040
5'-most EST
                   LIB3139-095-P1-N1-G11
                   BLASTN
Method
NCBI GI
                   g2582799
BLAST score
                   113
E value
                   1.0e-56
                   266
Match length
% identity
                   88
NCBI Description M.sativa mRNA for protein phosphatase 2C
Seq. No.
Contig ID
                   2983 5.R1040
5'-most EST
                   wrg7\overline{0}0786175.h2
                   BLASTN
Method
NCBI GI
                   g2582799
BLAST score
                   43
                   6.0e-15
E value
Match length
                   67
% identity
                  M.sativa mRNA for protein phosphatase 2C
NCBI Description
Seq. No.
                   3913
Contig ID
                   2983 6.R1040
5'-most EST
                   uC-gmrominsoy208a02b1
Seq. No.
                   3914
Contig ID
                   2984 1.R1040
5'-most EST
                   LIB3065-004-Q1-N1-H9
Seq. No.
                   3915
Contig ID
                   2988 1.R1040
5'-most EST
                   LIB3028-036-Q1-B1-G8
Seq. No.
                   3916
Contig ID
                   2989 1.R1040
5'-most EST
                   LIB3170-042-Q1-J1-B12
Method
                   BLASTX
NCBI GI
                   g1279640
BLAST score
                   666
E value
                   6.0e-70
Match length
                   153
% identity
                   (X92204) NAM [Petunia x hybrida]
NCBI Description
Seq. No.
                   3917
```

2989\_2.R1040

Contig ID

```
5'-most EST
                   kl1701211357.hl
Method
                   BLASTX
                   q1944132
NCBI GI
BLAST score
                   558
                   3.0e-57
E value
                   162
Match length
% identity
                   68
                   (AB002560) CUC2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3918
                   2992 1.R1040
Contig ID
                   LIB3167-029-P1-K1-G2
5'-most EST
Method
                   BLASTX
                   g3282505
NCBI GI
BLAST score
                   196
                   8.0e-15
E value
Match length
                   139
% identity
                   (AF020786) polyphenol oxidase precursor [Prunus armeniaca]
NCBI Description
Seq. No.
                   3919
                   2993 1.R1040
Contig ID
                   jC-gmf102220139a10a1
5'-most EST
Method
                   BLASTX
                   g4314378
NCBI GI
                   451
BLAST_score
                   1.0e-44
E value
                   231
Match length
% identity
                   43
                   (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                   3920
Seq. No.
                   2998 1.R1040
Contig ID
                   vzy700752164.hl
5'-most EST
Method
                   BLASTX
                   g1531758
NCBI GI
BLAST score
                   751
                   6.0e-80
E value
Match length
                   182
% identity
                   (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   3921
Seq. No.
                   2999 1.R1040
Contig ID
                   pxt700944601.hl
5'-most EST
                   BLASTX
Method
                   g1518059
NCBI GI
                   287
BLAST score
E value
                   2.0e-25
                   121
Match length
% identity
                   (U65650) blue-copper binging protein III [Arabidopsis
NCBI Description
                   thaliana] >gi_3395770 (AF039404) uclacyanin 3 [Arabidopsis
                   thaliana]
```

Seq. No.

```
Contig ID
                   3000 1.R1040
                   ncj700979531.h2
5'-most EST
Method
                   BLASTX
                   q3290209
NCBI GI
BLAST score
                   282
                   5.0e-25
E value
Match length
                   98
% identity
                   58
                   (U78947) MADS-box protein 1 [Malus domestica]
NCBI Description
                   3923
Seq. No.
Contig ID
                   3001 1.R1040
5'-most EST
                   jex700906677.hl
Method
                   BLASTX
NCBI GI
                   q3.928543
BLAST score
                   1541
E value
                   1.0e-172
Match length
                   473
% identity
                   61
                   (AB016819) UDP-qlucose qlucosyltransferase [Arabidopsis
NCBI Description
                   thalianal
Seq. No.
                   3924
                   3002 1.R1040
Contig ID
                   jex700909978.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4263772
BLAST score
                   517
E value
                   2.0e-52
Match length
                   162
% identity
                   60
                   (AC006218) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3925
                   3005 1.R1040
Contig ID
5'-most EST
                   zzp7\overline{0}0834539.h1
Method
                   BLASTX
NCBI GI
                   g3746062
BLAST score
                   229
E value
                   1.0e-26
Match length
                   112
% identity
                   (AC005311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   3926
Seq. No.
                   3008 1.R1040
Contig ID
5'-most EST
                   leu701156067.h1
Seq. No.
                   3927
Contig ID
                   3013 1.R1040
5'-most EST
                   LIB3092-055-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   q3415115
BLAST score
                   489
E value
                   3.0e-49
                   139
Match length
```

% identity

NCBI GI

```
NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]
Seq. No.
                 3928
                  3021 1.R1040
Contig ID
                  LIB3106-113-Q1-K1-E8
5'-most EST
                  BLASTX
Method
                  g4510381
NCBI GI
BLAST score
                  343
E value
                  1.0e-31
Match length
                  123
% identity
                  61
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                  3929
Seq. No.
                  3022 1.R1040
Contig ID
5'-most EST
                  LIB3107-013-Q1-K1-G9
Method
                  BLASTX
                  g3913518
NCBI GI
BLAST score
                  563
E value
                  2.0e-65
                  196
Match length
                  70
% identity
                  3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
NCBI Description
                  (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                  (DPNPASE) >gi 1103921 (U40433) 3'(2'),5'-bisphosphate
                  nucleotidase [Arabidopsis thaliana]
                  3930
Seq. No.
Contig ID
                  3022 2.R1040
                  wrg700790744.hl
5'-most EST
                  BLASTX
Method
                  q3913518
NCBI GI
                  291
BLAST score
                  4.0e-26
E value
Match length
                  91
% identity
                  3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
NCBI Description
                  (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                  (DPNPASE) >gi 1103921 (U40433) 3'(2'),5'-bisphosphate
                  nucleotidase [Arabidopsis thaliana]
Seq. No.
                  3027 1.R1040
Contig ID
5'-most EST
                  bth700848545.h1
                  BLASTX
Method
NCBI GI
                  q3128218
BLAST score
                  617
                  5.0e-64
E value
Match length
                  204
% identity
                  (AC004077) putative end13 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3932
Contiq ID
                  3030 1.R1040
5'-most EST
                  LIB3167-013-P1-K1-D5
Method
                  BLASTX
```

q4325341

```
699
BLAST score
E value
                  8.0e-74
Match length
                  162
% identity
NCBI Description
                   (AF128393) similar to the Drosophila DES-1 protein
                   (GB:X94180) [Arabidopsis thaliana]
Seq. No.
                  3033 1.R1040
Contig ID
                  zhf700957311.h1
5'-most EST
                  BLASTX
Method
                  g2979552
NCBI GI
BLAST score
                  1169
                  1.0e-128
E value
                  302
Match length
                  74
% identity
NCBI Description
                  (AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.
                  3934
                  3034 1.R1040
Contig ID
                  leu7\overline{0}1149079.h1
5'-most EST
                  BLASTX
Method
                  g3128175
NCBI GI
BLAST score
                  176
                  2.0e-12
E value
                  99
Match length
                  38
% identity
                   (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                  3034 2.R1040
5'-most EST
                  leu701146445.hl
                  3936
Seq. No.
Contig ID
                  3034 3.R1040
5'-most EST
                  LIB3039-053-Q1-E1-F6
Seq. No.
                  3937
Contig ID
                  3035 1.R1040
5'-most EST
                  LIB3167-029-P1-K1-D3
Seq. No.
                  3938
Contig ID
                  3036 1.R1040
5'-most EST
                  jC-gmro02910038h11a1
Method
                  BLASTX
NCBI GI
                  q461899
BLAST score
                  585
E value
                  4.0e-60
Match length
                  169
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
                  PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase
                   (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi 405131
                   (L14845) cyclophilin [Arabidopsis thaliana] >gi 1322278
```

(U42724) cyclophilin [Arabidopsis thaliana]

```
3939
Seq. No.
Contig ID
                   3037 1.R1040
                   epx7\overline{0}1108588.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4006871
BLAST score
                   700
                   2.0e-73
E value
Match length
                   355
                   47
% identity
                   (Z99707) patatin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   3041 1.R1040
5'-most EST
                   jC-gmf102220140b12d1
                   BLASTX
Method
NCBI GI
                   q1483228
BLAST score
                   142
                   6.0e-11
E value
Match length
                   52
                   77
% identity
                   (X99653) MADS3 protein [Betula pendula]
NCBI Description
                   3941
Seq. No.
Contig ID
                   3041 2.R1040
5'-most EST
                   LIB3109-022-Q1-K1-G8
                   BLASTX
Method
NCBI GI
                   q1483228
BLAST score
                   237
E value
                  ~7.0e-20
Match length
                   78
                   63
% identity
                   (X99653) MADS3 protein [Betula pendula]
NCBI Description
Seq. No.
                   3942
                   3043 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220127a03a1
                   3943
Seq. No.
Contig ID
                   3047 1.R1040
5'-most EST
                   kl1701206723.h1
Method
                   BLASTX
                   g2501497
NCBI GI
BLAST score
                   466
                   1.0e-48
E value
Match length
                   258
                   40
% identity
                   FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID
NCBI Description
                   3-O-GLUCOSYLTRANSFERASE) (ANTHOCYANIN RHAMNOSYL
                   TRANSFERASE)
Seq. No.
                   3944
Contig ID
                   3048 1.R1040
5'-most EST
                   pcp700994804.hl
                   3945
Seq. No.
                   3048 2.R1040
Contig ID
                   vzy7\overline{0}0756210.h1
5'-most EST
```

```
Seq. No.
                   3946
Contig ID
                  3049 1.R1040
5'-most EST
                  q5057499
Method
                  BLASTX
NCBI GI
                  q2982469
BLAST score
                  255
                  8.0e-22
E value
Match length
                  58
                  84
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3947
Contig ID
                  3050 1.R1040
5'-most EST
                  g4293435
                  BLASTX
Method
                  g3980393
NCBI GI
BLAST score
                   397
E value
                  2.0e-38
Match length
                  130
                  56
% identity
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                  3948
Seq. No.
Contig ID
                  3051 1.R1040
5'-most EST
                  crh700855414.h1
Seq. No.
                  3949
Contig ID
                   3052 1.R1040
5'-most EST
                  uC-qmflminsoy065f12b1
Method
                  BLASTX
                  q4249382
NCBI GI
BLAST score
                  1169
                  0.0e+00
E value
Match length
                  533
                  75
% identity
                  (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb_AC004481. [Arabidopsis thaliana]
                   3950
Seq. No.
                  3052 2.R1040
Contig ID
5'-most EST
                  rry700808361.hl
Method
                  BLASTX
NCBI GI
                  g4249382
BLAST score
                  571
                  5.0e-59
E value
Match length
                  140
% identity
                  76
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  3951
Seq. No.
```

3052 3.R1040

 $pmv7\overline{0}0889172.h1$ 

Contig ID

5'-most EST

Match length

```
Method
                  BLASTX
                  g4249382
NCBI GI
BLAST score
                  656
                  1.0e-68
E value
                  175
Match length
% identity
                  77
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  3952
Seq. No.
Contig ID
                  3052 4.R1040
                  asn701131917.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4249382
BLAST score
                  302
E value
                  2.0e-27
Match length
                  72
% identity
                  75
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
Seq. No.
Contig ID
                   3052 5.R1040
5'-most EST
                  uC-gmropic089b11b1
                  BLASTX
Method
NCBI GI
                  q4249382
BLAST score
                  476
E value
                  8.0e-48
Match length
                  113
% identity
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb_AC004481. [Arabidopsis thaliana]
                   3954
Seq. No.
Contig ID
                   3052 6.R1040
5'-most EST
                  LIB3\overline{1}39-089-P1-N1-F8
Method
                  BLASTX
NCBI GI
                  q4249382
BLAST score
                  283
E value
                   2.0e-25
Match length
                  70
% identity
                  81
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
Seq. No.
                   3955
Contig ID
                   3052 8.R1040
                  bth700849121.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4519191
BLAST score
                  41
E value
                   7.0e-14
```

```
% identity
                   85
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K9P8, complete sequence
                   3956
Seq. No.
                   3052 9.R1040
Contig ID
5'-most EST
                   eep700869859.hl
                   BLASTX
Method
                   g4249382
NCBI GI
BLAST score
                  :321
                   7.0e-30
E value
Match length
                   71
                   87
% identity
NCBI Description
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
Seq. No.
                   3957
                   3052 10.R1040
Contig ID
5'-most EST
                   uC-qmropic104b03b1
                   3958
Seq. No.
Contig ID
                   3052 11.R1040
5'-most EST
                   sat701008109.hl
                   3959
Seq. No.
Contig ID
                   3054 1.R1040
5'-most EST
                  LIB3028-036-Q1-B1-A11
                   3960
Seq. No.
Contig ID
                   3056 1.R1040
5'-most EST
                  LIB3028-028-Q1-B1-D7
Method
                  BLASTX
NCBI GI
                   g1209756
BLAST score
                   694
E value
                   4.0e-73
Match length
                  162
% identity
NCBI Description
                   (U43629) integral membrane protein [Beta vulgaris]
                  3961
Seq. No.
                   3060 1.R1040
Contig ID
5'-most EST
                  LIB3092-020-Q1-K1-A9
                  3962
Seq. No.
                  3061 1.R1040
Contig ID
                  leu701148824.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4406531
BLAST score
                  346 .
E value
                  0.0e+00
Match length
                  977
% identity
                  85
                  Vigna radiata NADPH-protochlorophyllide oxidoreductase
NCBI Description
                  mRNA, chloroplast gene encoding chloroplast protein,
```

complete cds

BLAST score

```
Seq. No.
                   3963
Contig ID
                   3061 2.R1040
5'-most EST
                   q5057756
                  BLASTN
Method
NCBI GI
                   q4406531
BLAST score
                   160
E value
                   1.0e-84
Match length
                   429
                  87
% identity
                  Vigna radiata NADPH-protochlorophyllide oxidoreductase
NCBI Description
                  mRNA, chloroplast gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   3964
Contig ID
                   3061 3.R1040
5'-most EST
                  LIB3092-032-Q1-K1-B12
Method
                  BLASTN
NCBI GI
                  q4406531
BLAST score
                  156
                   4.0e-82
E value
Match length
                   431
% identity
                  93
NCBI Description
                  Vigna radiata NADPH-protochlorophyllide oxidoreductase
                  mRNA, chloroplast gene encoding chloroplast protein,
                  complete cds
                  3965
Seq. No.
Contig ID
                   3061 4.R1040
5'-most EST
                  q5752868
Method
                  BLASTN
NCBI GI
                  q4406531
BLAST score
                  206
E value
                  1.0e-112
Match length
                  322
                  91
% identity
                  Vigna radiata NADPH-protochlorophyllide oxidoreductase
NCBI Description
                  mRNA, chloroplast gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  3966
Contig ID
                  3064 1.R1040
5'-most EST
                  uC-gmrominsoy115f07b1
Method
                  BLASTX
NCBI GI
                  q4538947
BLAST score
                  440
                  4.0e-43
E value
Match length
                  133
% identity
NCBI Description
                  (AL049483) putative mitochondrial carrier protein
                   [Arabidopsis thaliana]
                  3967
Seq. No.
                  3066 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy188c08b1
Method
                  BLASTX
                  g3253095
NCBI GI
```

% identity

NCBI Description

```
E value
                   9.0e-95
                   307
Match length
% identity
                   57
                   (AB015643) Polygalacturonase-inhibiting protein [Citrus sp.
NCBI Description
                   cv. sannumphung]
Seq. No.
                   3968
                   3069 1.R1040
Contig ID
                   LIB3040-047-Q1-E1-C9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4467119
BLAST score
                   1303
                   1.0e-144
E value
Match length
                   261
% identity
                   90
NCBI Description
                   (AL035538) Histone deacetylase [Arabidopsis thaliana]
Seq. No.
                   3969
                   3070 1.R1040
Contiq ID
5'-most EST
                   LIB3106-095-Q1-K1-D9
Seq. No.
                   3970
Contig ID
                   3071 1.R1040
5'-most EST
                   LIB3051-094-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2275196
BLAST score
                   693
E value
                   5.0e-73
Match length
                   171
% identity
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   3971
                   3071 2.R1040
Contig ID
                   LIB3028-004-Q1-B1-E5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2275196
BLAST score
                   150
E value
                   4.0e-13
Match length
                   67
% identity
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   3972
Seq. No.
                   3072 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy026a05b1
Method
                   BLASTX
NCBI GI
                   g2244993
BLAST score
                   318
                   5.0e-29
E value
Match length
                   115
```

[Arabidopsis thaliana]

(Z97341) similarity to AMP-activated protein kinase beta

NCBI GI

```
3973
Seq. No.
Contig ID
                   3075 1.R1040
                   LIB3107-025-Q1-K1-E10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3033397
BLAST score
                   281
E value
                   5.0e-25
Match length
                   72
                   76
% identity
                   (AC004238) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3075 2.R1040
Contig ID
5'-most EST
                   LIB3106-096-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   q3033397
BLAST score
                   252
E value
                   1.0e-21
Match length
                   60
                   80
% identity
                   (AC004238) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3975
Contig ID
                   3076 1.R1040
5'-most EST
                   jC-gmro02910063c10a1
Seq. No.
                   3976
Contig ID
                   3076 2.R1040
5'-most EST
                   wvk700686545.h1
                   3977
Seq. No.
                   3077 1.R1040
Contig ID
                   leu7\overline{0}1154357.h1
5'-most EST
Method
                   BLASTN
                   g3290208
NCBI GI
BLAST score
                   126
                   3.0e-64
E value
                   230
Match length
% identity
                   89
NCBI Description
                   Malus domestica MADS-box protein 1 mRNA, complete cds
                   3978
Seq. No.
                   3077 2.R1040
Contiq ID
                   leu701151545.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3646333
                   91
BLAST score
                   2.0e-43
E value
Match length
                   189
% identity
                   90
                  Malus domestica mRNA for MADS box protein MdMADS8
NCBI Description
                   3979
Seq. No.
                   3078 1.R1040
Contig ID
                   LIB3028-035-Q1-B1-E11
5'-most EST
Method
                   BLASTX
```

g3068717

```
338
BLAST score
                   1.0e-31
E value
                   100
Match length
                   65
% identity
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   3980
Seq. No.
                   3079 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy114c11b1
                   3981
Seq. No.
Contig ID
                   3079 2.R1040
                   uC-gmropic090b10b1
5'-most EST
                   3982
Seq. No.
Contig ID
                   3081 1.R1040
5'-most EST
                   ncj700975617.hl
                   3983
Seq. No.
                   3081 2.R1040
Contig ID
5'-most EST
                   zsg701121309.h1
                   3984
Seq. No.
                   3081 3.R1040
Contig ID
5'-most EST
                   gsv7\overline{0}1044734.h1
Seq. No.
                   3985
Contig ID
                   3083 1.R1040
                   LIB3\overline{1}07-060-Q1-K1-F12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4539296
BLAST score
                   375
E value
                   6.0e-36
Match length
                   110
                   57
% identity
                   (AL049480) putative pathogenesis-related protein
NCBI Description
                   [Arabidopsis thaliana]
                   3986
Seq. No.
                   3085 1.R1040
Contig ID
5'-most EST
                   LIB3028-035-Q1-B1-E9
Seq. No.
                   3987
                   3085 2.R1040
Contig ID
                   zhf7\overline{0}0956091.h1
5'-most EST
                   3988
Seq. No.
Contig ID
                   3090 1.R1040
5'-most EST
                   jC-gmst02400030g12a1
Method
                   BLASTX
NCBI GI
                   g3785975 ·
BLAST score
                   254
E value
                   2.0e-21
Match length
                   248
```

(AC005560) hypothetical protein [Arabidopsis thaliana]

27

% identity

NCBI Description

```
Seq. No.
                  3989
Contig ID
                  3093 1.R1040
5'-most EST
                  pcp700995355.h1
Method
                  BLASTX
NCBI GI
                  q2500036
BLAST score
                  801
                  4.0e-87
E value
Match length
                  186
                  81
% identity
                  DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146)
NCBI Description
                  dihydroorotase [Arabidopsis thaliana]
                  >gi_3292818_emb_CAA19808_ (AL031018) dihydroorotase
                  [Arabidopsis thaliana]
                  3990
Seq. No.
Contig ID
                  3094 1.R1040
5'-most EST
                  qsv701045588.hl
                  BLASTN
Method
NCBI GI
                  q1041244
BLAST score
                  268
                  1.0e-149
E value
                  657
Match length
                  87
% identity
NCBI Description A.glutinosa mRNA for enolase
Seq. No.
Contig ID
                  3094 2.R1040
5'-most EST
                  vwf700674352.hl
Method
                  BLASTX
NCBI GI
                  q3023713
BLAST score
                  466
                  2.0e-55
E value
                  147
Match length
                  67
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
Seq. No.
                  3992
Contig ID
                  3094 3.R1040
                  q4293723
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1041244
BLAST score
                  142
E value
                  6.0e-74
Match length
                  375
                  87
% identity
NCBI Description
                  A.glutinosa mRNA for enolase
                  3993
Seq. No.
Contig ID
                  3094 6.R1040
5'-most EST
                  kmv700741338.h1
                  BLASTX
Method
NCBI GI
                  q3912997
BLAST score
                  147
                  2.0e-09
E value
Match length
                  37
```

% identity 81

NCBI Description FLORAL HOMEOTIC PROTEIN AGL15 >gi\_2129535\_pir\_\_S71200 AGL15 protein - Arabidopsis thaliana >gi\_790635 (U22528) AGL15 [Arabidopsis thaliana]

Seq. No. 3994

Contig ID 3094\_7.R1040 5'-most EST txt700734472.h1

Method BLASTN
NCBI GI g533473
BLAST score 36
E value 6.0e-11
Match length 68
% identity 88

NCBI Description Mesembryanthemum crystallinum 2-phospho-D-glycerate

hydrolase, enolase, mRNA, complete cds

Seq. No. 3995

Contig ID 3095 1.R1040 5'-most EST zzp700832658.h1

Seq. No. 399

Contig ID 3096 1.R1040

5'-most EST jC-gmf102220079b08d1

Seq. No. 3997

Contig ID 3096\_2.R1040

5'-most EST jC-gmf102220080b03d1

Seq. No. 3998

Contig ID 3099\_1.R1040 5'-most EST fua701043125.h1

Method BLASTX
NCBI GI g586765
BLAST score 175
E value 4.0e-12
Match length 79
% identity 48

NCBI Description HYPOTHETICAL 10.2 KD PROTEIN IN RPS1-NAD4L INTERGENIC

REGION (ORF 86A) >gi\_282786\_pir\_\_S25987 hypothetical protein 86a - liverwort (Marchantia polymorpha)

mitochondrion >gi 786215 (M68929) ORF86a [Marchantia

polymorpha]

Seq. No. 3999

Contig ID 3100\_1.R1040 5'-most EST leu701150468.h1

Seq. No. 4000

Contig ID 3100 2.R1040

5'-most EST LIB3139-113-P1-N1-B10

Seq. No. 4001

Contig ID 3100 3.R1040

5'-most EST LIB3049-012-Q1-E1-F7

Seq. No. 4002

```
Contig ID
                  3102 1.R1040
                  LIB3028-023-Q1-B1-E2
5'-most EST
Method
                  BLASTX
                  g2244964
NCBI GI
BLAST score
                  743
                  1.0e-78
E value
Match length
                  233
% identity
                  61
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  4003
Seq. No.
Contig ID
                  3104 1.R1040
                  LIB3093-030-Q1-K1-E2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4185141
BLAST score
                  1794
E value
                  0.0e+00
Match length
                  655
% identity
                  59
                  (AC005724) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  4004
                  3104 2.R1040
Contig ID
                  vzy700754865.hl
5'-most EST
Method
                  BLASTX
                  g4185141
NCBI GI
BLAST score
                  214
E value
                  5.0e-17
Match length
                  64
                  92
% identity
                  (AC005724) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  4005
Seq. No.
                  3104 5.R1040
Contig ID
                  epx701104351.hl
5'-most EST
                  BLASTN
Method
                  g1698547
NCBI GI
BLAST score
                  38
                  5.0e-12
E value
Match length
                  86
                  86
% identity
                  Nicotiana tabacum calmodulin-binding protein (TCB60) mRNA,
NCBI Description
                  complete cds
                  4006
Seq. No.
                  3107 1.R1040
Contig ID
                  2DC-01-Q1-B1-D7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g418399
BLAST score
                  257
E value
                  7.0e-22
                  110
Match length
                  51
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT)
NCBI Description
                  >gi 320705 pir S30826 hypothetical protein YEL051w - yeast
```

(Saccharomyces cerevisiae) >gi\_1042219\_bbs\_168845 vacuolar proton-translocating ATPase V1 subunit, V H(+) -ATPase V1 subunit=VMA8 product [Saccharomyces cerevisiae=baker's yeast, Peptide, 256 aa] >gi\_603628 (U18779) Vma8p: subunit D of vacuolar H-ATPase [Saccharomyces cerevisiae]

```
Seq. No.
                   4007
                   3107 2.R1040
Contig ID
                   2DC - \overline{0}1 - Q1 - E1 - D7
5'-most EST
                   4008
Seq. No.
Contig ID
                   3108 1.R1040
5'-most EST
                   uaw700663331.hl
                   BLASTX
Method
NCBI GI
                   q4567281
BLAST score
                   388
E value
                   3.0e-37
Match length
                   167
% identity
                   50
                   (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                   4009
Seq. No.
Contig ID
                   3110 1.R1040
5'-most EST
                   zhf700957271.h1
                   BLASTX
Method
NCBI GI
                   q3776005
BLAST score
                   1083
E value
                   0.0e+00
Match length
                   403
% identity
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   4010
Seq. No.
Contig ID
                   3110 4.R1040
5'-most EST
                   uC-gmropic062f10b1
                   4011
Seq. No.
                   3110 5.R1040
Contig ID
5'-most EST
                   zsg701125976.hl
Method
                   BLASTX
NCBI GI
                   q3776005
BLAST score
                   261
                   7.0e-23
E value
Match length
                   63
% identity
                   83
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   4012
Seq. No.
                   3112 1.R1040
Contig ID
5'-most EST
                  uxk700671938.h1
Method
                   BLASTX
                   q3549665
NCBI GI
BLAST score
                   263
                   1.0e-22
E value
                   206
Match length
% identity
                   (AL031394) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
                   4013
                   3113 1.R1040
Contig ID
5'-most EST
                  LIB3050-001-Q1-E1-C2
Method
                  BLASTX
NCBI GI
                  q3075391
BLAST score
                   1544
E value
                   1.0e-172
Match length
                  579
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4014
Contig ID
                   3113 2.R1040
5'-most EST
                   jC-gmle01810053a05d1
Seq. No.
                   4015
Contig ID
                   3113 3.R1040
5'-most EST
                  q4396396
Seq. No.
                   4016
Contig ID
                   3116 1.R1040
5'-most EST
                  q5677064
Method
                  BLASTX
NCBI GI
                  q2288999
BLAST score
                  221
E value
                   5.0e-18
Match length
                   44
% identity
                  86
                  (AC002335) electron transfer flavoprotein ubiquinone
NCBI Description
                  oxidoreductase isolog [Arabidopsis thaliana]
                   4017
Seq. No.
Contig ID
                   3116 2.R1040
                  dpv7\overline{0}1100529.h1
5'-most EST
                   4018
Seq. No.
                  3116 4.R1040
Contig ID
5'-most EST
                  LIB3028-035-Q1-B1-C11
Seq. No.
                   4019
                   3117 1.R1040
Contig ID
                   uC-gmflminsoy091d09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3063392
BLAST score
                   1625
                  0.0e+00
E value
Match length
                   437
                   75
% identity
                  (AB012932) Ca2+/H+ exchanger [Vigna radiata]
NCBI Description
                   4020
Seq. No.
                  3117 2.R1040
Contig ID
                   jC-gmle01810093c11a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q438216
```

511 ·

BLAST score

E value 0.0e + 00997 Match length % identity 88 P.sativum mRNA for T subunit of glycine decarboxylase NCBI Description multi-enzyme complex Seq. No. 4021 3117 3.R1040 Contig ID LIB3030-009-Q1-B1-C9 5'-most EST Method BLASTN g3063391 NCBI GI BLAST score 228 1.0e-125 E value 754 Match length % identity 88 Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds NCBI Description Seq. No. 3117 4.R1040 Contig ID 5'-most EST epx701110201.hl Method BLASTN NCBI GI g438216 BLAST score 108 E value 1.0e-53 Match length 251 % identity P.sativum mRNA for T subunit of glycine decarboxylase NCBI Description multi-enzyme complex Seq. No. 4023 3117 5.R1040 Contig ID jC-qmle01810017f08a2 5'-most EST Method BLASTN NCBI GI q3063391 BLAST score 69 2.0e-30 E value 269 . Match length % identity 81 Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds NCBI Description 4024 Seq. No. 3117 6.R1040 Contig ID hrw701063289.hl 5'-most EST BLASTN Method q438253 NCBI GI BLAST score 103 9.0e-51 E value Match length 263

85 % identity

S.tuberosum mRNA for T subunit of glycine decarboxylase NCBI Description

multi-enzyme complex

4025 Seq. No.

3117 7.R1040 Contig ID ssr700560831.hl 5'-most EST

Method BLASTN q3063391 NCBI GI

. .

```
BLAST score
                  157
E value
                  8.0e-83
Match length
                  333
                  93
% identity
NCBI Description Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds
                  4026
Seq. No.
                  3117_8.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy059h12b1
Method
                  BLASTN.
                  g3063391
NCBI GI
BLAST score
                  296
E value
                  1.0e-165
Match length
                  551
                  92
% identity
NCBI Description
                  Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds
                  4027
Seq. No.
                  3117 14.R1040
Contig ID
5'-most EST
                  fde700875255.hl
Method
                  BLASTN
NCBI GI
                  g3063391
BLAST score
                  80
                  4.0e-37
E value
Match length
                  152
                  93
% identity
NCBI Description
                 Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds
                  4028
Seq. No.
                  3117 15.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy075b09b1
Method
                  BLASTN
                  g3063391
NCBI GI
BLAST score
                  107
E value
                  5.0e-53
                  330
Match length
% identity
                  83
NCBI Description
                  Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds
                  4029
Seq. No.
Contig ID
                  3117 17.R1040
5'-most EST
                  uC-gmflminsoy082b03b1
Method
                  BLASTN
                  g3063391
NCBI GI
BLAST score
                  32
E value
                  1.0e-08
Match length
                  52
% identity
NCBI Description
                  Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds
                  4030
Seq. No.
Contig ID
                  3119 1.R1040
5'-most EST
                  LIB3028-035-Q1-B1-A9
                  4031
Seq. No.
```

3119 2.R1040

LIB3106-104-Q1-K1-E2

Contig ID

5'-most EST

Contig ID

5'-most EST

```
Seq. No.
                      4032
Contig ID
                      3119 3.R1040
 5'-most EST
                      jex700908254.h1
Method
                     BLASTX
NCBI GI
                     q1077162
BLAST score
                     153
E value
                     7.0e-10
Match length
                     111
% identity
                     probable membrane protein YDL015c - yeast (Saccharomyces
cerevisiae) >gi_683682_emb_CAA88344_ (Z48432) homolog of
NCBI Description
                     rat synaptic glycoprotein SC2 (S45663) [Saccharomyces
                     cerevisiae] >gi_1430981_emb CAA98573 (Z74063) ORF YDL015c
                     [Saccharomyces cerevisiae]
Seq. No.
                     4033
Contig ID
                     3119 7.R1040
5'-most EST
                     dpv701099354.h1
Seq. No.
                     4034
Contig ID
                     3121 1.R1040
5'-most EST
                     fde700871532.hl
Seq. No.
                     4035
Contig ID
                     3126 1.R1040
5'-most EST
                     LIB3139-034-P1-N1-A11
Method
                     BLASTX
NCBI GI
                     g1729980
BLAST score
                     1027
E value
                     1.0e-112
Match length
                     223
% identity
NCBI Description
                     THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175
                     thaumatin-like protein - Arabidopsis thaliana >gi_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana]
                     >gi_1094863_prf__2106421A thaumatin-like protein
                     [Arabidopsis thaliana]
Seq. No.
                     4036
Contig ID
                     3126_2.R1040
                     LIB3028-035-Q1-B1-A1
5'-most EST
Method
                     BLASTX
NCBI GI
                     g1729980
BLAST score
                     367
E value
                     8.0e-35
Match length
                     73
% identity
                     THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana >gi_536825
NCBI Description
                     (L34693) thaumatin-like protein [Arabidopsis thaliana]
                     >gi_1094863_prf__2106421A thaumatin-like protein
                     [Arabidopsis thaliana]
Seq. No.
                     4037
```

3127 1.R1040

uC-gmflminsoy018e04b1

```
BLASTX
Method
NCBI GI
                  a4371293
BLAST score
                  150
E value
                  3.0e-09
Match length
                  280
                  24
% identity
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  4038
                  3128 1.R1040
Contig ID
5'-most EST
                  LIB3093-038-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q2827709
BLAST score
                  479
E value
                  5.0e-48
Match length
                  150
% identity
                  61
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  4039
                  3130 1.R1040
Contig ID
5'-most EST
                  LIB3028-035-Q1-B1-A2
Seq. No.
                  4040
                  3132 1.R1040
Contig ID
5'-most EST
                  crh700850157.hl
Seq. No.
                  4041
                  3132 2.R1040
Contig ID
5'-most EST
                  ncj700982157.h1
Method
                  BLASTX
NCBI GI
                  q4220481
BLAST score
                  141
E value
                  9.0e-09
Match length
                  66
% identity
                  53
NCBI Description
                 (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  4042
                  3136 1.R1040
Contig ID
5'-most EST
                  leu701146141.hl
Seq. No.
                  4043
                  3136 2.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy022g09b1
Seq. No.
                  4044
                  3137 1.R1040
Contiq ID
5'-most EST
                  LIB3109-001-Q1-K4-C2
Method
                  BLASTX
NCBI GI
                  q2245378
BLAST score
                  1277
E value
                  1.0e-141
Match length
                  353
% identity
                  74
```

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

E value

```
4045
Seq. No.
                   3137 2.R1040
Contig ID
                   xpa700794082.h1
5'-most EST
Method
                   BLASTX
                   g2245378
NCBI GI
                   873
BLAST score
                   4.0e-94
E value
                   183
Match length
% identity
                   86
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
                   4046
Seq. No.
                   3137 3.R1040
Contig ID
                   kl1701207433.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245378
                   389
BLAST score
                   1.0e-37
E value
Match length
                   93
                   77
% identity
NCBI Description
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
                   4047
Seq. No.
Contig ID
                   3138_1.R1040
                   jC-gmro02910037g07a1
5'-most EST
Method
                   BLASTX
                   q2739046
NCBI GI
BLAST score
                   127
                   1.0e-14
E value
                   190
Match length
% identity
                   34
                   (AF024652) polyphosphoinositide binding protein Ssh2p
NCBI Description
                   [Glycine max]
                   4048
Seq. No.
Contig ID
                   3138 2.R1040
5'-most EST
                   bth700844103.h1
                   4049
Seq. No.
                   3138 3.R1040
Contig ID
5'-most EST
                   vwf700675341.hl
Method
                   BLASTX
NCBI GI
                   q3687237
BLAST score
                   655
E value
                   1.0e-68
Match length
                   167
% identity
                   71
NCBI Description
                   (AC005169) putative Cys3His zinc-finger protein
                   [Arabidopsis thaliana]
                   4050
Seq. No.
Contig ID
                   3138 4.R1040
5'-most EST
                   LIB3028-034-Q1-B1-G10
Method
                   BLASTX
NCBI GI
                   g1710858
BLAST score
                   215
```

1.0e-16

Method

NCBI GI

BLASTX

q4220481

```
208
Match length
                   28
% identity
                  PUTATIVE SEC14 CYTOSOLIC FACTOR
NCBI Description
                   (PHOSPHATIDYLINOSITOL/PHOSPHATIDYL-CHOLINE TRANSFER
                   PROTEIN) (PI/PC TP) >gi 1177668 emb CAA93167 (Z69086)
                  unknown [Schizosaccharomyces pombe]
Seq. No.
                   4051
                  3145 1.R1040
Contig ID
                  LIB3028-034-Q1-B1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4490738
BLAST score
                  144
E value
                   6.0e-09
Match length
                  127
                  36
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4052
Contig ID
                  3146 1.R1040
5'-most EST
                  sat701008976.hl
Method
                  BLASTX
NCBI GI
                  g3033375
BLAST score
                  395
E value
                  3.0e-38
Match length
                  142
% identity
                  58
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  4053
                  3147 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220077g05a1
Method
                  BLASTX
NCBI GI
                  q3435096
BLAST score
                  259
E value
                  2.0e-22
Match length
                  75
% identity
                  67
                  (AF033587) SRZ-80 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  3147 2.R1040
Contig ID
5'-most EST
                  LIB3106-026-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2582643
BLAST score
                  408
                  6.0e-40
E value
Match length
                  108
% identity
                  73
                  (AJ002377) RSZp21 protein [Arabidopsis thaliana]
NCBI Description
                  4055
Seq. No.
Contig ID
                  3150 1.R1040
5'-most EST
                  seb700651221.hl
```

NCBI Description

```
211
BLAST score
                   6.0e-17
E value
Match length
                   79
                   53
% identity
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   4056
Seq. No.
                   3154 1.R1040
Contig ID
5'-most EST
                   LIB3028-034-Q1-B1-E3
                   4057
Seq. No.
Contig ID
                   3155_1.R1040
                   uC-gmflminsoy042b11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q886130
BLAST score
                   915
E value
                   9.0e-99
Match length
                   282
                   61
% identity
NCBI Description
                   (U28148) putative pectinesterase [Medicago sativa]
                   4058
Seq. No.
                   3156_1.R1040
Contig ID
5'-most EST
                   LIB3\overline{1}06-089-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3759184
BLAST score
                   886
E value
                   2.0e-95
Match length
                   275
% identity
                   61
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
                   4059
Seq. No.
                   3156_2.R1040
Contig ID
5'-most EST
                   dpv7\overline{0}1100326.h1
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   212
                   7.0e-17
E value
Match length
                   101
                   50
% identity
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
                   4060
Seq. No.
                   3156 3.R1040
Contig ID
5'-most EST
                   gsv701048028.hl
Seq. No.
                   4061
Contig ID
                   3158 1.R1040
5'-most EST
                   LIB3051-075-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   q1542941
BLAST score
                   1321
                   1.0e-173
E value
Match length
                   396
% identity
```

(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

```
4062
Seq. No.
                  3158 2.R1040
Contig ID
                  LIB3109-048-Q1-K1-C1
5'-most EST
                  BLASTX
Method
                  q1542941
NCBI GI
BLAST score
                  444
                  5.0e-44
E value
                  118
Match length
                  79
% identity
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
                   4063
Seq. No.
                   3163 1.R1040
Contig ID
                   sat701006382.hl
5'-most EST
                   4064
Seq. No.
                   3164 1.R1040
Contig ID
                   uC-gmrominsoy238d12b1
5'-most EST
                   BLASTX
Method
                   q2191145
NCBI GI
                   442
BLAST score
                   2.0e-43
E value
Match length
                   266
                   43
% identity
                   (AF007269) A_IG002N01.4 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   3165 1.R1040
                   LIB3028-034-Q1-B1-F5
5'-most EST
                   BLASTX
Method
                   q2244765
NCBI GI
                   275
BLAST score
                   3.0e-24
E value
                   72
Match length
% identity
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4066
Contig ID
                   3166 1.R1040
                   LIB3106-005-Q1-K1-D4
5'-most EST
Method
                   BLASTX
                   q584825
NCBI GI
BLAST score
                   727
                   1.0e-76
E value
Match length
                   147
                   88
% identity
                   B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                   >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                   carota]
                   4067
Seq. No.
                   3166 2.R1040
Contig ID
                   kl1701203510.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g584825
```

July .

750

BLAST score

Contig ID

```
3.0e-79
E value
Match length
                   149
                   92
% identity
                  B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
NCBI Description
                   >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus
                   carota]
                   4068
Seq. No.
                   3166_3.R1040
Contig ID
5'-most EST
                   jC-gmro02910054h09d1
                   4069
Seq. No.
Contig ID
                   3166 4.R1040
5'-most EST
                  LIB3092-034-Q1-K1-G1
Method
                   BLASTX
                   g584825
NCBI GI
BLAST score
                   196
E value
                   9.0e-15
Match length
                  75
                   81
% identity
NCBI Description
                  B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
                  >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                  carota]
                   4070
Seq. No.
                   3166 5.R1040
Contig ID
5'-most EST
                  ncj7\overline{0}0980819.h1
                   4071
Seq. No.
                   3166 6.R1040
Contig ID
5'-most EST
                   jC-gmro02910075c03d1
                   4072
Seq. No.
                   3167_1.R1040
Contig ID
5'-most EST
                   fC-gmst700888545a4
Method
                  BLASTN
                  g440592
NCBI GI
BLAST score
                   513
                   0.0e+00
E value
                  785
Match length
                  82
% identity
NCBI Description
                  V.faba mRNA (VfAGPC) for ADP-glucose pyrophosphorylase
                   4073
Seq. No.
Contig ID
                   3168 1.R1040
5'-most EST
                  ncj700981229.hl
Method
                  BLASTN
NCBI GI
                  g2565339
BLAST score
                  133
                  3.0e-68
E value
Match length
                   460
% identity
NCBI Description
                  Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
                  cds
                  4074
Seq. No.
```

3168\_2.R1040

```
uC-gmronoir060h06b1
5'-most EST
Method
                   BLASTN
                   g2565339
NCBI GI
                   237
BLAST score
                   1.0e-130
E value
Match length
                   457
                   88
% identity
                  Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
NCBI Description
                   4075
Seq. No.
                   3168 3.R1040
Contig ID
                  LIB3039-011-Q1-E1-G8
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2565339
BLAST score
                  228
E value
                  1.0e-125
Match length
                   452
                  88
% identity
                  Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
NCBI Description
                  4076
Seq. No.
                  3168 4.R1040
Contig ID
                  LIB3051-098-Q1-K1-A3
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2565339
                                                  7-1
BLAST score
                  161
                  3.0e-85
E value
Match length
                  313
                  88
% identity
                  Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
NCBI Description
                  4077
Seq. No.
                  3168 5.R1040
Contig ID
5'-most EST
                  LIB3170-002-Q1-K1-G2
Method
                  BLASTN
NCBI GI
                  g2565339
BLAST score
                  163
                  3.0e-86
E value
                  399
Match length
                  85
% identity
                  Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
NCBI Description
                  4078
Seq. No.
Contig ID
                  3168 8.R1040
5'-most EST
                  LIB3T67-002-Q1-K1-H3
                  4079
Seq. No.
                  3169 1.R1040
Contig ID
5'-most EST
                  uC-gmropic0001a09b1
                  BLASTX
Method
                  g2852640
NCBI GI
BLAST score
                  355
E value
                  4.0e-33
```

Match length

```
Match length
                   188
% identity
                   40
NCBI Description
                   (AF007157) unknown [Homo sapiens]
                   4080
Seq. No.
Contig ID
                   3171 1.R1040
5'-most EST
                   ncj7\overline{0}0980010.h1
                   4081
Seq. No.
Contig ID
                   3176 1.R1040
5'-most EST
                   LIB3106-051-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3450889
BLAST score
                   1510
                   1.0e-168
E value
Match length
                   408
                   76
% identity
                   (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
                   4082
Seq. No.
Contig ID
                   3176 2.R1040
5'-most EST
                   LIB3040-023-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   g3450889
BLAST score
                   314
                   9.0e-29
E value
Match length
                   94
                   70
% identity
                   (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
                   4083
Seq. No.
                   3179 1.R1040
Contig ID
                   fua701042962.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2580582
BLAST score
                   1109
E value
                   1.0e-121
Match length
                   353
                   58
% identity
                   (AF000975) 7-0-methyltransferase [Medicago sativa]
NCBI Description
                   4084
Seq. No.
                   3180 1.R1040
Contig ID
5'-most EST
                   LIB3028-034-Q1-B1-D7
                   4085
Seq. No.
Contig ID
                   3182_1.R1040
5'-most EST
                   jC-gmf102220126f08a1
                   4086
Seq. No.
                   3188 1.R1040
Contig ID
5'-most EST
                   rca701002090.h1
Method
                   BLASTX
NCBI GI
                   q2118974
BLAST score
                   230
E value
                   1.0e-18
```

BLAST score

```
70
 % identity
                   histone H1.41 - garden pea >gi_556345 (L34578) histone H1
NCBI Description
                    [Pisum sativum]
                   4087
Seq. No.
                   3188 2.R1040
Contig ID
                   LIB3170-017-Q1-K1-A4
 5'-most EST
Method
                   BLASTN
NCBI GI
                   q3204126
BLAST score
                   48
E value
                   1.0e-17
Match length
                   226
% identity
                   85
                   Cicer arietinum mRNA for histone H1
NCBI Description
                   4088
Seq. No.
                   3188 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy243f12b1
Method
                   BLASTN
NCBI GI
                   g3204126
                   39
BLAST score
E value
                   1.0e-12
Match length
                   87
                   86
% identity
NCBI Description
                   Cicer arietinum mRNA for histone H1
                   4089
Seq. No.
                   3189_1.R1040
Contig ID
                   uC-gmrominsoy200g09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4510349
                   227
BLAST score
                   1.0e-18
E value
                   89
Match length
% identity
                   60
NCBI Description
                    (AC006921) putative bZIP transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                    4090
                   3189 2.R1040
Contig ID
5'-most EST
                   ssr700554626.hl
Method
                   BLASTX
NCBI GI
                   g542200
BLAST score
                   552
E value
                   2.0e-56
Match length
                   196
% identity
                   57
NCBI Description
                   hypothetical protein - garden asparagus
                   >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                   officinalis]
Seq. No.
                   4091
                   3189 3.R1040
Contig ID
5'-most EST
                   LIB3109-015-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g629733
```

Contig ID

```
E value
                  0.0e+00
Match length
                  461
                  81
% identity
                  sulfate adenylyltransferase (EC 2.7.7.4) met3-2 - potato
NCBI Description
                  >gi_2130000_pir__S67498 sulfate adenylyltransferase (EC
                  2.7.7.4) (clone StMet3-2) - potato >gi_479090_emb_CAA55655_
                   (X79053) sulfate adenylyltransferase [Solanum tuberosum]
                  4092
Seq. No.
Contig ID
                  3189 4.R1040
                  zhf700954358.h1
5'-most EST
                  BLASTN
Method
                  g170216
NCBI GI
BLAST score
                  185
                  1.0e-99
E value
                  381
Match length
                  87
% identity
                  Nicotiana sylvestris (clone 6PCEP52-7) ubiquitin fusion
NCBI Description
                  protein (UbiCEP52-7) mRNA, complete cds
                  4093
Seq. No.
Contig ID
                  3189 5.R1040
5'-most EST
                  zzp700831422.h1
                  BLASTX
Method
NCBI GI
                  g542200
BLAST score
                  616
                  4.0e-64
E value
Match length
                  164
% identity
                  69
                  hypothetical protein - garden asparagus
NCBI Description
                  >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
                  4094
Seq. No.
Contig ID
                  3189 6.R1040
5'-most EST
                  LIB3072-055-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q3158376
BLAST score
                  404
                  3.0e-39
E value
Match length
                  118
% identity
                  66
NCBI Description
                  (AF035385) unknown [Arabidopsis thaliana]
                  4095
Seq. No.
Contig ID
                  3189_7.R1040
5'-most EST
                  jC-gmst02400031b07d1
Method
                  BLASTX
NCBI GI
                  g4033365
BLAST score
                  335
E value
                  5.0e-31
Match length
                  71
                  83
% identity
                  (AJ223499) ATP sulfurylase [Brassica juncea]
NCBI Description
                  4096
Seq. No.
```

3189 13.R1040

BLAST score

```
5'-most EST
                  sat701004906.h1
                   4097
Seq. No.
Contig ID
                   3191 1.R1040
                  jC-gmle01810087a10d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2245092
BLAST score
                  195
E value
                   6.0e-15
Match length
                  136
% identity
                   34
NCBI Description
                   (Z97343) unnamed protein product [Arabidopsis thaliana]
                  4098
Seq. No.
Contig ID
                   3193 1.R1040
5'-most EST
                  LIB3053-003-Q1-N1-B6
                  4099
Seq. No.
                  3196 1.R1040
Contig ID
5'-most EST
                  LIB3028-034-Q1-B1-C10
Method
                  BLASTX
NCBI GI
                  g1123105
BLAST score
                  142
E value
                  8.0e-09
Match length
                  111
% identity
                  33
                  (U42438) similar to S. cerevisiae longevity-assurance
NCBI Description
                  protein 1 (SP:P38703) [Caenorhabditis elegans]
                  4100
Seq. No.
Contig ID
                  3198 1.R1040
5'-most EST
                  LIB3040-009-Q1-E1-E5
Method
                  BLASTN
NCBI GI
                  g499692
BLAST score
                  148
E value
                  4.0e-77
Match length
                  343
                  87
% identity
                  Vicia faba cyclophilin mRNA, complete cds
NCBI Description
                  4101
Seq. No.
Contig ID
                  3200 1.R1040
5'-most EST
                  LIB3028-033-Q1-B1-F12
Method
                  BLASTX
NCBI GI
                  g2642157
BLAST score
                  1285
E value
                  1.0e-142
Match length
                  286
% identity
NCBI Description
                  (AC003000) ankyrin-like protein [Arabidopsis thaliana]
                  4102
Seq. No.
                  3201 1.R1040
Contig ID
                  fua701042634.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2498892
```

Seq. No.

```
E value
                   4.0e-87
Match length
                   303
% identity
                   23
NCBI Description
                   SEC13-RELATED PROTEIN
                   4103
Seq. No.
                   3201 2.R1040
Contig ID
5'-most EST
                   zzp700833353.hl
Method
                   BLASTX
NCBI GI
                   q3150415
BLAST score
                   466
E value
                   1.0e-46
                   104
Match length
% identity
                   29
NCBI Description
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
                   >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
Seq. No.
                   4104
                   3201 3.R1040
Contig ID
5'-most EST
                   LIB3051-020-Q1-E1-D9
Method
                   BLASTX
NCBI GI
                   q3150415
BLAST score
                   352
E value
                   2.0e-33
Match length
                   82
% identity
                   79
NCBI Description
                   (ACO04165) sec13-related protein [Arabidopsis thaliana]
                   >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
                   4105
Seq. No.
                   3203 1.R1040
Contig ID
5'-most EST
                   crh700849943.h1
Seq. No.
                   4106
                   3203 2.R1040
Contig ID
                   zvp7\overline{0}0764113.h1
5'-most EST
Seq. No.
                   4107
Contig ID
                   3205 1.R1040
5'-most EST
                   eep700865877.hl
Method
                   BLASTX
NCBI GI
                   g2529663
BLAST score
                   611
E value
                   3.0e-63
Match length
                   223
                   52
% identity
                   (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana] >gi 3738277 (AC005309) putative lysophospholipase
                   [Arabidopsis thaliana]
                   4108
Seq. No.
                   3208 1.R1040
Contig ID
5'-most EST
                   g4292897
```

E value

```
Contig ID
                  3210 1.R1040
                  LIB3106-068-P1-K1-A7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2267567
BLAST score
                  379
                  2.0e-36
E value
Match length
                  86
                  83
% identity
                   (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
Seq. No.
                  4110
Contig ID
                  3210 5.R1040
5'-most EST
                  ssr7\overline{0}0553813.h1
Method
                  BLASTX
                  g2267567
NCBI GI
BLAST score
                  226
E value
                  3.0e-29
Match length
                  84
% identity
                  81
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
                  4111
Seq. No.
Contig ID
                  3212 1.R1040
                  leu701149930.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q535454
BLAST score
                  541
E value
                  3.0e-55
Match length
                  147
% identity
                  68
                  (U13940) cysteine proteinase [Alnus glutinosa]
NCBI Description
Seq. No.
                  4112
                  3213 1.R1040
Contig ID
                  LIB3092-045-Q1-K1-F11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1711355
BLAST score
                  405
E value
                  1.0e-41
Match length
                  208
% identity
                  46
                  SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
NCBI Description
                  >gi_421786_pir__S34678 short-chain alcohol dehydrogenase -
                  Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain
                  alcohol dehydrogenase [Picea abies]
                  4113
Seq. No.
                  3214 1.R1040
Contig ID
5'-most EST
                  LIB3106-078-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q1709825
BLAST score
                  534
```

2.0e-54

Contig ID

```
167
Match length
                  63
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  4114
                  3214 3.R1040
Contig ID
5'-most EST
                  LIB3072-009-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q1709825
BLAST score
                  350
E value
                  5.0e-33
Match length
                  125
                  62
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  4115
                  3216 1.R1040
Contig ID
5'-most EST
                  jex700906615.hl
Seq. No.
                  4116
Contig ID
                  3217 1.R1040
                  q5606400
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3281846
BLAST score
                  701
E value
                  3.0e-73
Match length
                  623
                  48
% identity
NCBI Description
                  (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
Seq. No.
                  4117
Contig ID
                  3217 2.R1040
5'-most EST
                  rca700996583.hl
Method
                  BLASTX
NCBI GI
                  q3281846
BLAST score
                  260
E value
                  4.0e-22
Match length
                  233
% identity
                  31
                  (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4118
                  3217 3.R1040
Contig ID
5'-most EST
                  jex700904220.h1
Seq. No.
                  4119
                  3217 5.R1040
Contig ID
5'-most EST
                  uC-gmropic021a01b1
Seq. No.
                  3217 7.R1040
Contig ID
5'-most EST
                  jC-gmle01810089h08a1
Seq. No.
                  3217 8.R1040
```

```
5'-most EST
                    pmv700894463.h1
 Method
                    BLASTX
 NCBI GI
                    g1777443
 BLAST score
                    228
 E value
                    1.0e-18
 Match length
                    48
 % identity
 NCBI Description
                    (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
                    DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569
                    (U79156) CCA1 [Arabidopsis thaliana]
 Seq. No.
                    4122
 Contig ID
                    3217 9.R1040
 5'-most EST
                    ncj700977410.h1
Seq. No.
                    4123
Contig ID
                    3217 12.R1040
5'-most EST
                    LIB3138-130-Q1-N1-D2
Method
                    BLASTN
NCBI GI
                    g3281845
BLAST score
                    43
E value
                    6.0e-15
Match length
                    83
% identity
                    88
NCBI Description
                   Arabidopsis thaliana mRNA for LATE ELONGATED HYPOCOTYL MYB
                    transcription factor
Seq. No.
                    4124
Contig ID
                   3217 16.R1040
                   zhf7\overline{0}0953467.h1
5'-most EST
Seq. No.
                   4125
Contig ID
                   3217_17.R1040
                   wvk700683912.h1
5'-most EST
Seq. No.
                   4126
Contig ID
                   3219 1.R1040
5'-most EST
                   jC-gmst02400015f08a1
Method
                   BLASTX
NCBI GI
                   g1706082
BLAST score
                   836
E value
                   2.0e-89
Match length
                   313
% identity
                   53
NCBI Description
                   SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
                   >gi_629787_pir__S44191 serine-type carboxypeptidase (EC
3.4.16.1) II-3 - barley >gi_619350_bbs_153536
                   CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
                   cv. Alexis, aleurone, Peptide, 516 aa]
                   >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
                   [Hordeum vulgare]
Seq. No.
                   4127
Contig ID
                   3220 1.R1040
5'-most EST
                   LIB3073-009-Q1-K1-C11
Method
                   BLASTX
NCBI GI
```

g4544418

5'-most EST

```
BLAST score
                   401
E value
                  9.0e-39
Match length
                  145
% identity
                  56
NCBI Description
                   (AC006955) hypothetical protein [Arabidopsis thaliana]
                  4128
Seq. No.
                  3221_1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy103f05b1
Method
                  BLASTX
                  g2980770
NCBI GI
BLAST score
                  1519
E value
                  1.0e-169
Match length
                  430
% identity
                  69
NCBI Description
                   (AL022198) putative protein kinase [Arabidopsis thaliana]
                  4129
Seq. No.
                  3221 2.R1040
Contig ID
5'-most EST
                  fC-gmro7000750362r1
Method
                  BLASTX
NCBI GI
                  q2980770
BLAST score
                  339
E value
                  2.0e-31
Match length
                  94
% identity
                  69
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  4130
Seq. No.
                  3221_3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy117f06b1
                  BLASTX
Method
NCBI GI
                  g2980770
BLAST score
                  190
E value
                  3.0e-14
Match length
                  77
% identity
NCBI Description
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  4131
Contig ID
                  3223 1.R1040
5'-most EST
                  jC-gmf102220141g06a1
Method
                  BLASTX
NCBI GI
                  g2232354
BLAST score
                  439
E value
                  2.0e-43
Match length
                  159
% identity
NCBI Description
                  (AF006081) UDPG glucosyltransferase [Solanum berthaultii]
Seq. No.
                  4132
Contig ID
                  3224 1,R1040
5'-most EST
                  uC-gmrominsoy136g03b1
Seq. No.
                  4133
                  3224 2.R1040
Contig ID
```

dpv701102995.hl

BLAST score

936

```
4134
Seq. No.
                   3225 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220079g05d1
Seq. No.
                   3225 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy024d08b1
Seq. No.
Contig ID
                   3226 1.R1040
5'-most EST
                   LIB3040-047-Q1-E1-F12
Method
                   BLASTN
NCBI GI
                   q1666172
BLAST score
                   103
                   2.0e-50
E value
Match length
                   259
                   85
% identity
                   N.plumbaginifolia mRNA for BTF3-like transcription factor
NCBI Description
Seq. No.
                   4137
                   3226 2.R1040
Contig ID
5'-most EST
                   txt700736278.h1
Method
                   BLASTX
NCBI GI
                   q2982299
BLAST score
                   396
E value
                   2.0e-38
Match length
                   137
                   72
% identity
NCBI Description
                   (AF051234) transcription factor BTF3 homolog [Picea
                   mariana]
                   4138
Seq. No.
                   3227 1.R1040
Contig ID
5'-most EST
                   g4307584
Method
                   BLASTX
NCBI GI
                   q2864616
BLAST score
                   230
E value
                   6.0e-19
Match length
                   69
% identity
                   65
                   (AL021811) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   3228 1.R1040
5'-most EST
                   LIB3040-019-Q1-E1-C7
Seq. No.
Contig ID
                   3229 1.R1040
5'-most EST
                   LIB3028-033-Q1-B1-E12
                   4141
Seq. No.
Contig ID
                   3230 1.R1040
5'-most EST
                   zhf700955020.h1
Method
                   BLASTX
NCBI GI
                   g1619300
```

```
E value
                    1.0e-101
 Match length
                    218
 % identity
                    82
                    (X95269) LRR protein [Lycopersicon esculentum]
 NCBI Description
 Seq. No.
                    4142
                    3230 2.R1040
 Contig ID
                    zzp7\overline{0}0834740.h1
 5'-most EST
                    4143
 Seq. No.
 Contig ID
                    3232 1.R1040'
                    wrg700790475.h2
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g1655637
 BLAST score
                    380
 E value
                    9.0e-80
 Match length
                    188
 % identity
                    80
                    (Z54179) orf [Mus musculus]
 NCBI Description
                    4144
 Seq. No.
                    3232 2.R1040
 Contig ID
 5'-most EST
                    jsh701067294.h1
                    4145
 Seq. No.
                    3232 4.R1040
 Contig ID
 5'-most EST
                    LIB3028-015-Q1-B1-G5
Method
                    BLASTX
                    q1655637
 NCBI GI
 BLAST score
                    428
                    3.0e-42
 E value
 Match length
                    100
                    81
 % identity
                    (Z54179) orf [Mus musculus]
 NCBI Description
                    4146
 Seq. No.
                    3233 1.R1040
 Contig ID
 5'-most EST
                    crh7\overline{0}0855064.h1
 Method
                    BLASTX
 NCBI GI
                    g2980770
 BLAST score
                    485
                    1.0e-48
 E value
                    155
 Match length
 % identity
                    66
                    (AL022198) putative protein kinase [Arabidopsis thaliana]
 NCBI Description
                    4147
 Seq. No.
                    3233 2.R1040
 Contig ID
                    jC-gmle01810016b03d1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2980770
 BLAST score
                    304
                    2.0e-27
 E value
 Match length
                    83
                    70
 % identity
 NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
```

5'-most EST

```
Seq. No.
                  4148
                  3235_1.R1040
Contig ID
                  LIB3028-032-Q1-B1-H10
5'-most EST
                  4149
Seq. No.
                  3237 1.R1040
Contig ID
                  wrg7\overline{0}0790785.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3746791
BLAST score
                  279
                  2.0e-24
E value
Match length
                  186
% identity
                  32
                  (AF081788) putative spliceosome associated protein [Homo
NCBI Description
                  sapiens] >gi 3985930 dbj BAA34863 (AB020623) DAM1 [Homo
                  sapiens]
                  4150
Seq. No.
                  3238 1.R1040
Contig ID
                  jC-gmf102220084a05a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3844596
BLAST score
                  369
                  7.0e-35
E value
Match length
                  153
% identity
                  47
                   (U28941) contains similarity to human copine I (GB:U83246)
NCBI Description
                   [Caenorhabditis elegans]
                  4151
Seq. No.
                  3238 2.R1040
Contig ID
5'-most EST
                  LIB3028-032-Q1-B1-H4
Method
                  BLASTX
                  g1176658
NCBI GI
BLAST score
                  399
E value
                  1.0e-38
Match length
                  158
% identity
                  54
                  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                  >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
Seq. No.
                  4152
                  3238_3.R1040
Contig ID
                  uC-gmrominsoy108d01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3844596
BLAST score
                  185
E value
                  1.0e-13
Match length
                  67
                  54
% identity
                   (U28941) contains similarity to human copine I (GB:U83246)
NCBI Description
                   [Caenorhabditis elegans]
                  4153
Seq. No.
Contig ID
                  3238 4.R1040
```

: 3

jex700904237.h1

Seq. No.

4159

```
Seq. No.
                   4154
                   3239 1.R1040
Contig ID
                   LIB3040-022-Q1-E1-F10
5'-most EST
Method
                   BLASTN
                   g498895
NCBI GI
BLAST score
                   120
E value
                   1.0e-60
Match length
                   392
                   83
% identity
NCBI Description
                   Pisum sativum histone H2A homolog mRNA, complete cds
                   4155
Seq. No.
                   3239 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy058d06b1
Method
                   BLASTN
                   g498895
NCBI GI
BLAST score
                   116
E value
                   2.0e-58
Match length
                   368
% identity
                   83
                  Pisum sativum histone H2A homolog mRNA, complete cds
NCBI Description
                   4156
Seq. No.
                   3239 3.R1040
Contig ID
5'-most EST
                   LIB3106-110-Q1-K1-B8
Method
                   BLASTN
NCBI GI
                   q498895
BLAST score
                   117
                   9.0e-59
E value
Match length
                   385
                   83
% identity
NCBI Description
                  Pisum sativum histone H2A homolog mRNA, complete cds
                   4157
Seq. No.
Contig ID
                   3239 4.R1040
5'-most EST
                   uC-gmropic062d07b1
Method
                   BLASTN
NCBI GI
                   q498895
BLAST score
                   113
E value
                   2.0e-56
Match length
                   385
% identity
                   82
NCBI Description
                   Pisum sativum histone H2A homolog mRNA, complete cds
Seq. No.
                   4158
Contig ID
                   3239 5.R1040
5'-most EST
                   zvj700605109.h2
Method
                   BLASTN
NCBI GI
                   g498895
BLAST score
                   103
E value
                   1.0e-50
Match length
                   323
                   83
% identity
                   Pisum sativum histone H2A homolog mRNA, complete cds
NCBI Description
```

```
3240 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220138h05a1
Method
                   BLASTX
NCBI GI
                   g3158476
BLAST score
                   1185
                   1.0e-130
E value
Match length
                   286
                   80
% identity
                   (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                   4160
Seq. No.
                   3240 2.R1040
Contig ID
5'-most EST
                   q4298424
                   BLASTN
Method
                   g1402832
NCBI GI
BLAST score
                   98
E value
                   2.0e-47
Match length
                   290
                   83
% identity
NCBI Description
                   Beta vulgaris plasma membrane major intrinsic protein 1
                   mRNA, complete cds
Seq. No.
                   4161
                   3240_5.R1040
Contig ID
5'-most EST
                   g4313924
                   BLASTX
Method
                   g1657948
NCBI GI
BLAST score
                   348
E value
                   1.0e-32
Match length
                   153
% identity
                   58
                   (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
                   4162
Seq. No.
                   3240 9.R1040
Contig ID
5'-most EST
                   pxt700943836.hl
Seq. No.
                   4163
Contig ID
                   3241 1.R1040
5'-most EST
                   sat7\overline{0}1012981.h1
Method
                   BLASTX
NCBI GI
                   q3776578
BLAST score
                   382
E value
                   2.0e-36
Match length
                   136
% identity
NCBI Description
                   (ACO05388) ESTs gb_F13915 and gb_F13916 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   4164
Contig ID
                   3243 1.R1040
5'-most EST
                   uaw700665294.h1
Method
                   BLASTX
NCBI GI
                   q3252807
BLAST score
                   364
E value
                   1.0e-34
Match length
                   184
```

Seq. No.

4171

```
% identity
                   43
NCBI Description
                   (AC004705) hypothetical protein [Arabidopsis thaliana]
                   4165
Seq. No.
                   3247 1.R1040
Contig ID
5'-most EST
                   leu701154509.hl
                   BLASTX
Method
NCBI GI
                   g3212851
BLAST score
                   236
                   1.0e-19
E value
Match length
                   74
% identity
                   62
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   4166
Seq. No.
                   3247 2.R1040
Contig ID
                   leu7\overline{0}1149937.h1
5'-most EST
                   4167
Seq. No.
Contig ID
                   3248 1.R1040
                   k11701208893.h1
5'-most EST
Method
                   BLASTX
                   g2244806
NCBI GI
BLAST score
                   590
E value
                   2.0e-60
Match length
                   299
                   43
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
     v.
Seq. No.
                   4168
Contig ID
                   3248 2.R1040
                   g5605815
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244806
BLAST score
                   333
E value
                   6.0e-31
Match length
                   104
                   58
% identity
NCBI Description
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
                   4169
Seq. No.
                   3251 1.R1040
Contig ID
5'-most EST
                   zpv700762784.hl
                   4170
Seq. No.
Contig ID
                   3252 1.R1040
5'-most EST
                   jex700908866.hl
Method
                   BLASTN
NCBI GI
                   q4097582
BLAST score
                   205
E value
                   1.0e-111
Match length
                   596
% identity
                   84
NCBI Description
                  Nicotiana tabacum geranylgeranylated protein NTGP3 mRNA,
                   complete cds
```

```
3252 2.R1040
Contig ID
                   hyd7\overline{0}0730610.h1
5'-most EST
Method
                   BLASTN
                   g1370199
NCBI GI
BLAST score
                   129
                   3.0e-66
E value
                   321
Match length
% identity
                   85
NCBI Description
                  L.japonicus mRNA for small GTP-binding protein, RAC1
Seq. No.
                   4172
                   3253 1.R1040
Contig ID
                   LIB3050-004-Q1-E1-H5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3242723
BLAST score
                   526
E value
                   1.0e-53
Match length
                   158
% identity
                   59
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   4173
                   3254 1.R1040
Contig ID
5'-most EST
                   LIB3040-027-Q1-E1-G3
Method
                   BLASTN
NCBI GI
                   q1711035
BLAST score
                   172
E value
                   1.0e-91
Match length
                   388
% identity
                   86
                   Pisum sativum hydroxyproline rich glycoprotein PsHRGP1
NCBI Description
                   mRNA, partial cds
Seq. No.
                   4174
Contig ID
                   3254 2.R1040
5'-most EST
                   LIB3170-001-Q1-K1-D12
Method
                   BLASTN
NCBI GI
                   q1711035
BLAST score
                   188
E value
                   1.0e-101
Match length
                   392
                   87
% identity
                   Pisum sativum hydroxyproline rich glycoprotein PsHRGP1
NCBI Description
                   mRNA, partial cds
Seq. No.
                   4175
                   3254 3.R1040
Contig ID
5'-most EST
                   LIB3139-056-P1-N1-D3
Method
                   BLASTN
NCBI GI
                   g1711035
BLAST score
                   74
                   2.0e-33
E value
Match length
                   118
% identity
                   91
                   Pisum sativum hydroxyproline rich glycoprotein PsHRGP1
NCBI Description
```

mRNA, partial cds

```
4176
Seq. No.
                  3254 4.R1040
Contig ID
                  LIB3049-048-Q1-E1-G11
5'-most EST
                  BLASTX
Method
                  g4490705
NCBI GI
BLAST score
                  305
                  2.0e-40
E value
                  128
Match length
                  68
% identity
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  4177
Seq. No.
                  3255 1.R1040
Contig ID
5'-most EST
                  vzy700751859.h1
                  4178
Seq. No.
                  3256 1.R1040
Contig ID
5'-most EST
                  ssr700555088.h1
Method
                  BLASTX
NCBI GI
                  g3941289
BLAST score
                  292
                  3.0e-26
E value
Match length
                  117
% identity
                  50
NCBI Description
                  (AF018093) similarity to SCAMP37 [Pisum sativum]
                  4179
Seq. No.
                  3256 2.R1040
Contig ID
5'-most EST
                  LIB3049-041-Q1-E1-F3
Method
                  BLASTX
                  g2443878
NCBI GI
BLAST score
                  164
E value
                  3.0e-11
Match length
                  92
                  47
% identity
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  4180
Seq. No.
                  3260 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810004e08a1
Method
                  BLASTX
                  g2160148
NCBI GI
BLAST score
                  791
E value
                  3.0e-84
Match length
                  239
% identity
NCBI Description
                  (ACO00375) EST gb H37044 comes from this gene. [Arabidopsis
                  thaliana]
                  4181
Seq. No.
Contig ID
                  3260 2.R1040
5'-most EST
                  ejt700606288.h1
                  4182
Seq. No.
                  3262 1.R1040
Contig ID
```

Contig ID

```
zhf700962774.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4455800
BLAST score
                  360
                  9.0e-34
E value
Match length
                  145
                  49
% identity
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  4183
Seq. No.
Contig ID
                  3264 2.R1040
                  pcp700992416.hl
5'-most EST
                  4184
Seq. No.
Contig ID
                  3264 4.R1040
                  zhf700962567.h1
5'-most EST
                  4185
Seq. No.
Contig ID
                  3269 1.R1040
5'-most EST
                  LIB3138-070-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  g3915601
BLAST score
                  570
E value
                  1.0e-58
                  207
Match length
                  54
% identity
                  ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD
NCBI Description
                  SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38)
                  >gi 1498259 (L07541) replication factor C, 38-kDa subunit
                   [Homo sapiens] >gi_4506489_ref_NP_002906.1_pRFC3_
                   replication factor C (activator 1) 3 (38kD)
                   4186
Seq. No.
                   3273 1.R1040
Contig ID
                   asn7\overline{0}1131893.h1
5'-most EST
Method
                  BLÁSTX
NCBI GI
                   q3831453
                   549
BLAST score
                   4.0e-56
E value
                   179
Match length
                   65
% identity
NCBI Description
                   (AC005700) unknown protein [Arabidopsis thaliana]
                   4187
Seq. No.
                   3273 2.R1040
Contig ID
5'-most EST
                   zsg701119359.hl
Method
                   BLASTX
NCBI GI
                   q2388580
BLAST score
                   211
                   9.0e-17
E value
Match length
                   67
% identity
                   (AC000098) Similar to Sequence 10 from patent 5477002
NCBI Description
                   (gb 1253956). [Arabidopsis thaliana]
Seq. No.
```

3274 1.R1040

```
5'-most EST
                  trc700563862.h1
Method
                  BLASTX
NCBI GI
                  q2501568
BLAST score
                  219
E value
                  1.0e-17
Match length
                  72
% identity
                  57
NCBI Description
                  HYPOTHETICAL 28.8 KD PROTEIN SLL0506
                  >gi_1001342_dbj_BAA10829_ (D64006) hypothetical protein
                   [Synechocystis sp.]
Seq. No.
Contig ID
                  3275 1.R1040
5'-most EST
                  uC-qmrominsoy300b11b1
Method
                  BLASTX
NCBI GI
                  a3953466
BLAST score
                  1063
E value
                  1.0e-116
Match length
                  287
% identity
                  70
NCBI Description (ACO02328) F20N2.11 [Arabidopsis thaliana]
Seq. No.
                  4190
Contig ID
                  3276 1.R1040
5'-most EST
                  qsv701055179.h1
Method
                  BLASTX
NCBI GI
                  q1498053
BLAST score
                  835
E value
                  1.0e-89
Match length
                  207
% identity
                  79
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  4191
Contig ID
                  3280 1.R1040
5'-most EST
                  LIB3073-023-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  q3242659
BLAST score
                  960
E value
                  1.0e-104
Match length
                  302
% identity
NCBI Description (AB015599) spermidine synthase [Coffea arabica]
Seq. No.
                  4192
Contig ID
                  3281 1.R1040
5'-most EST
                  LIB3106-067-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q416731
BLAST score
                  311
E value
                  4.0e-28
Match length
                  167
% identity
                  38
NCBI Description
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >qi 82655 pir JQ1107
                  18.3K protein precursor, pollen - maize
                  >gi 255569 bbs 113677 (S44171) pollen specific protein [Zea
```

mays=corn, Peptide, 170 aa] [Zea mays]

Match length

30

## 4193 Seq. No. 3281 2.R1040 Contig ID 5'-most EST LIB3051-088-Q1-K1-C12 4194 Seq. No. 3281 3.R1040 Contig ID 5'-most EST LIB3051-062-Q1-K1-A11 Seq. No. 4195 3281 4.R1040 Contig ID 5'-most EST LIB3051-039-Q1-K1-E9 Method BLASTX NCBI GI a416731 BLAST score 308 1.0e-27 E value Match length 158 39 % identity POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi\_82655\_pir\_\_JQ1107 NCBI Description 18.3K protein precursor, pollen - maize >gi\_255569 bbs\_113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays] >gi\_1588669\_prf\_\_2209273A Zm13 [Zea mays] Seq. No. 4196 3281 5.R1040 Contig ID 5'-most EST $q575\overline{2}512$ Method BLASTX NCBI GI g1352316 BLAST score 654 3.0e-68 E value Match length 152 % identity 85 DR1 PROTEIN HOMOLOG >gi\_633026\_dbj\_BAA07288\_ (D38110) Dr1 NCBI Description [Arabidopsis thaliana] 4197 Seq. No. Contig ID 3281 6.R1040 5'-most EST zzp700831164.hl Method BLASTX NCBI GI q1352316 BLAST score 552 E value 3.0e-56 Match length 154 75 % identity NCBI Description DR1 PROTEIN HOMOLOG >gi\_633026\_dbj\_BAA07288\_ (D38110) Dr1 [Arabidopsis thaliana] 4198 Seq. No. Contig ID 3281 14.R1040 5'-most EST jsh701065943.hl Method BLASTX NCBI GI q1352316 BLAST score 138 E value 1.0e-08

>gi 1588669 prf 2209273A Zm13 [Zea mays]

% identity

97

```
% identity
NCBI Description
                   DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1
                   [Arabidopsis thaliana]
                   4199
Seq. No.
Contig ID
                   3283 1.R1040
5'-most EST
                   uC-gmropic097h11b1
Method
                   BLASTX
NCBI GI
                   g1930081
BLAST score
                   1531
E value
                   1.0e-171
Match length
                   365
                   78
% identity
NCBI Description
                   (U92878) acyl-ACP thioesterase [Garcinia mangostana]
Seq. No.
                   3283 2.R1040
Contig ID
5'-most EST
                  LIB3028-047-Q1-B1-C11
Method
                  BLASTX
NCBI GI
                   g1930081
BLAST score
                   291
                   3.0e-26
E value
Match length
                   92
% identity
                   63
                   (U92878) acyl-ACP thioesterase [Garcinia mangostana]
NCBI Description
                   4201
Seq. No.
                   3283 3.R1040
Contig ID
5'-most EST
                  LIB3053-010-Q1-N1-A8
Method
                  BLASTX
NCBI GI
                   q1930081
BLAST score
                   489
E value
                   4.0e-49
Match length
                  143
                   65
% identity
                   (U92878) acyl-ACP thioesterase [Garcinia mangostana]
NCBI Description
Seq. No.
                   4202
Contig ID
                   3283_4.R1040
5'-most EST
                  uC-gmflminsoy029g06b1
Method
                  BLASTX
NCBI GI
                  q1930081
BLAST score
                  888
                                                                     .,-
E value
                  1.0e-130
Match length
                   327
% identity
NCBI Description
                   (U92878) acyl-ACP thioesterase [Garcinia mangostana]
Seq. No.
                  4203
Contig ID
                  3283 5.R1040
5'-most EST
                  LIB3170-042-Q1-J1-A11
Method
                  BLASTN
                  q4104241
NCBI GI
BLAST score
                  33
E value
                  7.0e-09
Match length
                  37
```

```
NCBI Description Gossypium hirsutum palmitoyl-acyl carrier protein
                   thioesterase (FatB1) mRNA, partial cds
                   4204
 Seq. No.
                   3283 6.R1040
 Contig ID
                   LIB3093-040-Q1-K1-E8
 5'-most EST
Seq. No.
                   4205
 Contig ID
                   3283 8.R1040
 5'-most EST
                   jC-qmro02910005b10a1
                   BLASTN.
Method
NCBI GI
                   q4104241
BLAST score
                   54
E value
                   3.0e-21
Match length
                   82
 % identity
                   91
                   Gossypium hirsutum palmitoyl-acyl carrier protein
NCBI Description
                   thioesterase (FatB1) mRNA, partial cds
Seq. No.
                   3283 9.R1040
 Contig ID
5'-most EST
                   jC-gmf102220103g09d1
Seq. No. 1
                   4207
Contig ID
                   3283 10.R1040
5'-most EST
                   LIB3170-030-Q1-K1-B8
Seq. No.
                   4208
Contig ID
                   3283 11.R1040
5'-most EST
                   uC-gmflminsoy059g08b1
Method
                   BLASTN
NCBI GI
                   q804947
BLAST score
                   39
E value
                   2.0e-12
Match length
                   43
% identity
                   98
                   A.thaliana mRNA for acyl-(acyl carrier protein)
NCBI Description
                   thioesterase
Seq. No.
                   4209
Contig ID
                   3283 12.R1040
5'-most EST
                   jC-qmf102220138b10a1
Seq. No.
                   4210
Contig ID
                   3283 13.R1040
5'-most EST
                   LIB3109-037-Q1-K1-G7
Seq. No.
                   4211
                   3288 1.R1040
Contig ID
5'-most EST
                   leu701145370.hl
Method
                   BLASTN
NCBI GI
                   q169106
BLAST score
                   442
E value
                   0.0e+00
Match length
                   906
% identity
                   90
NCBI Description
                   Pisum sativum IM30 protein mRNA, complete cds
```

```
4212
Seq. No.
                   3292 1.R1040
Contig ID
5'-most EST
                   1eu7\overline{0}1148679.h1
Method
                   BLASTX
                   g2062167
NCBI GI
                   1341
BLAST score
                   1.0e-148
E value
Match length
                   321
% identity
                   78
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   4213
Seq. No.
Contig ID
                   3292 2.R1040
                   LIB3107-013-Q1-K1-B11
5'-most EST
Method
                   BLASTX
                   g2062167
NCBI GI
                   300
BLAST score
E value
                   6.0e-27
                   68
Match length
                   82
% identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   4214
Seq. No.
                   3293 1.R1040
Contig ID
                   wrg700786729.h2
5'-most EST
                   BLASTN
Method
NCBI GI
                   q603218
BLAST score
                   183
                   3.0e-98
E value
                   457
Match length
% identity
                   Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
NCBI Description
                   complete cds
                    4215
Seq. No.
                    3296 1.R1040
Contig ID
                    leu7\overline{0}1153364.h1
5'-most EST
                    BLASTX
Method
                    g2760326
NCBI GI
                    582
BLAST score
E value
                    6.0e-60
                   261
Match length
                    48
% identity
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                    4216
Seq. No.
                    3297 1.R1040
Contig ID
                    LIB3\overline{0}28-032-Q1-B1-D3
5'-most EST
Method
                    BLASTX
                    g2239262
NCBI GI
                    444
BLAST score
                    7.0e-44
E value
                    207
Match length
% identity
                    43
```

```
NCBI Description
                   (Y13285) pectin methylesterase-like protein [Zea mays]
                    4217
Seq. No.
Contig ID
                    3298 1.R1040
5'-most EST
                    jC-gmro02910047c03d1
                    4218
Seq. No.
Contiq ID
                    3303 1.R1040
5'-most EST
                    seb7\overline{0}0653702.h1
Method
                    BLASTX
NCBI GI
                    q2130052
BLAST score
                    1922
E value
                    0.0e + 00
Match length
                    459
% identity
                    77
                    xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                    >gi 1296809 emb CAA64545 (X95257) xylose isomerase
                    [Hordeum vulgare]
Seq. No.
                    4219
                    3304 1.R1040
Contig ID
5'-most EST
                    k117\overline{0}1213675.h1
Method
                    BLASTX
NCBI GI
                    q1432056
BLAST score
                    174
E value
                    3.0e-12
Match length
                    88
% identity
                    51
NCBI Description
                   (U56834) WRKY3 [Petroselinum crispum]
Seq. No.
                    4220
Contig ID
                    3304 2.R1040
5'-most EST
                    LIB3028-032-Q1-B1-A2
Seq. No.
                    4221
Contig ID
                    3306 1.R1040
5'-most EST
                    sat701010447.hl
Method
                    BLASTX
NCBI GI
                    q1931639
BLAST score
                    637
E value
                    3.0e-66
Match length
                    310
                    41
% identity
NCBI Description
                    (U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.
                    4222
Contig ID
                    3315 1.R1040
5'-most EST
                    LIB3139-104-P1-N1-D1
Method
                    BLASTX
NCBI GI
                    q462013
BLAST score
                    3250
E value
                    0.0e + 00
Match length
                    816
% identity
                    79
NCBI Description
                    ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                   >gi_542022_pir_S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90
```

[Catharanthus roseus] 4223 Seq. No. 3315\_2.R1040 Contig ID 5'-most EST fC-qmro7000749772r1 BLASTX Method NCBI GI q462013 BLAST score 422 5.0e-42 E value Match length 106 80 % identity ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description >gi\_542022\_pir\_\_S39558 HSP90 homolog - Madagascar periwinkle >gi\_348696 (L14594) heat shock protein 90 [Catharanthus roseus] 4224 Seq. No. 3315 3.R1040 Contig ID hrw701058023.h1 5'-most EST BLASTX Method g462013 NCBI GI BLAST score 229 4.0e-19 E value 52 Match length % identity 88 ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description >gi\_542022\_pir\_\_S39558 HSP90 homolog - Madagascar periwinkle >gi\_348696 (L14594) heat shock protein 90 [Catharanthus roseus] Seq. No. 4225 3316 1.R1040 Contig ID  $jex7\overline{0}0907321.h1$ 5'-most EST Method BLASTX q4006877 NCBI GI BLAST score 347 E value 2.0e-32 Match length 111 37 % identity (Z99707) RNA-binding like protein [Arabidopsis thaliana] NCBI Description 4226 Seq. No. 3319 1.R1040 Contig ID jC-gmle01810060g11a1 5'-most EST BLASTX Method NCBI GI g3763926 BLAST score 302 E value 7.0e-27 Match length 313 % identity 35 (AC004450) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 4227

Contig ID 3319\_4.R1040 5'-most EST zpv700758505.h1

Method BLASTX NCBI GI g3763926

E value

```
BLAST score
                   207
E value
                   2.0e-16
Match length
                   129
% identity
                   29
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                   4228
Seq. No.
                   3322 1.R1040
Contig ID
5'-most EST
                   pmv700891362.hl
Seq. No.
                   4229
                   3323 1.R1040
Contig ID
5'-most EST
                   pmv700894690.hl
Method
                   BLASTX
NCBI GI
                   q4567205
BLAST score
                   582
                   5.0e-60
E value
Match length
                   154
% identity
                   72
NCBI Description
                   (AC007168) putative trehalose-6-phosphate phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                   4230
Contig ID
                   3323 2.R1040
5'-most EST
                   uC-gmrominsoy049f06b1
Method
                   BLASTX
NCBI GI
                   q4567205
BLAST score
                   425
E value
                   1.0e-41
Match length
                   113
% identity
                   72
NCBI Description
                   (AC007168) putative trehalose-6-phosphate phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                   4231
Contig ID
                   3323 3.R1040
5'-most EST
                   uC-gmropic046h07b1
                                                               ÷:
Method
                   BLASTX
NCBI GI
                   q2944180
BLAST score
                   148
E value
                   2.0e-09
Match length
                   109
% identity
                   39
NCBI Description
                   (AF007779) trehalose-6-phosphate phosphatase (Arabidopsis
                   thaliana]
Seq. No.
                   4232
Contig ID
                   3323 4.R1040
5'-most EST
                   uC-gmrominsoy310c07b1
Seq. No.
                   4233
Contig ID
                   3326 1.R1040
5'-most EST
                   LIB3138-016-Q1-N1-A5
Method
                   BLASTX
NCBI GI
                   g4115357
BLAST score
                   876
```

4.0e-94

NCBI GI

```
378
  Match length
  % identity
                     47
                     (AC005957) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     4234
  Seq. No.
                     3326 2.R1040
  Contig ID
                     wrg700788991.h2
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     g4115357
  BLAST score
                     265
  E value
                     6.0e-23
  Match length
                     69
  % identity
                     62
                     (AC005957) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
  Contig ID
                     3329 1.R1040
  5'-most EST
                     jC-gmf102220065b08a1
  Method
                     BLASTX
  NCBI GI
                     q1001478
  BLAST score
                     691
  E value
                     3.0e-72
  Match length
                     368
  % identity
                     39
  NCBI Description
                    (D63999) hypothetical protein [Synechocystis sp.]
  Seq. No.
                     4236
                     3330 1.R1040
  Contig ID
  5'-most EST
                     epx701104170.hl
  Method
                     BLASTX
  NCBI GI
                     g2388710
  BLAST score
                     2187
  E value
                     0.0e + 00
  Match length
                     500
  % identity
                     79
  NCBI Description
                     (AF017150) betaine aldehyde dehydrogenase [Amaranthus
                     hypochondriacus]
                     4237
  Seq. No.
                     3330 2.R1040
  Contig ID
  5'-most EST
                     leu701154014.hl
  Method
                     BLASTX
  NCBI GI
                     g118490
  BLAST score
                     417
                     7.0e-82
  E value
  Match length
                     236
  % identity
                     67
                     BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
· · NCBI Description
                     >qi 99517 pir S19135 betaine-aldehyde dehydrogenase (EC
                     1.2.1.8) precursor - beet >gi 17934_emb_CAA41377_ (X58463)
                     betaine aldehyd dehydrogenase [Beta vulgaris]
                     4238
  Seq. No.
                     3330 3.R1040
  Contig ID
                     jC-gmro02910038c11d1
  5'-most EST
  Method
                     BLASTX
```

g2388710

```
BLAST score
                  820
                   8.0e-88
E value
Match length
                  197
% identity
                   74
                   (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                  hypochondriacus]
Seq. No.
                   4239
Contig ID
                  3330 4.R1040
                  bth700844477.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1169286
BLAST score
                  143
                   3.0e-09
E value
Match length
                  35
                  71
% identity
                  BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
NCBI Description
                  >gi 1085671_pir__S49205 betaine-aldehyde dehydrogenase (EC
                  1.2.1.8) precursor - Atriplex hortensis
                  >gi 510574 emb CAA49425 (X69770) betaine-aldehyde
                  dehydrogenase [Atriplex hortensis]
Seq. No.
                  4240
Contig ID
                  3331 1.R1040
                  uaw700665055.hl
5'-most EST
Method
                  BLASTX
                  q4539322
NCBI GI
BLAST score
                  241
                  9.0e-32
E value
Match length
                  111
% identity
                  62
                   (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                  4241
Seq. No.
                  3333 1.R1040
Contig ID
5'-most EST
                  wrg700790526.h2
Method
                  BLASTX
NCBI GI
                  q3193316
BLAST score
                  642
E value
                  3.0e-95
Match length
                  284
% identity
                  65
                   (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  4242
Seq. No.
Contig ID
                  3335 1.R1040
5'-most EST
                  LIB3074-039-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q1653488
BLAST score
                  173
E value
                  3.0e-12
Match length
                  79
                  42
% identity
NCBI Description
                  (D90914) hypothetical protein [Synechocystis sp.]
```

4243

Seq. No.

```
Contig ID
                   3335 2.R1040
5'-most EST
                   leu701146566.h1
Seq. No.
                   4244
Contig ID
                   3336 1.R1040
5'-most EST
                   LIB3028-031-Q1-B1-E5
Method
                   BLASTX
NCBI GI
                   g4337025
BLAST score
                   590
E value
                   8.0e-61
Match length
                   192
% identity
                   59
NCBI Description
                   (AF123253) AIM1 protein [Arabidopsis thaliana]
Seq. No.
                   4245
Contig ID
                   3336 2.R1040
5'-most EST
                   jC-gmf102220054c05d1
Method
                   BLASTX
NCBI GI
                   g4337025
BLAST score
                   296
E value
                   1.0e-26
Match length
                   82
% identity
                   71
NCBI Description
                   (AF123253) AIM1 protein [Arabidopsis thaliana]
Seq. No.
                   4246
Contig ID
                  3340 1.R1040
5'-most EST
                  leu701156583.h1
Method
                  BLASTN
NCBI GI
                  g2961299
BLAST score
                  266
E value
                  1.0e-147
Match length
                  474
% identity
                  89
NCBI Description Cicer arietinum mRNA for ribosomal protein L24
Seq. No.
                  4247
Contig ID
                  3340 2.R1040 '
5'-most EST
                  LIB3073-016-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2961299
BLAST score
                  202
E value
                  1.0e-109
Match length
                  485
% identity
                  85
NCBI Description Cicer arietinum mRNA for ribosomal protein L24
Seq. No.
Contig ID
                  3341 1.R1040
5'-most EST
                  taw700659875.h1
Seq. No.
                  4249
Contig ID
                  3343 1.R1040
5'-most EST
                  jsh701066525.h1
Seq. No.
                  4250
Contig ID
                  3346 1.R1040
```

5'-most EST

```
Seq. No.
                   4251
                   3347 1.R1040
Contig ID
                   LIB3073-025-Q1-K1-F2
5'-most EST
                   4252
Seq. No.
Contig ID
                   3347 2.R1040
5'-most EST
                   uC-gmflminsoy032e12b1
Seq. No.
                   4253
                   3351 1.R1040
Contig ID
                   uC-qmflminsoy077f09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q285741
BLAST score
                   1135
E value
                   1.0e-124
Match length
                   415
% identity
                   59
NCBI Description
                   (D14550) EDGP precursor [Daucus carota]
Seq. No.
                   3351 2.R1040
Contig ID
                   leu701151416.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3850580
BLAST score
                   254
                   8.0e-22
E value
Match length
                   102
% identity
                   54
                   (AC005278) Strong similarity to gb D14550 extracellular
NCBI Description
                   dermal glycoprotein (EDGP) precursor from Daucus carota.
                   ESTs gb 84105 and gb AI100071 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   4255
                   3354 1.R1040
Contig ID
                   leu701153022.h1
5'-most EST
Method
                   BLASTX
                  g3894186
NCBI GI
BLAST score
                   861
E value
                   2.0e-92
Match length
                   260
% identity
                   63
NCBI Description
                   (AC005662) putative embryo-abundant protein [Arabidopsis
                  thaliana]
                   4256
Seq. No.
                   3356 1.R1040
Contig ID
5'-most EST
                  uC-gmropic030a08b1
Method
                   BLASTX
NCBI GI
                   g2062169
BLAST score
                   1308
                   1.0e-145
E value
Match length
                   364
% identity
                   38
                   (ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
```

LIB3051-046-Q1-K1-A6

```
4257
Seq. No.
                   3359 1.R1040
Contig ID
5'-most EST
                   LIB3106-022-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   q4567207
BLAST score
                   534
                   3.0e-54
E value
Match length
                   143
                   65
% identity
NCBI Description
                   (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   4258
                   3361 1.R1040
Contig ID
5'-most EST
                   hrw701059490.h1
                   4259
Seq. No.
                   3361 2.R1040 ·
Contig ID
5'-most EST
                  LIB3028-031-Q1-B1-D3
Seq. No.
                   4260
                   3362 1.R1040
Contig ID
                   leu7\overline{0}1155858.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3421104
BLAST score
                   1252
                   1.0e-138
E value
Match length
                   268
                   88
% identity
NCBI Description
                   (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
                  thaliana]
                   4261
Seq. No.
                   3362 2.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1152736.h1
Method
                  BLASTX
NCBI GI
                   g3421104 '
BLAST score
                   887
E value
                   1.0e-95
Match length
                  195
                   86
% identity
NCBI Description
                   (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
                   thaliana]
                   4262
Seq. No.
Contig ID
                   3362 3.R1040
5'-most EST
                  LIB3170-053-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g3421104
BLAST score
                   721
E value
                   2.0e-76
Match length
                  148
% identity
                   91
NCBI Description
                  (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
```

thaliana]

thaliana]

```
4263
  Seq. No.
                     3362 4.R1040
  Contig ID
                     LIB3065-005-Q1-N1-F8
5'-most EST
  Method
                     BLASTX
  NCBI GI
                     q3421104
  BLAST score
                     435
                     5.0e-43
  E value
                     107
  Match length
  % identity
                     75
                     (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
  NCBI Description
                     thaliana]
                     4264
  Seq. No.
                     3362_5.R1040
  Contig ID
  5'-most EST
                     jC-gmro02910037b10a1
  Method
                     BLASTX
  NCBI GI
                     g3421104
  BLAST score
                     522
  E value
                     3.0e-66
  Match length
                     141
  % identity
                     91
                     (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
  NCBI Description
                     thaliana]
                     4265
  Seq. No.
  Contig ID
                     3363 1.R1040
  5'-most EST
                     leu701156343.hl
                     4266
  Seq. No.
                     3364 1.R1040
  Contig ID
  5'-most EST
                     rca701001508.h1
  Method
                     BLASTX
  NCBI GI
                     g2194137
  BLAST score
                     291
                                    ķ. 🔻
                     2.0e-25
  E value
  Match length
                     89
  % identity
                     63
  NCBI Description
                     (AC002062) ESTs gb R29947, gb H76702 come from this gene.
                     [Arabidopsis thaliana]
  Seq. No.
                     4267
                     3364 2.R1040
  Contig ID
  5'-most EST
                     LIB3107-032-Q1-K1-G12
  Method
                     BLASTX
  NCBI GI
                     q2194137
  BLAST score
                     350
  E value
                     6.0e-33
  Match length
                     131
  % identity
                     59
                     (AC002062) ESTs gb R29947, gb H76702 come from this gene.
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                     4268
                     3364 3.R1040
  Contig ID
  5'-most EST
                     wrg700785911.h2
  Seq. No.
```

4269

```
Contig ID
                  3366 1.R1040
                  LIB3049-006-Q1-E1-H6
5'-most EST
                  4270
Seq. No.
                  3370 1.R1040
Contig ID
                  LIB3170-051-Q1-K1-A11
5'-most EST
                  4271
Seq. No.
                  3371 1.R1040
Contig ID
5'-most EST
                  zzp700836229.hl
Method
                  BLASTX
NCBI GI
                  g1707642
BLAST score
                  1420
E value
                  1.0e-158
Match length
                  571
% identity
                  48
NCBI Description
                  (Y07748) TMK [Oryza sativa]
                  4272
Seq. No.
                  3372 1.R1040
Contig ID
5'-most EST
                  LIB3167-031-P1-K1-H6
Method
                  BLASTX
                  g4098989
NCBI GI
                  833
BLAST score
                  3.0e-89
E value
Match length
                  215
                  71
% identity
                  (U81498) phenylalkylamine binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
                  4273
Seq. No.
                  3377 1.R1040
Contig ID
                  LIB3051-010-Q1-E1-B11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1685005
                  395
BLAST score
E value
                  4.0e-38
Match length
                  208
                  39
% identity
                  (U32644) immediate-early salicylate-induced
NCBI Description
                  glucosyltransferase [Nicotiana tabacum]
Seq. No.
                  4274
                  3378 1.R1040
Contig ID
5'-most EST
                  LIB3039-044-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g416662
BLAST score
                  216
E value
                  5.0e-17
Match length
                  173
                  40
% identity
                  21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin
NCBI Description
                  inhibitor homolog - soybean >gi_21909 emb_CAA39860_
                  (X56509) 21 kDa seed protein [Theobroma cacao]
                  4275
Seq. No.
```

3378 2.R1040

Contig ID

```
5'-most EST
                    LIB3039-049-Q1-E1-D10
                    4276
Seq. No.
Contig ID
                    3384 1.R1040
                    k117\overline{0}1205810.h1
5'-most EST
                    4277
Seq. No.
                    3386 1.R1040
Contig ID
5'-most EST
                    LIB3028-031-Q1-B1-C2
                    4278
Seq. No.
Contig ID
                    3388 1.R1040
5'-most EST
                    wvk7\overline{0}0680179.h2
                    BLASTX
Method
NCBI GI
                    g1001541
                    145
BLAST score
                    4.0e-09
E value
                    63
Match length
% identity
                    46
NCBI Description
                    (D64000) ABC transporter [Synechocystis sp.]
Seq. No.
                    4279
                    3390 1.R1040
Contig ID
5'-most EST
                    zsg701122962.h1
                    4280
Seq. No.
Contig ID
                    3394 1.R1040
5'-most EST
                    leu7\overline{0}1156190.h1
                    BLASTX
Method
                    g3170570
NCBI GI
BLAST score
                    155
                    6.0e-10
E value
                    107
Match length
% identity
                    35
                    (AF058302) FrnE [Streptomyces roseofulvus]
NCBI Description
                    4281
Seq. No.
Contig ID
                    3394 2.R1040
5'-most EST
                    LIB3170-058-Q1-K1-F5
                    4282
Seq. No.
                    3398 1.R1040
Contig ID
5'-most EST
                    leu7\overline{0}1153547.h1
                    BLASTX
Method
NCBI GI
                    g3845099
BLAST score
                    148
                    5.0e-09
E value
Match length
                    203
% identity
NCBI Description
                    (AE001373) predicted secreted protein [Plasmodium
                    falciparum]
Seq. No.
                    4283
Contig ID
                    3398 2.R1040
5'-most EST
                    gsv7\overline{0}1046010.h1
```

4284

Seq. No.

```
Contig ID
                   3399 1.R1040
                  uC-gmflminsoy093c05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2664214
BLAST score
                  1307
E value
                  1.0e-144
Match length
                  633
% identity
                  47
                  (AJ222646) G2484-1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4285
                  3399 5.R1040
Contig ID
5'-most EST
                  taw700654495.hl
Method
                  BLASTX
NCBI GI
                  q2664214
BLAST score
                  293
E value
                   4.0e-26
Match length
                  233
% identity
                  34
                  (AJ222646) G2484-1 [Arabidopsis thaliana]
NCBI Description
                  4286
Seq. No.
                  3400 1.R1040
Contig ID
                  LIB3107-022-Q1-K1-E8
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2605886
BLAST score
                  75
E value
                  1.0e-33
Match length
                  225
% identity
                  87
                  Pisum sativum dormancy-associated protein (DRM1) mRNA,
NCBI Description
                  complete cds
                  4287
Seq. No.
Contig ID
                  3400 2.R1040
5'-most EST
                  jC-gmro02910046d03a1
Method
                  BLASTN
                  g2995991
NCBI GI
                  52
BLAST score
                  3.0e-20
E value
                  68
Match length
                  94
% identity
NCBI Description
                  Arabidopsis thaliana dormancy-associated protein (DRM1)
                  gene, complete cds
                  4288
Seq. No.
                  3400 4.R1040
Contig ID
5'-most EST
                  LIB3049-013-Q1-E1-G7
Method
                  BLASTN
                  g2605886
NCBI GI
BLAST score
                  56
E value
                  2.0e-22
Match length
                  172
% identity
                  Pisum sativum dormancy-associated protein (DRM1) mRNA,
NCBI Description
                  complete cds
```

```
4289
Seq. No.
                   3400 5.R1040
Contig ID
                   jC-gmf102220091e01a1
5'-most EST
                   4290
Seq. No.
                   3400 6.R1040
Contig ID
                   jC-gmst02400049b11a1
5'-most EST
                  BLASTN
Method
NCBI GI
                   q2605886
BLAST score
                   56
                   1.0e-22
E value
Match length
                  182
                   87
% identity
                  Pisum sativum dormancy-associated protein (DRM1) mRNA,
NCBI Description
                   complete cds
                   4291
Seq. No.
Contig ID
                   3401 1.R1040 ·
                  LIB3109-006-Q1-K1-D12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3914467
BLAST score
                  1921
                   0.0e+00
E value
Match length
                   482
                  79
% identity
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
                  tabacum]
                   4292
Seq. No.
                   3401 3.R1040
Contig ID
5'-most EST
                  uxk7\overline{0}0669951.h1
                  BLASTX
Method
NCBI GI
                  g3914468
BLAST score
                  200
                  1.0e-19
E value
Match length
                  89
% identity
                   67
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot
                  >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus
                  carota]
                   4293
Seq. No.
Contig ID
                   3403 1.R1040
                  leu701149929.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q625547
BLAST score
                  1041
E value
                  1.0e-113
Match length
                  246
                  80
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I - common tobacco
                  >gi_493723_emb_CAA45523_ (X64198) photosystem I
                  light-harvesting chlorophyll a/b-binding protein [Nicotiana
```

tabacum]

Contig ID

5'-most EST

```
4294
Seq. No.
                   3403 2.R1040
Contig ID
                   epx7\overline{0}1104535.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g625547
BLAST score
                   144
                   7.0e-09
E value
                   66
Match length
% identity
                   50
                  chlorophyll a/b-binding protein type I - common tobacco
NCBI Description
                   >gi_493723_emb_CAA45523_ (X64198) photosystem I
                   light-harvesting chlorophyll a/b-binding protein [Nicotiana
                   tabacum]
                   4295
Seq. No.
                   3403 5.R1040
Contig ID
                   LIB3106-030-Q1-K1-G12
5'-most EST
Method
                   BLASTX
NCBI GI
                  g625547
BLAST score
                   301
E value
                   1.0e-27
Match length
                   97
% identity
                   63
NCBI Description
                  chlorophyll a/b-binding protein type I - common tobacco
                   >gi_493723_emb_CAA45523_ (X64198) photosystem I
                   light-harvesting chlorophyll a/b-binding protein [Nicotiana
                   tabacum]
                   4296
Seq. No.
                   3407 1.R1040
Contig ID
5'-most EST
                   zpv700761975.h1
Method
                   BLASTX
NCBI GI
                   g2352084
BLAST score
                   323
                   9.0e-30
E value
Match length
                   162
% identity
                   48
NCBI Description
                   (U96613) serine/threonine kinase [Arabidopsis thaliana]
                   4297
Seq. No.
                   3408 1.R1040
Contig ID
5'-most EST
                   LIB3028-030-Q1-B1-F12
                   4298
Seq. No.
                   3409 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220106h05a1
Method
                   BLASTX
NCBI GI
                   g3293031
BLAST score
                   1371
E value
                   1.0e-152
Match length
                   441
% identity
                   55
NCBI Description
                  (AJ007574) amino acid carrier [Ricinus communis]
Seq. No.
                   4299
```

3409 2.R1040

jC-gmf102220127b05d1

5'-most EST

```
BLASTX
Method
                   g4164408
NCBI GI
BLAST score
                   218
                   2.0e-17
E value
Match length
                   66
% identity
                   50
                  (AJ132228) amino acid carrier [Ricinus communis]
NCBI Description
                   4300
Seq. No.
Contig ID
                   3409 3.R1040
                   jC-gmf102220088d03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4164408
BLAST score
                   149
                   1.0e-09
E value
Match length
                   46
                   65
% identity
                   (AJ132228) amino acid carrier [Ricinus communis]
NCBI Description
                   4301
Seq. No.
Contig ID
                   3409 4.R1040
5'-most EST
                   pcp700991253.hl
                   4302
Seq. No.
Contig ID
                   3410 1.R1040
5'-most EST
                   uC-gmrominsoy279b04b1
Method
                   BLASTX
NCBI GI
                   q3281853
                   1167
BLAST score
                   1.0e-128
E value
Match length
                   259
% identity
                   92
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   4303
Seq. No.
Contig ID
                   3410 2.R1040
5'-most EST
                   hyd7\overline{0}0730125.h1
Method
                   BLASTX
NCBI GI
                   q3281853
BLAST score
                   318
                   4.0e-29
E value
Match length
                   62
% identity
                   97
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   4304
Seq. No.
Contig ID
                   3410 3.R1040
5'-most EST
                   jC-gmst02400069e07a1
Seq. No.
                   4305
                   3410 7.R1040
Contig ID
5'-most EST
                   kmv700738573.h1
                   4306
Seq. No.
                   3410 8.R1040
Contig ID
```

pmv700889945.h1

5'-most EST

```
4307
Seq. No.
                   3411 1.R1040
Contig ID
5'-most EST
                   LIB3049-004-Q1-E1-B11
                   4308
Seq. No.
                   3411 2.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1145786.h1
Seq. No.
                   4309
                   3415 1.R1040
Contig ID
5'-most EST
                   fua701038164.hl
Method
                   BLASTX
NCBI GI
                   q3281861
                   303
BLAST score
E value
                   1.0e-27
Match length
                   124
% identity
                   47
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   4310
Seq. No.
                   3415 2.R1040
Contig ID
                   ckk700605834.h2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4572681
                   209
BLAST score
E value
                   8.0e-17
Match length
                   65
                   57
% identity
                   (AC006954) putative ubiquitin carboxyl terminal hydrolase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   4311
                   3418_1.R1040
Contig ID
5'-most EST
                   uC-gmropic040a03b1
Seq. No.
                   4312
Contig ID
                   3418 3.R1040
5'-most EST
                   rca701002429.h1
                   4313
Seq. No.
Contig ID
                   3419 1.R1040
5'-most EST
                   leu7\overline{0}1152577.h1
                   4314
Seq. No.
                   3420 1.R1040
Contig ID
5'-most EST
                   LIB3051-109-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g3402701
BLAST score
                   302
E value
                   9.0e-28
Match length
                   105
% identity
                   64
NCBI Description
                   (AC004261) unknown protein [Arabidopsis thaliana]
                   4315
Seq. No.
Contig ID
                   3424 1.R1040
```

jC-gmro02910002e09a1

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                   q4467128
BLAST score
                   635
E value
                   4.0e-66
Match length
                   242
% identity
                   49
NCBI Description
                   (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                   4316
Contig ID
                   3431 1.R1040
5'-most EST
                  LIB3139-004-P1-N1-B5
                   4317
Seq. No.
Contig ID
                   3432 1.R1040
5'-most EST
                   uC-qmflminsoy031b04b1
                  BLASTX
Method
NCBI GI
                   q2497753
BLAST score
                   327
                   5.0e-30
E value
Match length
                   114
% identity
                   54
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                   [Prunus dulcis]
Seq. No.
                   4318
Contig ID
                   3433 1.R1040
5'-most EST
                  LIB3106-006-Q1-K2-F9
Method
                  BLASTX
NCBI GI
                  q3660471
BLAST score
                   2865
                   0.0e + 00
E value
Match length
                   630
% identity
                   85
                   (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   4319
Seq. No.
Contig ID
                   3433 3.R1040
5'-most EST
                  LIB3138-061-Q1-N1-H5
Method
                  BLASTX
NCBI GI
                  q3660471
BLAST score
                   304
E value
                   2.0e-27
Match length
                  108
% identity
                   56
NCBI Description
                   (AJ001809) succinate dehydrogenase flavoprotein alpha
                   subunit [Arabidopsis thaliana]
                   4320
Seq. No.
Contig ID
                   3437 1.R1040
5'-most EST
                  LIB3028-030-Q1-B1-E9
                  4321
Seq. No.
Contig ID
                  3439 1.R1040
5'-most EST
                  trc700563801.h1
```

```
g2244749
NCBI GI
BLAST score
                   2170
                   0.0e + 00
E value
Match length
                   471
% identity
                   87
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                   4322
Seq. No.
                   3439 2.R1040
Contig ID
                  _rlr700898970.h1
5'-most EST
Method
                   BLASTX
                   g2244749
NCBI GI
BLAST score
                   264
E value
                   2.0e-22
Match length
                   146
% identity
                   83
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4323
                   3439 3.R1040
Contig ID
5'-most EST
                   jC-gmle01810087a12a1
Method
                   BLASTX
                   g2244749
NCBI GI
BLAST score
                   611
E value
                   1.0e-63
                   128
Match length
% identity
                   88
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                   4324
Seq. No.
                   3441 1.R1040
Contig ID
                   LIB3028-030-Q1-B1-B7
5'-most EST
                   4325
Seq. No.
                   3442 1.R1040
Contig ID
5'-most EST
                   fde7\overline{0}0876469.h1
Method
                   BLASTX
                   g2443329
NCBI GI
BLAST score
                   664
E value
                   3.0e-69
                   290
Match length
% identity
                   51
                  (D86122) Mei2-like protein [Arabidopsis thaliana]
NCBI Description
                   4326
Seq. No.
                   3443 1.R1040
Contig ID
5'-most EST
                   LIB3109-029-Q1-K1-F9
Seq. No.
                   4327
                   3443 2.R1040
Contig ID
                   zhf700958208.hl
5'-most EST
Seq. No.
                   4328
                   3444 1.R1040
Contig ID
                   hrw701063179.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3122673
```

```
BLAST score
                   855
E value
                   6.0e-92
Match length
                   204 -
                   79
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   4329
Seq. No.
Contig ID
                   3444_2.R1040
                  LIB3170-004-Q1-K1-D9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2982318
BLAST score
                  536
E value
                   2.0e-54
Match length
                  182
% identity
                   61
                   (AF051244) probable 60S ribosomal protein L15 [Picea
NCBI Description
                  mariana]
                   4330
Seq. No.
Contig ID
                   3444 3.R1040
5'-most EST
                   jC-gmro02910067a02a1
Method
                  BLASTX
NCBI GI
                  g3122673
BLAST score
                   664
E value
                  1.0e-85
Match length
                  203
                   78
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   4331
                   3444 4.R1040
Contig ID
                  LIB3106-107-Q1-K1-E7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3122673
BLAST score
                  830
E value
                  5.0e-89
Match length
                  204
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   4332 `
Seq. No.
                  3444 5.R1040
Contig ID
                  LIB3138-070-P1-N1-D1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3122673
BLAST score
                  267
                  4.0e-23
E value
                  55
Match length
% identity
                  91
NCBI Description
                  60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  4333
Seq. No.
                  3444 6.R1040
Contig ID
```

Contig ID

```
5'-most EST
                    vzy700753239.h1
                    4334
Seq. No.
                    3444 9.R1040
Contig ID
5'-most EST
                    leu7\overline{0}1144830.h1
                    BLASTX
Method
NCBI GI
                    g3122673
BLAST score
                    233
E value
                    1.0e-19
Match length
                    96
% identity
                    55
NCBI Description
                    60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                    (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                    4335
                    3446 2.R1040
Contig ID
5'-most EST
                    LIB3028-030-Q1-B1-C12
                    4336
Seq. No.
Contig ID
                    3447 1.R1040
5'-most EST
                    LIB3049-048-Q1-E1-A6
Seq. No.
                    4337
Contig ID
                    3447 3.R1040
5'-most EST
                    LIB3093-053-Q1-K1-E3
                    4338
Seq. No.
                    3448 1.R1040
Contig ID
5'-most EST
                    g4397081
Seq. No.
                    4339
                    3453 1.R1040
Contig ID
5'-most EST
                    uC-gmflminsoy041f03b1
                    BLASTX
Method
NCBI GI
                    g2829204
BLAST score
                    337
E value
                    2.0e-31
Match length
                    123
                    51
% identity
                    (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                    4340
                    3454 1.R1040
Contig ID
5'-most EST
                    zhf700954310.hl
Method
                    BLASTX
NCBI GI
                    q1362105
BLAST score
                    529
E value
                    1.0e-53
Match length
                    257
% identity
                    42
                   alcohol dehydrogenase (EC 1.1.1.1) - common tobacco (fragment) >gi_551257_emb_CAA57446_ (X81853) alcohol
NCBI Description
                    dehydrogenase [Nicotiana tabacum]
Seq. No.
                    4341
```

3455 1.R1040

NCBI GI

```
5'-most EST
                    LIB3028-030-Q1-B1-D10
Method
                    BLASTX
NCBI GI
                    a1708971
BLAST score
                    351
                    6.0e-33
E value
Match length
                    162
                    44
% identity
NCBI Description
                    (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
                    (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                    >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
                    black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                    (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                    serotina] >gi 1090776 prf 2019441A mandelonitrile lyase
                    [Prunus serotina]
Seq. No.
                    4342
                    3462 2.R1040
Contig ID
5'-most EST
                    LIB3106-048-Q1-K1-A6
Method
                    BLASTX
NCBI GI
                    q2827712
BLAST score
                    711
E value
                    1.0e-128
Match length
                    265
                    79
% identity
NCBI Description
                    (AL021684) endoxyloglucan tranferase-like protein
                    [Arabidopsis thaliana]
                    4343
Seq. No.
                    3465 1.R1040
Contig ID
5'-most EST
                    wvk700681629.hl
                    BLASTX
Method
NCBI GI
                    q3600032
BLAST score
                    290
E value
                    5.0e-26
Match length
                    161
% identity
                    42
                    (AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:
NCBI Description
                    ATP-synt B.hmm, score: 10.89) [Arabidopsis thaliana]
Seq. No.
Contig ID
                    3467 1.R1040
                    leu701154244.h1
5'-most EST
Method
                    BLASTN
NCBI GI
                    g2961297
BLAST score
                    49
E value
                    5.0e-18
Match length
                    305
% identity
                    86
NCBI Description
                   Cicer arietinum mRNA for unidentified protein
Seq. No.
                    4345
                    3467 2.R1040
Contig ID
5'-most EST
                    uC-gmropic011g03b1
Method
                    BLASTN
```

q2961297

5'-most EST

```
45
BLAST score
                   8.0e-16
E value
                   89
Match length
% identity
                   93
                   Cicer arietinum mRNA for unidentified protein
NCBI Description
                   4346
Seq. No.
                   3467 4.R1040
Contig ID
                   uC-gmropic016g06b1
5'-most EST
Seq. No.
                   4347
Contig ID
                   3468_1.R1040
                   g4313544
5'-most EST
Method
                   BLASTX
NCBI GI
                   g548437
BLAST score
                   164
E value
                   4.0e-11
Match length
                   103
                   40
% identity
NCBI Description
                   OSH1 PROTEIN >gi_1078479_pir__S53463 SWH1 protein (version
                   1) - yeast (Saccharomyces cerevisiae) >gi_456143 (L28920)
                   Oshlp [Saccharomyces cerevisiae]
                   4348
Seq. No.
Contig ID
                   3469 1.R1040
5'-most EST
                   LIB3030-003-Q1-B1-H5
                   4349
Seq. No.
Contig ID
                   3472 1.R1040
                   jC-g\overline{m}ro02910039g08a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245378
BLAST score
                   1106
E value
                   1.0e-121
Match length
                   545
% identity
                   54
NCBI Description
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
                   4350
Seq. No.
                   3472 2.R1040
Contig ID
                   jC-gmro02910046h09d1
5'-most EST
                   4351
Seq. No.
                   3476 1.R1040
Contig ID
                   LIB3028-029-Q1-B1-G4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3193298
BLAST score
                   312
E value
                   2.0e-28
Match length
                   120
                   48
% identity
NCBI Description
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
                   4352
Seq. No.
                   3476 2.R1040
Contig ID
```

 $epx7\overline{0}1104722.h1$ 

Seq. No.

4359

```
4353
Seq. No.
Contig ID
                   3478 1.R1040
5'-most EST
                   LIB3092-037-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   g4262239
                   980
BLAST score
                   1.0e-106
E value
Match length
                   232
                   81
% identity
                   (AC006200) putative membrane transporter [Arabidopsis
NCBI Description
                   thaliana]
                   4354
Seq. No.
                   3480 1.R1040
Contig ID
5'-most EST
                   LIB3170-088-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   q2245066
BLAST score
                   774
E value
                   5.0e-82
Match length
                   426
% identity
                   39
NCBI Description
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
                   4355
Seq. No.
Contig ID
                   3480 4.R1040
5'-most EST
                   gsv701046710.hl
                   4356
Seq. No.
Contig ID
                   3483 1.R1040
                   euj700697977.h1
5'-most EST
Seq. No.
                   4357
Contig ID
                   3484 1.R1040
                   sat701007584.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2499805
BLAST score
                   173
                   8.0e-12
E value
Match length
                   201
                   28
% identity
NCBI Description
                  PROTEIN ARGININE N-METHYLTRANSFERASE 2
                   >gi_1655625_emb_CAA67599_ (X99209) arginine
                  methyltransferase [Homo sapiens]
                   4358
Seq. No.
                   3484 2.R1040
Contig ID
5'-most EST
                  LIB3051-015-Q1-E1-H10
Method
                   BLASTX
NCBI GI
                   a2499804
BLAST score
                   388
E value
                   3.0e-37
Match length
                  163
% identity
                   48
                  PROTEIN ARGININE N-METHYLTRANSFERASE 1 >gi 1390025 (U60882)
NCBI Description
                  protein arginine N-methyltransferase [Rattus norvegicus]
```

Contig ID

```
Contig ID
                  3486 1.R1040
                  LIB3107-014-Q1-K1-B5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1531758
BLAST score
                  360
                  7.0e-34
E value
                  105
Match length
% identity
                   68
                   (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                  unknown protein [Arabidopsis thaliana]
                   4360
Seq. No.
Contig ID
                   3486 2.R1040
                   zhf700953621.hl
5'-most EST
Seq. No.
                   4361
                  3487 1.R1040
Contig ID
                  uaw700666850.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2341042
BLAST score
                  231
                  2.0e-18
E value
                  292
Match length
% identity
                   30
                   (AC000104) F19P19.26 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4362
                  3488 1.R1040
Contig ID
                   smc7\overline{0}0746571.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2833220
BLAST score
                  247
                  5.0e-21
E value
                  80
Match length
                  53
% identity
                  HYPOTHETICAL 35.7 KD PROTEIN IN DNL4-SLG1 INTERGENIC REGION
NCBI Description
                  >gi_2132030_pir__S61990 hypothetical protein YOR006c -
                  yeast (Saccharomyces cerevisiae) >gi 1151002 (U43491)
                  hypothetical protein UND313 [Saccharomyces cerevisiae]
                  >gi_1420098_emb_CAA99194_ (Z74914) ORF YOR006c
                   [Saccharomyces cerevisiae]
Seq. No.
                   4363
Contig ID
                  3494 1.R1040
5'-most EST
                  jC-gmst02400027g11a1
Method
                  BLASTX
NCBI GI
                  g3004549
BLAST score
                   500
E value
                  3.0e-50
Match length
                  165
                   61
% identity
NCBI Description
                   (AC003673) unknown protein [Arabidopsis thaliana]
                  >gi 4185152 (AC005724) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                   4364
```

3494 2.R1040

```
5'-most EST
                  uC-gmflminsoy055h11b1
Method
                  BLASTX
NCBI GI
                  q3004549
                  597
BLAST score
                   2.0e-61
E value
Match length
                  278
                   44
% identity
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4185152 (AC005724) unknown protein [Arabidopsis
                  thaliana]
                  4365
Seq. No.
                  3494 3.R1040
Contig ID
                  uC-gmropic019g05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3004549
BLAST score
                  187
                  5.0e-14
E value
                  56
Match length
% identity
                   64
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4185152 (AC005724) unknown protein [Arabidopsis
                  thaliana]
                  4366
Seq. No.
                  3494 5.R1040
Contig ID
5'-most EST
                  dpv7\overline{0}1099759.h1
Method
                  BLASTX
NCBI GI
                  g3004549
BLAST score
                  149
                  3.0e-18
E value
Match length
                  73
                  68
% identity
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4185152 (AC005724) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  4367
Contig ID
                  3495 1.R1040
5'-most EST
                  zhf700956320.h1
Method
                  BLASTX
NCBI GI
                  q3559805
BLAST score
                  473
E value
                  3.0e-47
Match length
                  97
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  4368
Contig ID
                  3496 1.R1040
                  LIB3139-113-P1-N1-E11
5'-most EST
Method
                  BLASTX
                  g2459443
NCBI GI
BLAST score
                  736
                  5.0e-78
E value
```

210

Match length

NCBI GI

```
% identity
                   67
                   (AC002332) putative NAD(P)-dependent cholesterol
NCBI Description
                  dehydrogenase [Arabidopsis thaliana]
                   4369
Seq. No.
                   3496 2.R1040
Contig ID
                  epx701106813.hl
5'-most EST
                  BLASTX
Method
                  g2459443
NCBI GI
                   233
BLAST score
                  9.0e-20
E value
                  51
Match length
                  84
% identity
                   (AC002332) putative NAD(P)-dependent cholesterol
NCBI Description
                  dehydrogenase [Arabidopsis thaliana]
                   4370
Seq. No.
Contig ID
                   3497 1.R1040
                  hrw701063210.h1
5'-most EST
                  BLASTN
Method
                  g3860322
NCBI GI
BLAST score
                   110
                   1.0e-54
E value
                  242
Match length
                  86
% identity
NCBI Description
                  Cicer arietinum mRNA for hypothetical protein, clone
                  Can40-1
                   4371
Seq. No.
Contig ID
                   3497 2.R1040
                  yza700764025.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3860322
                   44
BLAST score
                  3.0e-15
E value
                   64
Match length
% identity
                  92
NCBI Description
                  Cicer arietinum mRNA for hypothetical protein, clone
                  Can40-1
                   4372
Seq. No.
                   3498 1.R1040
Contig ID
5'-most EST
                  g4397123
Method
                  BLASTX
NCBI GI
                  g3646451
BLAST score
                  172
                  7.0e-12
E value
Match length
                  96
                  39
% identity
                  (AL031603) mRNA cap methyltransferase [Schizosaccharomyces
NCBI Description
                  pombe]
                  4373
Seq. No.
Contig ID
                  3499 1.R1040
5'-most EST
                  LIB3050-008-Q1-E1-A7
Method
                  BLASTX
```

g4079809

5'-most EST

```
BLAST score
                  285
                  3.0e-25
E value
Match length
                  196
% identity
                  3
                  (AF071172) HERC2 [Homo sapiens]
NCBI Description
                  4374
Seq. No.
                  3500 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220065e10d1
                  4375
Seq. No.
                  3502 1.R1040
Contig ID
                  ncj700981882.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q131187
BLAST score
                  732
E value
                  2.0e-77
                  220
Match length
                  67
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi_72681_pir__F1SP3 photosystem I chain III precursor -
                  spinach >gi_21303_emb_CAA31523_ (X13133) PSI subunit IV
                  preprotein (AA -77 to 154) [Spinacia oleracea]
                  >gi_226166_prf__1413236A photosystem I reaction center IV
                   [Spinacia oleracea]
Seq. No.
                  4376
                  3506 1.R1040
Contig ID
5'-most EST
                  LIB3028-029-Q1-B1-C7
                  4377
Seq. No.
                  3508 1.R1040
Contig ID
5'-most EST
                  zhf700965192.hl
                  BLASTX
Method
NCBI GI
                  g2253583
BLAST score
                  172
E value
                  3.0e-12
Match length
                  82
% identity
NCBI Description
                  (U78721) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  4378
                  3514 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy053c08b1
Method
                  BLASTX
NCBI GI
                  g886130
BLAST score
                  561
E value
                  2.0e-80
Match length
                  327
                  47
% identity
                  (U28148) putative pectinesterase [Medicago sativa]
NCBI Description
Seq. No.
                  4379
                  3514 2.R1040
Contig ID
```

LIB3028-029-Q1-B1-D4

```
4380
Seq. No.
                   3515 1.R1040
Contig ID
                  leu701151350.hl
5'-most EST
                  BLASTN
Method
                  g3264758
NCBI GI
BLAST score
                  116
                   2.0e-58
E value
                  360
Match length
                  83
% identity
NCBI Description Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA,
                  complete cds
                   4381
Seq. No.
                   3517 2.R1040
Contig ID
                  LIB3139-056-P1-N1-B1
5'-most EST
Seq. No.
                  4382
                  3518 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910022g03a1
Method
                  BLASTX
                  g3075392
NCBI GI
                  179
BLAST score
                  5.0e-16
E value
                  71
Match length
                   66
% identity
                   (AC004484) putative steroid dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                   4383
Seq. No.
Contig ID
                  3522 1.R1040
5'-most EST
                  LIB3056-010-Q1-N1-A1
                  BLASTX
Method
NCBI GI
                  g3834310
BLAST score
                  716
                  1.0e-75
E value
Match length
                  141
% identity
                  99
NCBI Description
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                  gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                  gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  4384
Contig ID
                  3522 2.R1040
5'-most EST
                  LIB3056-004-Q1-N1-A12
Method
                  BLASTX
NCBI GI
                  g3834310
BLAST score
                  712
E value
                  4.0e-75
Match length
                  141
                  99
% identity
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                  gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                  gb_N37265, gb_H36151, gb_Z34711, gb_AAO40983, and gb_T22122
                  come from this gene. [Arabidopsis thaliana]
```

4385

Seq. No.

NCBI GI

```
Contig ID
                   3522 3.R1040
5'-most EST
                   pxt700943960.h1
Method
                   BLASTX
NCBI GI
                   q3834310
BLAST score
                   240
E value
                   8.0e-30
Match length
                   71
% identity
NCBI Description
                    (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                   gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb_AAO40983, and gb_T22122 come from this gene. [Arabidopsis thaliana]
                   4386
Seq. No.
Contig ID
                   3524 1.R1040
5'-most EST
                   LIB3028-029-Q1-B1-B12
Seq. No.
                   4387
Contig ID
                   3527 1.R1040
5'-most EST
                   V4R-02-Q1-B1-D2
Method
                   BLASTX
NCBI GI
                   g3702631
BLAST score
                   350
E value
                   7.0e-33
Match length
                   214
% identity
                   36
                    (AL031824) protein transport protein sec23 homolog
NCBI Description
                    [Schizosaccharomyces pombe]
                   4388
Seq. No.
Contig ID
                   3529 1.R1040
5'-most EST
                   jex700903469.hl
                   4389
Seq. No.
Contig ID
                   3530_1.R1040
5'-most EST
                   jC-gmle01810020e10d1
                   4390
Seq. No.
Contig ID
                   3530 2.R1040
5'-most EST
                   LIB3092-004-Q1-K1-A3
Seq. No.
                   4391
Contig ID
                   3531 1.R1040
5'-most EST
                   crh700855207.hl
Method
                   BLASTX
NCBI GI
                   g3757523
BLAST score
                   247
E value
                   1.0e-20
Match length
                   61
% identity
                   74
                   (AC005167) putative transportin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4392
                   3531 2.R1040
Contig ID
5'-most EST
                   ncj700981843.hl
Method
                   BLASTX
```

g3757523

```
BLAST score
                   345
                   2.0e-36
E value
                   104
Match length
% identity
                   73
                   (AC005167) putative transportin [Arabidopsis thaliana]
NCBI Description
                   4393
Seq. No.
                   3533 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{1}38-119-Q1-N1-G1
Method
                   BLASTX
NCBI GI
                   q2598589
BLAST score
                   426
E value
                   8.0e-42
Match length
                   143
% identity
                   58
                   (Y15367) MtN19 [Medicago truncatula]
NCBI Description
                   4394
Seq. No.
Contig ID
                   3533 2.R1040
5'-most EST
                   LIB3051-087-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2598589
BLAST score
                   359
E value
                   4.0e-34
Match length
                   134
                   51
% identity
NCBI Description
                   (Y15367) MtN19 [Medicago truncatula]
                   4395
Seq. No.
Contig ID
                   3533 3.R1040
5'-most EST
                   LIB3051-062-Q1-K1-H4
Method
                   BLASTX
                   g2598589
NCBI GI
BLAST score
                   220
E value
                   8.0e-18
Match length
                   75
% identity
                   51
                   (Y15367) MtN19 [Medicago truncatula]
NCBI Description
                   4396
Seq. No.
Contig ID
                   3536 1.R1040
5'-most EST
                   LIB3051-077-Q1-K1-D11
Method
                   BLASTN
NCBI GI
                   g20355
BLAST score
                   49
                   2.0e-18
E value
Match length
                   125
% identity
                   85
                   Rice rgp1 mRNA for a ras-related GTP-binding protein
NCBI Description
                   4397
Seq. No.
Contig ID
                   3537 1.R1040
                   jC-g\overline{m}le01810080e09d1
5'-most EST
Method
                   BLASTX
                   g2739382
NCBI GI
BLAST score
                   396
```

3.0e-38

E value

\*\*\*\*\*

```
233
 Match length
                    42
 % identity
                    (AC002505) myosin heavy chain-like protein [Arabidopsis
 NCBI Description
                    thaliana]
                    4398
 Seq. No.
                    3538 1.R1040
 Contig ID
                    uaw700660890.h1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g1256509
 BLAST score
                    546
 E value
                    1.0e-105
 Match length
                    220
 % identity
                    81
                   (X92943) pectate lyase [Musa acuminata]
 NCBI Description
                    4399
 Seq. No.
                    3538 2.R1040
 Contig ID
                    LIB3028-029-Q1-B1-A9
 5'-most EST
                    BLASTX
 Method
                    g2463509
 NCBI GI
 BLAST score
                    975
                    1.0e-106
 E value
 Match length
                    226
 % identity
                    77
 NCBI Description
                   (Y09541) pectate lyase [Zinnia elegans]
                    4400
 Seq. No.
                    3539 1.R1040
 Contig ID
 5'-most EST
                    pxt700945309.h1
                    BLASTX
 Method
                    g2880043
 NCBI GI
                    942
 BLAST score
                    1.0e-102
 E value
                    272
 Match length
                    65
 % identity
NCBI Description
                    (AC002340) putative 3-hydroxyisobutyryl-coenzyme A.
                    hydrolase [Arabidopsis thaliana]
                    4401
 Seq. No.
                    3539 2.R1040
 Contig ID
 5'-most EST
                    bth700843808.h1
                    4402
 Seq. No.
                    3542 1.R1040
 Contig ID
                    zsg701125459.hl
 5'-most EST
 Seq. No.
                    4403
                    3543 1.R1040
 Contig ID
                    LIB3028-028-Q1-B1-H8
 5'-most EST
 Method
                    BLASTX
                    g4263781
 NCBI GI
 BLAST score
                    346
                    2.0e-32
 E value
                    191
 Match length
                    41
 % identity
                   (AC006068) putative membrane transport protein [Arabidopsis
 NCBI Description
```

5'-most EST

## thaliana] Seq. No. 4404 Contig ID 3545 1.R1040 5'-most EST bth700843502.h1 Method BLASTX NCBI GI g100535 BLAST score 313 E value 2.0e-28 Match length 79 % identity 78 hypothetical protein - swollen duckweed NCBI Description >gi\_1929057\_emb\_CAA32236\_ (X14075) longest ORF (1) [Lemna gibba] 4405 Seq. No. Contig ID 3546 1.R1040 LIB3051-065-Q1-K1-E9 5'-most EST Method BLASTX NCBI GI g481762 BLAST score 249 E value 3.0e-21 Match length 135 35 % identity beta-adaptin 1 - fruit fly (Drosophila melanogaster) NCBI Description >gi\_434902\_emb\_CAA53509\_ (X75910) beta-adaptin Drosophila 1 [Drosophila melanogaster] 4406 Seq. No. 3547 1.R1040 Contig ID 5'-most EST jC-qmst02400046a06a1 Method BLASTX NCBI GI g2339978 BLAST score 1270 E value 1.0e-150 Match length 357 % identity 75 NCBI Description (Y11336) RGA1 protein [Arabidopsis thaliana] 4407 Seq. No. 3547 2.R1040 Contig ID 5'-most EST $vzy7\overline{0}0751203.h1$ Method BLASTX NCBI GI g2569938 BLAST score 217 3.0e-17 E value Match length 47 % identity NCBI Description (Y15193) GAI [Arabidopsis thaliana] 4408 Seq. No. Contig ID 3549 1.R1040 5'-most EST trc700563015.hl Seq. No. 4409 3552 1.R1040 Contig ID

LIB3107-080-Q1-K1-D10

```
BLASTX
Method
                   g4544369
NCBI GI
                   643
BLAST score
                   6.0e-67
E value
                   274
Match length
                   48
% identity
                   (AC006920) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   4410
Seq. No.
                   3555 1.R1040
Contig ID
                   LIB3106-079-P1-K1-D3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g537313
BLAST score
                   651
                   3.0e-68
E value
                   151
Match length
                   83
% identity
                   (L36159) unknown protein [Medicago sativa]
NCBI Description
                   4411
Seq. No.
                   3558 1.R1040
Contig ID
                   leu7\overline{0}1150138.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2266666
BLAST score
                   686
                   5.0e-72
E value
Match length
                   227
% identity
                   58
                   (Y14202) hypothetical protein [Hordeum vulgare]
NCBI Description
                   4412
Seq. No.
                   3558 2.R1040
Contig ID
                   jC-gmle01810085f08a1
5'-most EST
Method
                   BLASTX
                   g4335745
NCBI GI
BLAST score
                   576
E value
                   6.0e-59
Match length
                   308
                   40
% identity
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   4413
Seq. No.
                   3558 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy138d07b1
Method
                   BLASTX
NCBI GI
                   g4115368
BLAST score
                   510
E value
                   1.0e-51
                   170
Match length
% identity
                   55
                   (AC005957) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   4414
Seq. No.
                   3558 4.R1040
Contig ID
                   LIB3\overline{1}70-085-Q1-J1-D6
5'-most EST
```

% identity

```
4415
Seq. No.
Contig ID
                   3558 5.R1040
5'-most EST
                   jC-gmro02910032f01a1
Method
                   BLASTX
NCBI GI
                   g4335745
BLAST score
                   221
E value
                   2.0e-25
Match length
                   162
% identity
                   41
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.
                   4416
                   3558 8.R1040
Contig ID
5'-most EST
                   leu701149426.h1
Method
                   BLASTX
NCBI GI
                   g4115367
BLAST score
                   167
E value
                   1.0e-11
Match length
                   82
% identity
                   43
NCBI Description
                   (AC005957) unknown protein [Arabidopsis thaliana]
Seq. No.
                   4417
Contig ID
                   3561_1.R1040
5'-most EST
                   uC-qmropic108f06b1
Method
                   BLASTX
NCBI GI
                   g1149595
BLAST score
                   207
E value
                   3.0e-16
Match length
                   141
                   35
% identity
NCBI Description
                   (Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase
                   [Brassica napus]
Seq. No.
                   4418
Contig ID
                   3562 1.R1040
5'-most EST
                   LIB3028-028-Q1-B1-G5
Method
                   BLASTX
NCBI GI
                   g4140691
BLAST score
                   350
E value
                   6.0e-33
Match length
                   148
% identity
                   (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
NCBI Description
Seq. No.
                   4419
                   3564 1.R1040
Contig ID
5'-most EST
                   zsq701123081.hl
Method
                   BLASTX
NCBI GI
                   q3298540
BLAST score
                   985
E value
                   1.0e-107
Match length
                   239
```

Seq. No.

```
NCBI Description
                  (AC004681) unknown protein [Arabidopsis thaliana]
                   4420
Seq. No.
Contig ID
                   3565 2.R1040
                   LIB3040-044-Q1-E1-F8
5'-most EST
Method
                   BLASTX
                   g3482979
NCBI GI
BLAST score
                   571
E value
                   2.0e-58
Match length
                   215
% identity
                   53
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4567258_gb_AAD23672.1_AC007070 21 (AC007070)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   4421
                   3565 3.R1040
Contig ID
5'-most EST
                  LIB3028-028-Q1-B1-G8
                   4422
Seq. No.
Contig ID
                   3568 1.R1040
                  LIB3053-009-Q1-N1-C1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2864612
BLAST score
                   518
                   3.0e-52
E value
Match length
                   229
                   48
% identity
NCBI Description
                   (AL021811) L-ascorbate peroxidase - like protein
                   [Arabidopsis thaliana] >gi_4049334_emb_CAA22559_ (AL034567)
                  L-ascorbate peroxidase-like protein [Arabidopsis thaliana]
                   4423
Seq. No.
                   3568 2.R1040
Contig ID
5'-most EST
                  LIB3106-106-Q1-K1-E12
Seq. No.
                   4424
                   3571 1.R1040
Contig ID
5'-most EST
                  LIB3028-028-Q1-B1-E3
Method
                  BLASTX
NCBI GI
                  q3894168
BLAST score
                   243
                   3.0e-20
E value
Match length
                   148
% identity
                   36
NCBI Description
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
                   thaliana]
Seq. No.
                   4425
Contig ID
                   3573 1.R1040
5'-most EST
                  LIB3028-028-01-B1-E5
Seq. No.
                   4426
Contig ID
                   3573 2.R1040
5'-most EST
                  jex700903945.hl
```

% identity

```
Contig ID
                   3575 1.R1040
5'-most EST
                   LIB3049-011-Q1-E1-F7
Method
                   BLASTX
                   q2289003
NCBI GI
                   1619
BLAST score
                   0.0e+00
E value
                   496
Match length
                   65
% identity
                   (AC002335) membrane transporter D1 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   4428
Seq. No.
                   3575 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810086b11d1
Seq. No.
                   4429
                  3579 1.R1040
Contig ID
                  LIB3167-077-P1-K2-E5
5'-most EST
Method
                   BLASTX
NCBI GI
                  g2582665
BLAST score
                   1377
                   1.0e-153
E value
Match length
                   336
                   82
% identity
                   (Z82983) thi [Citrus sinensis]
NCBI Description
                   4430
Seq. No.
                   3579 2.R1040
Contig ID
                  ncj700979158.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   q3212869
                   704
BLAST score
E value
                   2.0e-74
                  160
Match length
                   82
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4431
Contig ID
                   3579_3.R1040
                   jC-gmst02400052h01d1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g1289203
                  93
BLAST score
                  1.0e-44
E value
                  213
Match length
% identity
                  A.glutinosa mRNA for thiazole biosynthetic enzyme
NCBI Description
                   4432
Seq. No.
Contig ID
                   3579 4.R1040
5'-most EST
                   jC-gmro02910034h10d1
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  2167
E value
                  0.0e + 00
Match length
                  487
```

NCBI Description

```
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                   4433
Seq. No.
                   3579 5.R1040
Contig ID
5'-most EST
                   LIB3106-114-Q1-K1-B9
                   BLASTN
Method
                   g596077
NCBI GI
BLAST score
                   63
                   8.0e-27
E value
Match length
                   159
                   86
% identity
                   Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA,
NCBI Description
                   complete cds
                   4434
Seq. No.
                   3579 7.R1040
Contig ID
                   LIB3106-077-P1-K1-E6
5'-most EST
                   BLASTX
Method
                   g2582665
NCBI GI
BLAST score
                   216
                   5.0e-17
E value
Match length
                   115
                   65
% identity
                   (Z82983) thi [Citrus sinensis]
NCBI Description
Seq. No.
                   4435
Contig ID
                   3579 11.R1040
                   jC-gmst02400043c02a1
5'-most EST
Method
                   BLASTX
                   g3212869
NCBI GI
BLAST score
                   334
E value
                   3.0e-31
Match length
                   73
% identity
                   81
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4436
Contig ID
                   3581 1.R1040
                   epx701109079.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1617270
BLAST score
                   2744
E value
                   0.0e+00
Match length
                   659
                   76
% identity
                   (X94624) acyl-CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                   4437
Contig ID
                   3582 1.R1040
                   LIB3170-026-Q1-K1-B2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2511594
BLAST score
                   1026
                   1.0e-112
E value
                   233
Match length
% identity
                   85
```

(Y13694) multicatalytic endopeptidase complex, proteasome

precursor, beta subunit [Arabidopsis thaliana] >gi 2827525 emb CAA16533 (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi 3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

4438 Seq. No.

3585 1.R1040 Contig ID zzp700830591.hl 5'-most EST

BLASTX Method NCBI GI g2501460 BLAST score 442 4.0e-43 E value Match length 556 % identity 28

PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP NCBI Description

(UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC

PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP)

(HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE)

>gi 1545952 emb CAA96580 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]

>gi 4507857 ref\_NP\_003461.1 pUSP7\_ Herpes virus-associated

ubiquitin-specific protease

4439 Seq. No.

Contig ID 3586 1.R1040

5'-most EST LIB3139-107-P1-N1-B1

Method BLASTX q1403522 NCBI GI BLAST score 908 5.0e-98 E value 200 Match length % identity 81

(X57187) chitinase [Phaseolus vulgaris] $_{\rm ki}$ NCBI Description

4440 Seq. No.

3590 1.R1040 Contig ID 5'-most EST  $k117\overline{0}1205931.h1$ 

4441 Seq. No.

3591 1.R1040 Contig ID 5'-most EST  $vzy7\overline{0}0756151.h1$ 

Method BLASTX NCBI GI g1905910 BLAST score 714 1.0e-75 E value Match length 182 73 % identity

(AD000092) putative human phenylalanine tRNA synthetase NCBI Description

[Homo sapiens]

4442 Seq. No.

Contig ID 3593 1.R1040 5'-most EST rca701000704.hl

Method BLASTX NCBI GI q1589913 BLAST score 596

BLAST score

```
E value
                   9.0e-63
Match length
                   182
                   71
% identity
                   (U69694) ATP-sulfurylase precursor [Brassica oleracea]
NCBI Description
                   4443
Seq. No.
                   3594 1.R1040
Contig ID
                   LIB3170-061-Q1-J1-B8
5'-most EST
                   BLASTX
Method'
NCBI GI
                   g3183217
BLAST score
                   462
                   1.0e-45
E value
                   250
Match length
                   40
% identity
                   HYPOTHETICAL PROTEIN KIAA0103 >gi_285943_dbj_BAA03493_
NCBI Description
                   (D14659) KIAA0103 [Homo sapiens]
                   4444
Seq. No.
                   3594 2.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0987648.h1
Method
                   BLASTX
NCBI GI
                   g3319457
BLAST score
                   141
                   1.0e-08
E value
                   77
Match length
% identity
                   39
NCBI Description
                   (AF077542) contains similarity to O-linked GlcNAc
                   transferases [Caenorhabditis elegans]
                   4445
Seq. No.
                   3596_1.R1040
Contig ID
5'-most EST
                   g5677719
Method
                   BLASTX
                   g4567207
NCBI GI
BLAST score
                   564
                   9.0e-58
E value
Match length
                   154
% identity
                   (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   4446
Seq. No.
                   3596 3.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1150756.h1
Method
                   BLASTX
                   g4567207
NCBI GI
BLAST score
                   201
E value
                   9.0e-16
Match length
                   71
% identity
                   58
                   (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4447
Contig ID
                   3597 1.R1040
                   LIB3028-028-Q1-B1-D4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3150412
```

```
9.0e-39
E value
Match length
                   115
% identity
                   66
NCBI Description
                   (AC004165) putative Fe(II) transport protein (Arabidopsis
                   thaliana] >gi 3420044 (AC004680) putative Fe(II) transport
                   protein [Arabidopsis thaliana]
                   4448
Seq. No.
Contig ID
                   3598 1.R1040
                   leu701150063.h1
5'-most EST
Method -
                   BLASTX
NCBI GI
                   q4335734
BLAST score
                   458
E value
                   1.0e-45
Match length
                   151
% identity
                   41
NCBI Description
                   (AC006248) putative calmodulin [Arabidopsis thaliana]
                   4449
Seq. No.
Contig ID
                   3602 1.R1040
                   LIB3093-006-Q1-K1-F8
5'-most EST
Method
                   BLASTX
                   g2497538
NCBI GI
BLAST score
                   220
E value
                   1.0e-17
Match length
                   92
% identity
                   55
NCBI Description
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
                  pyruvate kinase [Glycine max]
Seq. No.
                   4450
                   3602 2.R1040
Contig ID
                   LIB3051-013-Q1-E1-C8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2497543
BLAST score
                   204
                   6.0e-16
E value
                   70
Match length
% identity
                   61
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379
NCBI Description
                   pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
Seq. No.
                   4451
Contig ID
                   3604 1.R1040
5'-most EST
                   epx7\overline{0}1105730.h1
Seq. No.
                   4452
Contig ID
                   3608_1.R1040
5'-most EST
                   uC-gmropic113g01b1
Method
                   BLASTX
NCBI GI
                   q135861
BLAST score
                   137
E value
                   1.0e-10
Match length
                   160
% identity
                   36
NCBI Description
                  INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7)
```

BLAST score

318

```
Seq. No.
                   4453
                   3608 2.R1040
Contig ID
                   LIB3028-010-Q1-B1-F3
5'-most EST
                   4454
Seq. No.
                   3610 1.R1040
Contig ID
5'-most EST
                   zsg701118611.hl
Method
                   BLASTX
NCBI GI
                   g119640
BLAST score
                   548
E value
                   1.0e-104
Match length
                   354
                   55
% identity
NCBI Description '1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
                  E8) >gi 82109 pir S01642 ripening protein E8 - tomato
                   >gi 19199 emb CAA31789 (X13437) E8 protein [Lycopersicon
                   esculentum]
                   4455
Seq. No.
                   3614_1.R1040
Contig ID
5'-most EST
                   g4397270
Seq. No.
                   4456
                   3617 1.R1040
Contig ID
5'-most EST
                  LIB3028-028-Q1-B1-C2
Method
                  BLASTX
NCBI GI
                   g4406777
BLAST score
                   272
E value
                   3.0e-24
Match length
                  89
                   63
% identity
                   (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   4457
Seq. No.
Contig ID
                   3619 1.R1040
5'-most EST
                   q4395762
Method
                  BLASTX
NCBI GI
                   q1362078
BLAST score
                   465
E value
                   3.0e-46
Match length
                  128
                   65
% identity
NCBI Description
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
                   - common nasturtium >gi_311835_emb_CAA48324_ (X68254)
                  cellulase [Tropaeolum majus]
                   4458
Seq. No.
Contig ID
                   3621 1.R1040
                  LIB3040-036-Q1-E1-D1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2497753
```

(TIS7 PROTEIN) >gi\_321269\_pir\_\_A44989 interferon-related protein TIS7 - mouse >gi\_54806\_emb\_CAA35258\_ (X17400) TIS7

protein (AA 1-449) [Mus sp.]

```
5.0e-29
E value
Match length
                  115
                  51
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                   [Prunus dulcis]
                  4459
Seq. No.
                  3621_2.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy081b04b1
Method
                  BLASTX
                  g2497753
NCBI GI
BLAST score
                  285
                  3.0e-25
E value
Match length
                  91
% identity
                  59
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi 1321915_emb_CAA65477_ (X96716) lipid transfer protein
                  [Prunus dulcis]
Seq. No.
                  4460
                  3624 1.R1040
Contig ID
5'-most EST
                  LIB3139-021-P1-N1-A8
Seq. No.
                  4461
                  3627 1.R1040
Contig ID
5'-most EST
                  LIB3049-030-Q1-E1-H4
Method
                  BLASTX
                  g4572675
NCBI GI
BLAST score
                  154
                  1.0e-09
E value
Match length
                  79
                  47
% identity
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                  4462
Seq. No.
Contig ID
                  3627 2.R1040
5'-most EST
                  LIB3028-028-Q1-B1-A11
                  BLASTX
Method
NCBI GI
                  q4572675
BLAST score
                  154
                  5.0e-10
E value
Match length
                  79
                  47
% identity
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                  4463
Seq. No.
Contig ID
                  3628 1.R1040
5'-most EST
                  leu701148293.h1
Method
                  BLASTX
NCBI GI
                  q1762933
BLAST score
                  265
E value
                  1.0e-22
Match length
                  188
                  39
% identity
NCBI Description (U66263) tumor-related protein [Nicotiana tabacum]
```

```
4464
Seq. No.
                   3628 2.R1040
Contig ID
                   bth700845465.hl
5'-most EST
Seq. No.
                   4465
                   3628 3.R1040
Contig ID
                   bth700849368.h1
5'-most EST
                   4466
Seq. No.
                   3629 1.R1040
Contig ID
5'-most EST
                   LIB3028-028-Q1-B1-A3
Seq. No.
                   4467
Contig ID
                   3631 1.R1040
5'-most EST
                   ncj700987071.hl
                   BLASTX
Method
NCBI GI
                   q3850587
BLAST score
                   509
E value
                   3.0e-51
Match length
                   221
% identity
                   56
                   (AC005278) Strong similarity to gi_2244780 hypothetical
NCBI Description
                   protein from Arabidopsis thaliana chromosome 4 contig
                   gb Z97335. [Arabidopsis thaliana]
                   4468
Seq. No.
Contig ID
                   3631 2.R1040
5'-most EST
                   k117\overline{0}1214264.h1
Method
                   BLASTX
                   g2244779
NCBI GI
BLAST score
                   373
E value
                   1.0e-35
Match length
                   130
                   58
% identity
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4469
Contig ID
                   3631 3.R1040
5'-most EST
                   LIB3028-028-Q1-B1-A4
Method
                   BLASTX
NCBI GI
                   g2244780
BLAST score
                   174
E value
                  2.0e-12
Match length
                   67
% identity
                   54
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4470
Contig ID
                   3635 1.R1040
5'-most EST
                   q5678054
Method
                   BLASTX
                   g3108053
NCBI GI
BLAST score
                   1536
E value
                   1.0e-171
Match length
                   324
                   92
% identity
NCBI Description
                   (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
```

E value

Match length

% identity

7.0e-52

282 84

## mays] 4471 Seq. No. Contig ID 3635 2.R1040 5'-most EST g4397429 Method BLASTN q602564 NCBI GI BLAST score 316 1.0e-177 . E value 987 Match length 83 % identity NCBI Description C.paradisi (Macf) INO1 gene 4472 Seq. No. 3635 3.R1040 Contig ID 5'-most EST LIB3055-012-Q1-N1-H8 Method BLASTN NCBI GI q602564 102 BLAST score 5.0e-50 E value 310 Match length 83 % identity C.paradisi (Macf) INO1 gene NCBI Description 4473 Seq. No. Contig ID 3635 4.R1040 5'-most EST jC-qmst02400014d06a1 Method BLASTN NCBI GI q602564 BLAST score 167 8.0e-89 E value Match length 431 85 % identity NCBI Description C.paradisi (Macf) INO1 gene 4474 Seq. No. 3635\_5.R1040 Contig ID 5'-most EST uC-gmflminsoy059b08b1 Method BLASTX NCBI GI g1170567 595 BLAST score 1.0e-61 E value Match length 124 89 % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >gi\_1085960\_pir\_\_S52648 INO1 protein - Citrus paradisi >gi\_602565\_emb\_CAA83565\_ (Z32632) INO1 [Citrus x paradisi] 4475 Seq. No. Contig ID 3635 6.R1040 5'-most EST LIB3107-036-Q1-K1-G12 BLASTN Method NCBI GI g602564 BLAST score 105

```
NCBI Description C.paradisi (Macf) INO1 gene
                   4476
Seq. No.
Contig ID
                   3635 8.R1040
5'-most EST
                   pmv700889442.h1
Method
                   BLASTX
NCBI GI
                   g1170567
BLAST score
                   193
E value
                   2.0e-23
Match length
                   62
% identity
                   97
NCBI Description
                   MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
                   >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi
                   >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                   4477
                   3635 9.R1040
Contig ID
5'-most EST
                   jC-gmro02910004c10a1
Method
                   BLASTX
NCBI GI
                   q4567202
BLAST score
                   294
                   8.0e-35
E value
Match length
                   127
% identity
                   93
                   (AC007168) putative myo-inositol 1-phosphate synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   4478
Contig ID
                   3635 12.R1040
5'-most EST
                   jC-qmle01810016q01a1
Method
                   BLASTN
NCBI GI
                   q602564
BLAST score
                   87
E value
                   4.0e-41
Match length
                   261
% identity
                   83
NCBI Description
                   C.paradisi (Macf) INO1 gene
Seq. No.
                   4479
Contig ID
                   3637 1.R1040
5'-most EST
                   LIB3040-008-Q1-E1-H2
Method
                   BLASTX
NCBI GI
                   q3913416
BLAST score
                   872
E value
                   9.0e-94
Match length
                   231
% identity
                   71
NCBI Description
                   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi_2129920_pir__S68990 adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle
                   >gi 758695 (U12573) S-adenosyl-L-methionine decarboxylase
                   proenzyme [Catharanthus roseus] >gi 1094441 prf 2106177A
                   Met(S-adenosyl) decarboxylase [Catharanthus roseus]
Seq. No.
                   4480
```

3637 2.R1040

LIB3170-078-Q1-K1-F4

Contig ID 5'-most EST

NCBI Description

fragment No

```
Method
                  BLASTN
NCBI GI
                  g758693
BLAST score
                  91
E value
                  2.0e-43
Match length
                  167
                  89
% identity
                  Catharanthus roseus S-adenosyl-L-methionine decarboxylase
NCBI Description
                  proenzyme mRNA, complete cds
                   4481
Seq. No.
Contig ID
                  3638 1.R1040
                  LIB3028-027-Q1-B2-F12
5'-most EST
                   4482
Seq. No.
Contig ID
                  3639 1.R1040
5'-most EST
                  leu701154652.h1
                  4483
Seq. No.
Contig ID
                  3642 1.R1040
5'-most EST
                  LIB3028-027-Q1-B2-G10
Method
                  BLASTN
NCBI GI
                  g1370171
BLAST score
                  151
E value
                  2.0e-79
Match length
                  315
                  87
% identity
                  L.japonicus mRNA for small GTP-binding protein, RAB1X
NCBI Description
                  4484
Seq. No.
                  3644 1.R1040
Contig ID
5'-most EST
                  LIB3093-018-Q1-K1-F1
                  4485
Seq. No.
                  3645_1.R1040
Contig ID
                  LIB3051-059-Q1-K2-D9
5'-most EST
Method
                  BLASTX
                  g3036802
NCBI GI
BLAST score
                  292
                   5.0e-26
E value
                  97
Match length
                   65
% identity
NCBI Description
                   (AL022373) putative protein [Arabidopsis thaliana]
                  >gi 3805864 emb CAA21484_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   4486
Seq. No.
Contig ID
                  3647_1.R1040
5'-most EST
                  LIB3170-022-Q1-J1-E5
Method
                  BLASTN
NCBI GI
                  q2245073
BLAST score
                  42
                  3.0e-14
E value
Match length
                  66
% identity
```

Arabidopsis thaliana DNA chromosome 4, ESSA I contig

BLAST score

```
4487
Seq. No.
Contig ID
                  3648 1.R1040
                  LIB3028-008-Q1-B1-A8
5'-most EST
Method
                  BLASTX
                  g3913733
NCBI GI
BLAST score
                  679
E value
                  2.0e-71
Match length
                  160
                  76
% identity
                  HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME
NCBI Description
                  (GLYOXALASE II) (GLX II) >gi_1924921_emb_CAA69644_ (Y08357)
                  hydroxyacylglutathione hydrolase [Arabidopsis thaliana]
Seq. No.
Contig ID
                  3649 1.R1040
                  uxk700667202.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  1694
E value
                  0.0e + 00
Match length
                  551
                  59
% identity
                  (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                  thaliana] >gi_2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
Seq. No.
                  4489
Contig ID
                  3649 2.R1040
5'-most EST
                  LIB3139-052-P1-N1-H6
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  143
                  1.0e-08
E value
Match length
                  53
                  53
% identity
NCBI Description
                  (AF005047) transport inhibitor response 1 [Arabidopsis
                  thaliana] >gi_2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
                  4490
Seq. No.
Contig ID
                  3653_1.R1040
5'-most EST
                  jC-gmro02910029d10a1
Method
                  BLASTX
NCBI GI
                  q4539330
BLAST score
                  863
                  1.0e-92
E value
Match length
                  304
% identity
                   (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  4491
Contig ID
                  3653 2.R1040
5'-most EST
                  LIB3028-027-Q1-B2-D1
Method
                  BLASTX
NCBI GI
                  q4567279
```

```
1.0e-27
E value
Match length
                   327
                   30
% identity
                   (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   4492
Seq. No.
                   3654_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910052a01d1
                   4493
Seq. No.
                   3656 1.R1040
Contig ID
5'-most EST
                   LIB3028-027-Q1-B2-D12
Method
                   BLASTX
                   g4490706
NCBI GI
BLAST score
                   396
E value
                   1.0e-38
Match length
                   113
                   73
% identity
NCBI Description
                   (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                   4494
                   3657 1.R1040
Contig ID
5'-most EST
                   LIB3107-072-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g3522956
BLAST score
                   1434
                   1.0e-159
E value
                   405
Match length
% identity
NCBI Description
                   (AC004411) putative pectinacetylesterase precursor
                   [Arabidopsis thaliana]
                   4495
Seq. No.
                   3657 2.R1040
Contig ID
5'-most EST
                   LIB3109-010-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   g3047082
BLAST score
                   453
E value
                   4.0e-45
Match length
                   132
% identity
                   (AF058914) similar to Vigna radiata pectinacetylesterase
NCBI Description
                   precursor (GB:X99348) [Arabidopsis thaliana]
                   4496
Seq. No.
Contig ID
                   3657 3.R1040
5'-most EST
                   hyd7\overline{0}0726654.h1
Method
                   BLASTX
NCBI GI
                   g3522956
BLAST score
                   641
E value
                   6.0e-67
Match length
                   145
% identity
                   81
NCBI Description
                   (AC004411) putative pectinacetylesterase precursor
```

[Arabidopsis thaliana]

```
4497
Seq. No.
Contig ID
                  3658 1.R1040
                  LIB3139-010-P1-N1-B5
5'-most EST
                  BLASTX
Method
                  g4417289
NCBI GI
BLAST score
                  530
                  9.0e-54
E value
                  197
Match length
                  58
% identity
                  (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4498
                  3658 2.R1040
Contig ID
                  fC-gmle700875159r1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4417289
BLAST score
                  263
                  8.0e-23
E value
                  73
Match length
% identity
                  62
                  (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                  4499
Seq. No.
                  3660 1.R1040
Contig ID
5'-most EST
                  LIB3049-041-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  522
E value
                  5.0e-53
                  208
Match length
                  53
% identity
NCBI Description
                  (AC000132) No definition line found [Arabidopsis thaliana]
                  4500
Seq. No.
                  3662_1.R1040
Contig ID
                  LIB3170-012-Q1-K1-C5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g464621
BLAST score
                  581
                  2.0e-79
E value
                  194
Match length
                  80
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                  [Mesembryanthemum crystallinum]
                  4501
Seq. No.
                  3662 2.R1040
Contig ID
                  fua701040224.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  874
E value
                  4.0e-94
Match length
                  215
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
```

Seq. No. Contig ID

```
ribosomal protein L10A [Arabidopsis thaliana]
                   4502
Seq. No.
                   3662 4.R1040
Contig ID
                   LIB3094-017-Q1-K1-H8
5'-most EST
                   BLASTX
Method
                   g464621
NCBI GI
BLAST score
                   231
                   7.0e-38
E value
                   101
Match length
                   80
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
                   ribosomal protein ML16 - common ice plant
                   >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   4503
Seq. No.
                   3662 5.R1040
Contig ID
                   hyd7\overline{0}0726772.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3860277
BLAST score
                   444
                   6.0e-44
E value
Match length
                   117
% identity
                   86
NCBI Description
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
                   thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   4504
Seq. No.
                   3662 7.R1040
Contig ID
5'-most EST
                   g5510388
                   BLASTX
Method
NCBI GI
                   g464621
BLAST score
                   247
E value
                   4.0e-21
Match length
                   56
                   88
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant
                   >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   4505
Seq. No.
Contig ID
                   3662 9.R1040
5'-most EST
                   uxk700672494.h1
Method
                  BLASTX
NCBI GI
                   g1709970
                   375
BLAST score
E value
                   8.0e-36
Match length
                  87
                   84
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L10A
                   4506
```

thaliana] >gi\_4314394\_gb\_AAD15604\_ (AC006232) putative

3662 12.R1040

```
LIB3053-003-Q1-N1-D8
5'-most EST
                   4507
Seq. No.
                   3664 1.R1040
Contig ID
5'-most EST
                   LIB3030-005-Q1-B1-H1
                   4508
Seq. No.
                   3671_1.R1040
Contig ID
5'-most EST
                   LIB3028-027-Q1-B2-B11
Method
                   BLASTX
NCBI GI
                   q3461839
BLAST score
                   437
E value
                   2.0e-43
                   129
Match length
% identity
                   60
                   (AC005315) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   4509
Seq. No.
                   3672 1.R1040
Contig ID
5'-most EST
                   LIB3039-026-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g2582665
BLAST score
                   1284
                   1.0e-142
E value
                   282
Match length
% identity
                   88
                  (Z82983) thi [Citrus sinensis]
NCBI Description
                   4510
Seq. No.
Contig ID
                   3673 1.R1040
                   LIB3028-027-Q1-B2-B2
5'-most EST
                   4511
Seq. No.
                   3674 1.R1040
Contig ID
5'-most EST
                   pcp700994538.h2
Seq. No.
                   4512
                   3676 1.R1040
Contig ID
                   hrw701060639.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3063467
BLAST score
                   467
                   2.0e-46
E value
                   126
Match length
                   73
% identity
NCBI Description
                  (AC003981) F22013.29 [Arabidopsis thaliana]
Seq. No.
                   4513
Contig ID
                   3682 1.R1040
5'-most EST
                   fde700873509.hl
Method
                   BLASTX
NCBI GI
                   q4263818
BLAST score
                   189
E value
                   4.0e-15
Match length
                  139
% identity
                   41
```

```
NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]
                  4514
Seq. No.
Contig ID
                  3694 1.R1040
5'-most EST
                  LIB3039-022-Q1-E1-D6
                  4515
Seq. No.
                  3694 2.R1040
Contig ID
5'-most EST
                  LIB3106-092-Q1-K1-G8
                  4516
Seq. No.
Contig ID
                  3694 4.R1040
                  LIB3049-017-Q1-E1-H1
5'-most EST
                  4517
Seq. No.
Contig ID
                  3695 1.R1040
5'-most EST
                  LIB3028-027-Q1-B2-A10
                  4518
Seq. No.
                  3697 1.R1040
Contig ID
5'-most EST
                  LIB3028-027-Q1-B1-A11
                  4519
Seq. No.
                  3700 1.R1040
Contig ID
5'-most EST
                  hyd7\overline{0}0728205.h1
Seq. No.
                  4520
                  3700 2.R1040
Contig ID
5'-most EST
                  LIB3050-024-Q1-K1-A2
                  4521
Seq. No.
Contig ID
                  3701 1.R1040
                  epx701109853.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2136139
BLAST score
                  168
E value
                  9.0e-12
Match length
                  144
% identity
                  sds22 protein homolog - human >gi_1085028_emb_CAA90626_
NCBI Description
                   (Z50749) yeast sds22 homolog [Homo sapiens]
                  >gi_1585165_prf__2124310A sds22 gene [Homo sapiens]
                  >gi_4506013_ref_NP_002703.1_pPPP1R7_ protein phosphatase 1,
                  regulatory subunit
                  4522
Seq. No.
Contig ID
                  3712_1.R1040
5'-most EST
                  LIB3049-033-Q1-E1-G7
Method
                  BLASTN
NCBI GI
                  g2565428
BLAST score
                  48
                  1.0e-17
E value
Match length
                  112
% identity
                  Onobrychis viciifolia glycine-rich protein mRNA, complete
NCBI Description
```

```
Seq. No.
                   4523
                   3712 3.R1040
Contig ID
                   LIB3073-026-Q1-K1-D8
5'-most EST
                   BLASTN
Method
                   g2565428
NCBI GI
BLAST score
                   46
                   9.0e-17
E value
                   106
Match length
                   86
% identity
                   Onobrychis viciifolia glycine-rich protein mRNA, complete
NCBI Description
                   4524
Seq. No.
                   3715 1.R1040
Contig ID
5'-most EST
                   q5753666
Method
                   BLASTN
NCBI GI
                   g408793
BLAST score.
                   472
                   0.0e + 00
E value
Match length
                   613
                   96
% identity
                  Glycine soja chloroplast 3-omega faty acid desaturase
NCBI Description
                   (Fad3) mRNA, complete cds
                   4525
Seq. No.
                   3715 2.R1040
Contig ID
5'-most EST
                   leu701149421.h1
Method
                   BLASTN
                   g408793
NCBI GI
                   375
BLAST score
                   0.0e + 00
E value
                   379
Match length
                   100
% identity
                  Glycine soja chloroplast 3-omega faty acid desaturase
NCBI Description
                   (Fad3) mRNA, complete cds
                   4526
Seq. No.
Contig ID
                   3716_1.R1040
                   jC-gmf102220061a11a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1709449
BLAST score
                   1754
                   0.0e + 00
E value
Match length
                   396
                   85
% identity
                  PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
NCBI Description
                   PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate
                   dehydrogenase El alpha subunit [Pisum sativum]
                   4527
Seq. No.
                   3716 2.R1040
Contig ID
                  LIB3170-041-Q1-K1-C9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1709449
BLAST score
                   1118
                   1.0e-175
E value
                   370
Match length
```

```
83
% identity
                   PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
NCBI Description
                   PRECURSOR (PDHE1-A) >gi 1263302 (U51918) pyruvate
                   dehydrogenase El alpha subunit [Pisum sativum]
                   4528
Seq. No.
                   3716 3.R1040
Contig ID
5'-most EST
                   fC-gmse700756337a2
                   BLASTN
Method
NCBI GI
                   g3851004
BLAST score
                   106
E value
                   2.0e-52
Match length
                   194
                   89
% identity
                   Zea mays pyruvate dehydrogenase El alpha subunit RNA,
NCBI Description
                   nuclear gene encoding mitochondrial protein, complete cds
                   4529
Seq. No.
Contig ID
                   3716 6.R1040
5'-most EST
                   uC-gmropic041f09b1
Seq. No.
                   4530
                   3721 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810094c05a1
Method
                   BLASTX
                   g4455246
NCBI GI
BLAST score
                   691
                   1.0e-72
E value
                   238
Match length
                   58
% identity
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   4531
Seq. No.
                   3721_2.R1040
Contig ID
                   LIB3\overline{1}38-031-Q1-N1-D2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4455246
BLAST score
                   334
                   3.0e - 31
E value
                   95
Match length
                   69
% identity
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   4532 .
Seq. No.
                   3721 3.R1040
Contig ID
5'-most EST
                   fua701043571.h1
Method
                   BLASTX
NCBI GI
                   g4455246
BLAST score
                   191
                   9.0e-15
E value
Match length
                   62
% identity
                   75
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4533
                   3723 1.R1040
Contig ID
```

jex700906481.hl

5'-most EST

NCBI GI

```
Method
                   BLASTX
NCBI GI
                   g3176098
BLAST score
                   722
                   2.0e-76
E value
Match length
                   191
                   47
% identity
                   (Y15036) annexin [Medicago truncatula]
NCBI Description
                   4534
Seq. No.
                   3723 2.R1040
Contig ID
                   ek17\overline{0}0968268.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3176098
BLAST score
                   244
                   5.0e-21
E value
Match length
                   64
                   77
% identity
                   (Y15036) annexin [Medicago truncatula]
NCBI Description
                   4535
Seq. No.
                   3724 1.R1040
Contig ID
                   k11701210733.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1666096
                   1012
BLAST score
E value
                   1.0e-110
Match length
                   297
% identity
                   68
                   (Y09113) dioxygenase [Marah macrocarpus]
NCBI Description
                   4536
Seq. No.
Contig ID
                   3724 2.R1040
                   sat701005739.hl
5'-most EST
Method
                   BLASTX
                   g1666096
NCBI GI
BLAST score
                   171
E value
                   2.0e-12
Match length
                   61
                   59
% identity
NCBI Description
                   (Y09113) dioxygenase [Marah macrocarpus]
                   4537
Seq. No.
Contig ID
                   3725 1.R1040
5'-most EST
                   uC-gmflminsoy026e06b1
Method
                   BLASTX
                   g2194118
NCBI GI
BLAST score
                   222
E value
                   6.0e-18
Match length
                   74
% identity
                   46
                   (AC002062) F20P5.4 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4538
                   3725 2.R1040
Contig ID
5'-most EST
                   k11701211135.h1
Method
                   BLASTX
```

g2194118

E value

```
BLAST score
                   221
 E value
                   1.0e-17
 Match length
                   95
                   40
 % identity
                    (AC002062) F20P5.4 gene product [Arabidopsis thaliana]
 NCBI Description
                   4539
 Seq. No.
 Contig ID
                   3726_1.R1040
 5'-most EST
                   jC-gmf102220057d05a1
 Method
                   BLASTX
                   g3881189
 NCBI GI
 BLAST score
                   573
 E value
                   5.0e-59
                   155
 Match length
                   68
 % identity
 NCBI Description
                    (Z99281) similar to ADP-ribosylation factor; cDNA EST
                   EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                   comes from this gene; cDNA EST EMBL: C09829 comes from this
                   gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
 Seq. No.
                   4540
 Contig ID
                   3726 2.R1040
                   pmv700889323.h1
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g3881189
 BLAST score
                   345
 E value
                   1.0e-32
 Match length
                   77
                   78
 % identity
                    (Z99281) similar to ADP-ribosylation factor; cDNA EST
 NCBI Description
                   EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                   comes from this gene; cDNA EST EMBL: C09829 comes from this
                   gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
                   4541
 Seq. No.
 Contig ID
                   3727 1.R1040
 5'-most EST
                   LIB3039-017-Q1-E1-A3
                   4542
 Seq. No.
                   3729 1.R1040
 Contig ID
 5'-most EST
                   wvk700686507.h1
                   BLASTN
 Method
                   g2618601
· NCBI GI
 BLAST score
                   35
 E value
                   2.0e-09
 Match length
                   87
                   85
 % identity
 NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MHJ24, complete sequence [Arabidopsis thaliana]
                   4543
 Seq. No.
 Contig ID
                   3730 1.R1040
 5'-most EST
                   LIB3049-005-Q1-E1-C1
                   BLASTX
 Method
 NCBI GI
                   g4455364
 BLAST score
                   817
```

2.0e-87

```
265
Match length
% identity
                   55
NCBI Description
                   (AL035524) senescence-associated protein-like [Arabidopsis
                   thaliana]
                   4544
Seq. No.
                   3730 2.R1040
Contig ID
                   epx701109821.hl
5'-most EST
Method
                   BLASTX
                   g3551954
NCBI GI
BLAST score
                   477
E value
                   2.0e-47
Match length
                   218
                   47
% identity
NCBI Description
                   (AF082030) senescence-associated protein 5 [Hemerocallis
                   hybrid cultivar]
                   4545
Seq. No.
                   3730 4.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy063e02b1
Method
                   BLASTX
NCBI GI
                   g4455364
BLAST score
                   354
E value
                   1.0e-33
Match length
                   97
                   68
% identity
NCBI Description
                   (AL035524) senescence-associated protein-like [Arabidopsis
                   thaliana]
                   4546
Seq. No.
                   3732_1.R1040
Contig ID
5'-most EST
                   uC-gmropic050g09b1
                   4547
Seq. No.
Contig ID
                   3733 1.R1040
5'-most EST
                   LIB3051-016-Q1-E1-C12
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   33
                   6.0e-09
E value
Match length
                   37
% identity
                   97
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   4548
Seq. No.
                   3742_1.R1040
Contig ID
5'-most EST
                   LIB3050-002-Q1-E1-E7
Method
                   BLASTX
NCBI GI
                   g2827528
BLAST score
                   383
E value
                   6.0e-37
Match length
                   98
% identity
                   76
NCBI Description
                   (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   3743_1.R1040
```

NCBI Description

```
LIB3049-038-Q1-E1-C6
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3413169
BLAST score
                  345
                  0.0e + 00
E value
Match length
                  577
                  90
% identity
                  Cicer arietinum mRNA for 40S ribosomal protein S6, partial
NCBI Description
Seq. No.
                  4550
                  3743 2.R1040
Contig ID
5'-most EST
                  LIB3039-019-Q1-E1-F7
                  BLASTN
Method
NCBI GI
                  q3413169
BLAST score
                  231
                  1.0e-127
E value
Match length
                  407
                  89
% identity
                  Cicer arietinum mRNA for 40S ribosomal protein S6, partial
NCBI Description
Seq. No.
                  4551
                  3743 3.R1040
Contig ID
5'-most EST
                  LIB3028-026-Q1-B1-F10
Method
                  BLASTN
NCBI GI
                  q3413169
BLAST score
                  137
                   6.0e-71
E value
Match length
                  229
                  90
% identity
NCBI Description
                  Cicer arietinum mRNA for 40S ribosomal protein S6, partial
Seq. No.
                   4552
                  3743 5.R1040
Contig ID
5'-most EST
                  LIB3051-020-Q1-E1-H7
Method
                  BLASTN
NCBI GI
                  g3413169
BLAST score
                  261
E value
                  1.0e-145
Match length
                   457
                  89
% identity
                  Cicer arietinum mRNA for 40S ribosomal protein S6, partial
NCBI Description
                   4553
Seq. No.
Contig ID
                   3743 6.R1040
5'-most EST
                  LIB3040-029-Q1-E1-F8
Seq. No.
                   4554
Contig ID
                  3746 1.R1040
5'-most EST
                  LIB3040-041-Q1-E1-D4
Method
                  BLASTN
NCBI GI
                  q2879810
BLAST score
                  155
E value
                   2.0e-81
Match length
                  319
% identity
                  87
```

Lupinus luteus mRNA for ribosomal protein L30

5'-most EST

```
4555
Seq. No.
                   3746 2.R1040
Contig ID
5'-most EST
                   LIB3073-012-Q1-K1-C3
Method
                   BLASTN
NCBI GI
                   q2879810
BLAST score
                   169
                   5.0e-90
E value
                   341
Match length
                   87
% identity
NCBI Description
                   Lupinus luteus mRNA for ribosomal protein L30
                   4556
Seq. No.
Contig ID
                   3747 1.R1040
5'-most EST
                   txt700735453.h1
                   BLASTX
Method
                   g3402683
NCBI GI
BLAST score
                   563
                   1.0e-57
E value
                   266
Match length
                   44
% identity
NCBI Description
                   (AC004697) patatin-like protein [Arabidopsis thaliana]
                   4557
Seq. No.
                   3747 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400077e07d1
Seq. No.
                   4558
                   3747 4.R1040
Contig ID
5'-most EST
                   LIB3039-037-Q1-E1-B12
                   4559
Seq. No.
Contig ID
                   3748 1.R1040
                   awf700837610.hl
5'-most EST
                   4560
Seq. No.
                   3748 2.R1040
Contig ID
5'-most EST
                   uC-gmropic008a11b1
                   4561
Seq. No.
                   3748 3.R1040
Contig ID
                   kmv7\overline{0}0743318.h1
5'-most EST
Seq. No.
                   4562
Contig ID
                   3749 1.R1040
5'-most EST
                   leu701154836.hl
Method
                   BLASTX
NCBI GI
                   g2160182
BLAST score
                   264
E value
                   8.0e-23
Match length
                   146
                   40
% identity
                   (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb_AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
                   4563
Seq. No.
                   3750 1.R1040
Contig ID
```

LIB3109-013-Q1-K1-E2

Method

```
BLASTX
NCBI GI
                  g731507
                  179
BLAST score
                  2.0e-12
E value
Match length
                  254
% identity
                  26
                  HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC
NCBI Description
                  REGION >gi 1077700 pir S50622 hypothetical protein YER119c
                  - yeast (Saccharomyces cerevisiae) >gi 603358 (U18916)
                  Yer119cp [Saccharomyces cerevisiae]
                  4564
Seq. No.
                  3751 1.R1040
Contig ID
                  LIB3028-026-Q1-B1-C6
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4262174
BLAST score
                  1482
                  1.0e-165
E value
Match length
                  398
                  70
% identity
                  (AC005508) 9058 [Arabidopsis thaliana]
NCBI Description
                  4565
Seq. No.
                  3753 1.R1040
Contig ID
5'-most EST
                  g4397335
Method
                  BLASTX
NCBI GI
                  g3319355
BLAST score
                  1481
E value
                  1.0e-165
Match length
                  314
                  89
% identity
NCBI Description
                  (AF077407) similar to chaperonin containing TCP-1 complex
                  gamma chain [Arabidopsis thaliana]
Seq. No.
                  4566
Contig ID
                  3753 2.R1040
5'-most EST
                  k11701207044.h1
Method
                  BLASTX
NCBI GI
                  q3319355
BLAST score
                  538
E value
                  7.0e-64
Match length
                  281
% identity
                  72
                  (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
                  gamma chain [Arabidopsis thaliana]
Seq. No.
                  4567
Contig ID
                  3753_3.R1040
5'-most EST
                  LIB3049-021-Q1-E1-H7
Method
                  BLASTX
                  g3319355
NCBI GI
BLAST score
                  789
E value
                  2.0e-84
Match length
                  172
                  87
% identity
                  (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
```

gamma chain [Arabidopsis thaliana]

% identity

```
Seq. No.
                   4568
                   3753 5.R1040
Contig ID
5'-most EST
                   zzp7\overline{0}0834785.h1
                   BLASTX
Method
NCBI GI
                   g3319355
BLAST score
                   250
                   2.0e-21
E value
Match length
                   55
% identity
                   85
NCBI Description
                   (AF077407) similar to chaperonin containing TCP-1 complex
                   gamma chain [Arabidopsis thaliana]
                   4569
Seq. No.
Contig ID
                   3753 6.R1040
5'-most EST
                   uxk700669084.hl
                   4570
Seq. No.
                   3754 1.R1040
Contig ID
5'-most EST
                   LIB3051-037-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   g2623158
BLAST score
                   165
E value
                   3.0e-11
Match length
                   110
% identity
                   31
                   (AF030177) N-acetylglucosaminyl transferase component Gpil
NCBI Description
                   [Homo sapiens] >gi 2911142 dbj BAA24948 (AB003723) GPI1
                   [Homo sapiens]
Seq. No.
                   4571
Contig ID
                   3755_1.R1040
5'-most EST
                   LIB3028-026-Q1-B1-D10
Method
                   BLASTX
NCBI GI
                   g1168314
BLAST score
                   357
E value
                   2.0e-33
Match length
                   235
% identity
                   18
NCBI Description
                   REGULATOR OF ACETYL-COA SYNTHETASE ACTIVITY
                   >gi_1084627_pir__S57116 probable carrier protein ACR1 -
                   yeast (Saccharomyces cerevisiae) >gi_1015794_emb_CAA89624_
                   (Z49595) ORF YJR095w [Saccharomyces cerevisiae]
Seq. No.
                   4572
Contig ID
                   3756 1.R1040
5'-most EST
                   LIB3028-026-Q1-B1-D12
Seq. No.
                   4573
                   3758 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy119b08b1
Method
                   BLASTX
NCBI GI
                   q4220527
BLAST score
                   943
E value
                   1.0e-102
Match length
                   342
```

Match length

```
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                   4574
Seq. No.
Contig ID
                   3760 1.R1040
5'-most EST
                   jC-gmf102220073g01a1
Method
                   BLASTX
                   g2208908
NCBI GI
BLAST score
                   614
E value
                   6.0e-64
Match length
                   132
                   89
% identity
NCBI Description
                   (AB004809) phosphate transporter [Catharanthus roseus]
                   4575
Seq. No.
Contig ID
                   3761 1.R1040
                  LIB3107-002-Q1-K1-D1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3024541
BLAST score
                   163
E value
                   8.0e-11
                   293
Match length
% identity
NCBI Description
                  RESTIN >gi_2338714 (AF014012) restin [Gallus gallus]
Seq. No.
                   4576
Contig ID
                   3765 1.R1040
                   zsg7\overline{0}1118781.h1
5'-most EST
Method
                   BLASTX
                   q4091008
NCBI GI
BLAST score
                   310
E value
                   5.0e-28
Match length
                   101
% identity
                   60
                   (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
                   4577
Seq. No.
Contig ID
                   3766 1.R1040
5'-most EST
                  LIB3109-035-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                   g2129927
BLAST score
                   2238
E value
                   0.0e+00
Match length
                   487
% identity
NCBI Description
                  zeta-carotene desaturase precursor - pepper
                  >gi_1176437_bbs_171885 zeta-carotene desaturase,
                  CapZDS=phytoene desaturase homolog [Capsicum annuum, early
                   ripening fruit, Peptide, 588 aa]
                   4578
Seq. No.
Contig ID
                   3771 1.R1040
5'-most EST
                  pxt700945660.hl
Method
                  BLASTX
NCBI GI
                  g2459429
BLAST score
                  599
E value
                   4.0e-62
```

NCBI GI

```
% identity
                   77
NCBI Description
                   (AC002332) unknown protein [Arabidopsis thaliana]
                   4579
Seq. No.
Contig ID
                   3771 2.R1040
5'-most EST
                  LIB3092-032-Q1-K1-F8
                  BLASTX
Method
NCBI GI
                  g2459429
BLAST score
                  580
E value
                  7.0e-60
                  147
Match length
% identity
                   74
NCBI Description
                   (AC002332) unknown protein [Arabidopsis thaliana]
                   4580
Seq. No.
Contig ID
                  3772 1.R1040
5'-most EST
                  LIB3093-037-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                   g3790587
BLAST score
                   996
E value
                   1.0e-108
Match length
                   347
% identity
                   61
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
NCBI Description
                  thaliana]
                   4581
Seq. No.
                   3772 2.R1040
Contig ID
5'-most EST
                  rca700997363.hl
Method
                  BLASTX
                  g3790587
NCBI GI
BLAST score
                  360
E value
                   5.0e-34
Match length
                  74
                  88
% identity
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
NCBI Description
                   thaliana]
                   4582
Seq. No.
                   3777 1.R1040
Contig ID
                   zhf700953648.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3877358
BLAST score
                  188
                   6.0e-14
E value
Match length
                  85
% identity
                  28
NCBI Description
                   (Z66520) similar to RBB3 like protein; cDNA EST EMBL: C08891
                  comes from this gene; cDNA EST EMBL: C09371 comes from this
                  gene; cDNA EST yk468f10.5 comes from this gene
                   [Caenorhabditis elegans]
Seq. No.
                   4583
Contig ID
                  3778 1.R1040
5'-most EST
                  smc700745972.h1
Method
                  BLASTX
```

g2443751

```
1368
BLAST score
                   1.0e-162
E value
Match length
                   351
% identity
                   (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
NCBI Description
                   (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   3778 2.R1040
5'-most EST
                   asn7\overline{0}1138372.h1
Method
                   BLASTX
NCBI GI
                   a2443751
BLAST score
                   292
E value
                   3.0e-26
Match length
                   60
                   92
% identity
                   (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
NCBI Description
                   (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.
                   4585
                   3778 3.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1157217.h1
Method
                   BLASTX
NCBI GI
                   q2443751
BLAST score
                   146
E value
                   2.0e-09
Match length
                   61
% identity
                   54
                   (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676
NCBI Description
                   (AC002535) putative fumarase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   3779 1.R1040
5'-most EST
                   epx701108935.hl
Method
                   BLASTX
NCBI GI
                   q1076534
BLAST score
                   1833
E value
                   0.0e + 00
Match length
                   433
% identity
NCBI Description
                   monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden
                   pea >gi_497120 (U06461) monodehydroascorbate reductase
                   [Pisum sativum]
Seq. No.
                   4587
Contig ID
                   3784 1.R1040
5'-most EST
                   LIB3093-032-Q1-K1-C6
Method
                   BLASTX
                   g2245378
NCBI GI
BLAST score
                   819
E value
                   3.0e-87
Match length
                   398
                   56
% identity
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4588
```

3786 1.R1040

Contig ID

5'-most EST

```
LIB3028-026-Q1-B1-A10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g586021
BLAST score
                   218
                   2.0e-17
E value
                   96
Match length
                   45
% identity
                   PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION
NCBI Description
                   PROTEIN C) >gi_2127242_pir__S66083 stage V sporulation protein - Bacillus subtilis >gi_467442_dbj_BAA05288_
                   (D26185) stage V sporulation [Bacillus subtilis]
                   >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant
                   blocks spore coat formation (stage V sporulation) [Bacillus
                   subtilis]
                   4589
Seq. No.
                   3787 1.R1040
Contig ID
5'-most EST
                   LIB3028-026-Q1-B1-A11
                   4590
Seq. No.
                   3789 1.R1040
Contig ID
                   jex700908228.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3256770
BLAST score
                   306
E value
                   3.0e-27
Match length
                   314
% identity
                   31
                   (AP000002) 318aa long hypothetical UDP-glucose 4-epimerase
NCBI Description
                   [Pyrococcus horikoshii]
Seq. No.
                   4591
                   3789 3.R1040
Contig ID
5'-most EST
                   trc700567883.hl
                   4592
Seq. No.
Contig ID
                   3789 4.R1040
5'-most EST
                   ncj700987768.hl
                   4593
Seq. No.
                   3789 6.R1040
Contig ID
5'-most EST
                   uC-gmronoir031f04b1
Seq. No.
                   4594
                   3794_1.R1040
Contig ID
5'-most EST
                   LIB3028-025-Q1-B1-H11
Method
                   BLASTX
NCBI GI
                   g3461817
BLAST score
                   287
E value
                   7.0e-26
Match length
                   66
% identity
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
                   4595
Seq. No.
Contig ID
                   3795 1.R1040
```

uC-gmflminsoy057d10b1

Contig ID

Stage Land

```
BLASTN
Method
NCBI GI
                   g556421
BLAST score
                   45
                   1.0e-15
E value
Match length
                   247
                   89
% identity
                   Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)
NCBI Description
                   mRNA, complete cds
                   4596
Seq. No.
                   3795 2.R1040
Contig ID
                   LIB3028-025-Q1-B1-F5
5'-most EST
Method
                   BLASTX
                   g4056499
NCBI GI
BLAST score
                   149
E value
                   2.0e-09
Match length
                   44
% identity
                   66
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
                   4597
Seq. No.
                   3798 1.R1040
Contig ID
5'-most EST
                   ncj700983420.hl
                   4598
Seq. No.
                   3798 2.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0978215.h1
                   4599
Seq. No.
                   3803 1.R1040
Contig ID
5'-most EST
                   hyd7\overline{0}0726639.h1
Method
                   BLASTX
                   g4539383
NCBI GI
BLAST score
                   535
E value
                   1.0e-54
                   189
Match length
% identity
                   54
NCBI Description
                   (AL035526) putative protein (fragment) [Arabidopsis
                   thaliana]
                   4600
Seq. No.
Contig ID
                   3806 1.R1040
                   leu701153143.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4115377
BLAST score
                   664
E value
                   2.0e-72
Match length
                   292
% identity
                   45
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   4601
Seq. No.
Contig ID
                   3806 2.R1040
5'-most EST
                   jC-gmst02400046c12d1
Seq. No.
                   4602
```

3808 1.R1040

5'-most EST

```
5'-most EST
                    zzp700831734.hl
Method
                    BLASTX
NCBI GI
                    g3341697
BLAST score
                    290
E value
                    3.0e-53
                    143
Match length
                    77
% identity
                    (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    4603
Seq. No.
                    3809 1.R1040
Contig ID
5'-most EST
                    eep7\overline{0}0867020.h1
Method
                    BLASTX
NCBI GI
                    g3386597
BLAST score
                    222
E value
                    7.0e-18
                    77
Match length
                    61
% identity
                    (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                    >gi_3702347 (AC005397) putative permease [Arabidopsis
                    thaliana]
                    4604
Seq. No.
                    3809 2.R1040
Contig ID
5'-most EST
                    xpa700793883.h1
Seq. No.
                    4605
                    3810 1.R1040
Contig ID
                    pxt700946473.hl
5'-most EST
                    BLASTX
Method
NCBI GI
                    g3461835
BLAST score
                    1325
E value
                    1.0e-146
                    408
Match length
                    64
% identity
                    (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                    >gi_3927840 (AC005727) putative protein kinase [Arabidopsis
                    thaliana]
                    4606
Seq. No.
                    3810 3.R1040
Contig ID
5'-most EST
                    taw7\overline{0}0657682.h1
                    4607
Seq. No.
Contig ID
                    3812 1.R1040
                    sat7\overline{0}1013536.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3123515
BLAST score
                    713
                    3.0e-75
E value
                    146
Match length
% identity
                    92
NCBI Description
                    (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
                    4608
Seq. No.
                    3812 2.R1040
Contig ID
```

 $ncj7\overline{0}0977319.h1$ 

```
BLASTN
Method
NCBI GI
                  g3006211
BLAST score
                  73
                   6.0e-33
E value
Match length
                  133
                  89
% identity
NCBI Description
                  Drosophila melanogaster (P1 DS02368 (D205)) DNA sequence,
                  complete sequence [Drosophila melanogaster]
Seq. No.
                  3813 1.R1040
Contig ID
                  rca700996410.hl
5'-most EST
                  4610
Seq. No.
                  3813 2.R1040
Contig ID
5'-most EST
                  LIB3040-041-Q1-E1-D1
Method
                  BLASTX
                  g3115852
NCBI GI
BLAST score
                  460
                  1.0e-45
E value
Match length
                  107
                  80
% identity
                  (AL022023) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4611
                  3813 3.R1040
Contig ID
                  q4277052
5'-most EST
                  BLASTX
Method
                  g3115852
NCBI GI
BLAST score
                  356
E value
                  9.0e-34
                  71
Match length
                  92
% identity
                   (AL022023) putative protein [Arabidopsis thaliana]
NCBI Description
                  4612
Seq. No.
Contig ID
                  3814 1.R1040
                  LIB3139-055-P1-N1-G5
5'-most EST
Method
                  BLASTX
                  a3738283
NCBI GI
BLAST score
                   421
E value
                  3.0e-41
Match length
                  83
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4613
Contig ID
                  3815_1.R1040
5'-most EST
                  jC-qmf102220085d03a1
Method
                  BLASTX
NCBI GI
                  q886132
BLAST score
                  408
E value
                  1.0e-39
Match length
                  235
                  42
% identity
NCBI Description
                  (U28149) putative surface protein [Medicago sativa]
```

```
4614
Seq. No.
Contig ID
                   3815 2.R1040
5'-most EST
                  LIB3028-025-Q1-B1-E5
Method
                   BLASTX
NCBI GI
                   q886132
BLAST score
                   252
E value
                   1.0e-21
Match length
                   97
% identity
                   52
NCBI Description
                   (U28149) putative surface protein [Medicago sativa]
                   4615
Seq. No.
Contig ID
                   3816 1.R1040
5'-most EST
                   bth700848583.hl
Method
                   BLASTX
NCBI GI
                   q2623297
BLAST score
                   260
E value
                   7.0e-22
Match length
                   101
% identity
                   52
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3790583 (AF079180) RING-H2 finger protein RHCla
                   [Arabidopsis thaliana]
                   4616
Seq. No.
                   3816 2.R1040
Contig ID
5'-most EST
                   epx701108636.hl
Method
                   BLASTX
NCBI GI
                   q3128178
BLAST score
                   201
E value
                   2.0e-15
Match length
                   58
% identity
                   57
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3816 3.R1040
Contig ID
                   LIB3028-025-Q1-B1-E6
5'-most EST
Seq. No.
                   4618
Contig ID
                   3819 1.R1040
                   LIB3049-052-Q1-E1-D5
5'-most EST
Method
                   BLASTX
                   g3257202
NCBI GI
BLAST score
                   209
E value
                   3.0e-16
Match length
                   121
                   40
% identity
                   (AP000003) 172aa long hypothetical protein [Pyrococcus
NCBI Description
                   horikoshii]
Seq. No.
                   4619
                   3823 1.R1040
Contig ID
                   LIB3028-025-Q1-B1-F2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3080438
                   401
BLAST score
```

Match length

```
E value
                   8.0e-39
                   140
Match length
                   65
% identity
NCBI Description
                   (AL022605) putative protein [Arabidopsis thaliana]
                   4620
Seq. No.
                   3824 1.R1040
Contig ID
                   k11701205335.h1
5'-most EST
Method
                   BLASTN
                   g287561
NCBI GI
BLAST score
                   181
                   3.0e-97
E value
                   325
Match length
                   89
% identity
NCBI Description
                   Vigna radiata auxin-regulated mRNA
                   4621
Seq. No.
                   3826_1.R1040
Contig ID
5'-most EST
                   uC-gmropic036b10b1
Method
                   BLASTX
                   g3395432
NCBI GI
BLAST score
                   1841
E value
                   0.0e+00
Match length
                   450
% identity
                   76
NCBI Description
                   (AC004683) unknown protein [Arabidopsis thaliana]
                   4622
Seq. No.
                   3826 2.R1040
Contig ID
                   2DC-01-Q1-E1-E1
5'-most EST
Method
                   BLASTX
                   g3915826
NCBI GI
BLAST score
                   1124
E value
                   1.0e-123
                   294
Match length
                   72
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L5
                   4623
Seq. No.
Contig ID
                   3826 3.R1040
                   fC-gmse700654972d1
5'-most EST
Method
                   BLASTX
                   g3395432
NCBI GI
BLAST score
                   278
                   1.0e-24
E value
Match length
                   65
% identity
                   77
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4624
                   3826 4.R1040
Contig ID
5'-most EST
                   jC-gmst02400017g01d1
Method
                   BLASTX
NCBI GI
                   q3914771
BLAST score
                   422
E value
                   2.0e-41
```

Match length

```
% identity
                   78
                   60S RIBOSOMAL PROTEIN L5 >gi_1881380_dbj_BAA19415
NCBI Description
                   (AB001583) ribosomal protein L5 [Solanum melongena]
Seq. No.
                   4625
                   3826 5.R1040
Contig ID
5'-most EST
                   g5753460
Method
                   BLASTX
NCBI GI
                   g3915826
BLAST score
                   575
                   3.0e-59
E value
                   140
Match length
                   74
% identity
                  60S RIBOSOMAL PROTEIN L5
NCBI Description
Seq. No.
                   4626
                   3826 6.R1040
Contig ID
                  LIB3094-047-Q1-K1-D3
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3915826
BLAST score
                   534
E value
                   1.0e-54
Match length
                  121
                   82
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
Seq. No.
                   4627
                   3826 8.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy121e11b1
Method
                  BLASTN
                   g1183936
NCBI GI
BLAST score
                   64
E value
                   2.0e-27
                  119
Match length
                  89
% identity
NCBI Description
                  P.sativum 5S rRNA gene
                   4628
Seq. No.
                   3826 12.R1040
Contig ID
5'-most EST
                   awf700841854.hl
                  BLASTX
Method
NCBI GI
                  q3914771
BLAST score
                   185
                  1.0e-13
E value
Match length
                   42
% identity
                  86
NCBI Description
                  60S RIBOSOMAL PROTEIN L5 >gi_1881380_dbj_BAA19415_
                   (AB001583) ribosomal protein L5 [Solanum melongena]
                   4629
Seq. No.
Contig ID
                   3826 13.R1040
5'-most EST
                   jex700908485.h1
Method
                  BLASTX
NCBI GI
                  q3395432
BLAST score
                   332
E value
                   7.0e-31
```

```
% identity
                   52
NCBI Description
                   (AC004683) unknown protein [Arabidopsis thaliana]
                   4630
Seq. No.
                   3826 19.R1040
Contig ID
5'-most EST
                   LIB3029-008-Q1-B1-G1
Method
                   BLASTX
                   g3914771
NCBI GI
                   253
BLAST score
                   1.0e-21
E value
Match length
                   67
                   73
% identity
                   60S RIBOSOMAL PROTEIN L5 >gi_1881380_dbj_BAA19415_
NCBI Description
                   (AB001583) ribosomal protein L5 [Solanum melongena]
Seq. No.
                   4631
Contig ID
                   3826 20.R1040
                   LIB3106-022-Q1-K1-E7
5'-most EST
                   4632
Seq. No.
                   3829 1.R1040 '
Contig ID
5'-most EST
                   LIB3039-020-Q1-E1-C4
Method
                   BLASTN
NCBI GI
                   g2565428
BLAST score
                   41
E value
                   1.0e-13
Match length
                   65
% identity
                   91
                  Onobrychis viciifolia glycine-rich protein mRNA, complete
NCBI Description
                   cds
                   4633
Seq. No.
                   3836 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400064a12d1
                   4634
Seq. No.
Contig ID
                   3838 1.R1040
5'-most EST
                   LIB3170-054-Q1-J1-D11
Method
                   BLASTX
NCBI GI
                   g2462835
BLAST score
                   180
                   5.0e-13
E value
Match length
                   104
                   32
% identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   4635
Seq. No.
Contig ID
                   3838 2.R1040
5'-most EST
                   LIB3028-025-Q1-B1-D3
                   4636
Seq. No.
Contig ID
                   3840 1.R1040
5'-most EST
                   q4396547
Method
                   BLASTN
                  g3860332
NCBI GI
BLAST score
                   134
```

5.0e-69

E value

% identity

```
Match length
                   361
% identity
                   84
NCBI Description Cicer arietinum mRNA for plantacyanin
                   4637
Seq. No.
                   3844 1.R1040
Contig ID
5'-most EST
                   LIB3170-079-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   q4220461
BLAST score
                   147
E value
                   3.0e-09
Match length
                   73
% identity
                   45
                   (AC006216) ESTs gb_T75642 and gb_AA650997 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   4638
Seq. No.
                   3845 1.R1040
Contig ID
5'-most EST
                   LIB3170-023-Q1-K1-F9
                   4639
Seq. No.
                   3845 2.R1040
Contig ID
                   LIB3039-032-Q1-E1-F2
5'-most EST
                   4640
Seq. No.
                   3846 1.R1040
Contig ID
5'-most EST
                   6HA - \overline{0}2 - Q1 - E1 - A7
Seq. No.
                   4641
                   3848 1.R1040
Contig ID
                   LIB3050-024-Q1-K1-C6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2500341
BLAST score
                   165
                   5.0e-11
E value
Match length
                   38
% identity
NCBI Description
                   50S RIBOSOMAL PROTEIN L36 >gi 1652406 dbj_BAA17328_
                   (D90905) 50S ribosomal protein L36 [Synechocystis sp.]
Seq. No.
                   4642
Contig ID
                   3849 1.R1040
5'-most EST
                   kmv700740822.h1
Seq. No.
                   4643
                   3854 1.R1040
Contiq ID
5'-most EST
                   uC-gmrominsoy241g01b1
                   4644
Seq. No.
Contig ID
                   3854 2.R1040
5'-most EST
                  LIB3052-002-Q1-B1-C2
Method
                   BLASTX
NCBI GI
                   g4572675
BLAST score
                   203
                   1.0e-15
E value
Match length
                  146
```

Match length

```
(AC006954) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    4645
 Seq. No.
 Contig ID
                    3854 3.R1040
 5'-most EST
                   LIB3053-003-Q1-N1-D3
                    4646
 Seq. No.
                    3855 1.R1040
 Contig ID
 5'-most EST
                    zhf700956406.hl
                   BLASTX
 Method
 NCBI GI
                    q3776581
 BLAST score
                    368
                    5.0e-35
 E value
 Match length
                    84
 % identity
                    75
                    (AC005388) Similar to Beta integral membrane protein
 NCBI Description
                   homolog gb U43629 from A. thaliana. [Arabidopsis thaliana]
 Seq. No.
                    4647
 Contig ID
                    3855 2.R1040
 5'-most EST
                   LIB3028-025-Q1-B1-B5
Method
                   BLASTX
NCBI GI
                   q3776581
 BLAST score
                   187
                    5.0e-14
 E value
Match length
                    46
 % identity
                   74
                    (AC005388) Similar to Beta integral membrane protein
 NCBI Description
                   homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]
 Seq. No.
                    4648
                    3857 1.R1040
 Contig ID
 5'-most EST
                   uC-gmflminsoy002b11b1
                    4649
 Seq. No.
 Contig ID
                    3857 2.R1040
5'-most EST
                    zhf700963527.h1
                    4650
 Seq. No.
 Contig ID
                    3858 1.R1040
 5'-most EST
                   uC-qmropic039f10b1
Method
                   BLASTX
 NCBI GI
                   g2809262
 BLAST score
                    698
 E value
                    3.0e-73
Match length
                   349
 % identity
                    44
NCBI Description
                    (AC002560) F21B7.31 [Arabidopsis thaliana]
 Seq. No.
                   4651
                   3858 2.R1040
 Contig ID
 5'-most EST
                   LIB3170-053-Q1-K1-F9
Method
                   BLASTX
 NCBI GI
                   g3201632
BLAST score
                   218
E value
                   9.0e-28
```

```
% identity
                   45
NCBI Description
                   (AC004669) putative 2A6 protein [Arabidopsis thaliana]
                   4652
Seq. No.
                   3858 3.R1040
Contig ID
5'-most EST
                   LIB3170-054-Q1-J1-C3
                   BLASTX
Method
NCBI GI
                   q2809262
BLAST score
                   308
E value
                   5.0e-28
Match length
                   124
                   53
% identity
                   (AC002560) F21B7.31 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4653
                   3861 1.R1040
Contig ID
5'-most EST
                   zhf700962573.h1
                   4654
Seq. No.
Contig ID
                   3861 2.R1040
5'-most EST
                   zhf700964117.h1
Seq. No.
                   4655
Contig ID
                   3861 3.R1040
5'-most EST
                   seb700648626.hl
Seq. No.
                   4656
Contig ID
                   3861 4.R1040
5'-most EST
                   LIB3050-011-Q1-E1-H6
Seq. No.
                   4657
                   3861 5.R1040
Contig ID
                   zhf700953349.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4454465
BLAST score
                   193
E value
                   6.0e-15
                   55
Match length
                   58
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   3862 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400044a05a1
Seq. No.
                   3863 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910007b04a1
                   4660
Seq. No.
                   3864 1.R1040
Contig ID
                   LIB3170-043-Q1-J1-C11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3941522
BLAST score
                   460
E value
                   5.0e-46
                   100
Match length
```

```
79
% identity
                   (AF062915) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   4661
Seq. No.
                   3868 1.R1040
Contig ID
5'-most EST
                   seb700653512.hl
                   BLASTX
Method
NCBI GI
                   q2842486
BLAST score
                   357
E value
                   1.0e-33
Match length
                   131
                   58
% identity
NCBI Description
                   (AL021749) putative protein [Arabidopsis thaliana]
Seq. No.
                   3868 2.R1040
Contig ID
5'-most EST
                   g4293429
Seq. No.
                   4663
Contig ID
                   3868_3.R1040
5'-most EST
                   uC-qmronoir064a11b1
Seq. No.
                   4664
Contig ID
                   3872 1.R1040
5'-most EST
                   jex700909729.hl
Method
                   BLASTX
NCBI GI
                   q1171161
BLAST score
                   654
E value
                   1.0e-68
Match length
                   175
% identity
                   (U41472) pectate lyase homolog [Medicago sativa]
NCBI Description
                   4665
Seq. No.
                   3876 1.R1040
Contig ID
5'-most EST
                   jex700904814.hl
Method
                   BLASTX
NCBI GI
                   q1171579
BLAST score
                   1857
E value
                   0.0e+00
Match length
                   478
% identity
                   73
                   (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   4666
Contig ID
                   3879 1.R1040
                   jex700905393.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2895576
BLAST score
                   557
E value
                   1.0e-56
Match length
                   433
                   29
% identity
                   (AF041337) vacuolar proton pump subunit SFD beta isoform
NCBI Description
```

[Bos taurus]

5'-most EST

```
4667
Seq. No.
                   3880 1.R1040
Contig ID
                   1eu7\overline{0}1145144.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q886130
BLAST score
                   443
E value
                   1.0e-43
Match length
                   224
% identity
                   42
NCBI Description
                   (U28148) putative pectinesterase [Medicago sativa]
Seq. No.
                   3882 1.R1040
Contig ID
5'-most EST
                  LIB3107-006-Q1-K1-E11
                   4669
Seq. No.
                   3882 2.R1040
Contig ID
5'-most EST
                  LIB3107-031-Q1-K1-H6
                   4670
Seq. No.
Contig ID
                   3888 1.R1040
                   zpv700759675.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1877279
BLAST score
                   367
E value
                   5.0e-35
Match length
                   115
% identity
                   58
                   (Z92770) fadE2 [Mycobacterium tuberculosis]
NCBI Description
Seq. No.
                   4671
Contig ID
                   3889 1.R1040
5'-most EST
                  uC-gmronoir064h11b1
Seq. No.
                   4672
                   3891 1.R1040
Contig ID
                  bth700847332.h1
5'-most EST
                   4673
Seq. No.
Contig ID
                   3897 1.R1040
5'-most EST
                  LIB3028-024-Q1-B1-C7
Seq. No.
                   4674
Contig ID
                   3899 1.R1040
5'-most EST
                   kl1701209291.hl
Method
                  BLASTX
NCBI GI
                  g2244973
BLAST score
                   324
                   1.0e-29
E value
                   123
Match length
% identity
                   (Z97340) similarity to extensin class 1 protein
NCBI Description
                   [Arabidopsis thaliana]
                   4675
Seq. No.
                   3900 1.R1040
Contig ID
```

leu701145246.h1

```
Seq. No.
                   4676
                   3900 2.R1040
Contig ID
                  LIB3028-021-Q1-B1-G11
5'-most EST
                   4677
Seq. No.
                   3900 3.R1040
Contig ID
5'-most EST
                   gsv701045626.hl
                   4678
Seq. No.
                   3902 1.R1040
Contig ID
5'-most EST
                  LIB3028-024-Q1-B1-D12
Method
                  BLASTX
                   g2960120
NCBI GI
BLAST score
                   563
                   1.0e-57
E value
                   248
Match length
                   47
% identity
                   (AL022121) glpK [Mycobacterium tuberculosis]
NCBI Description
                   4679
Seq. No.
                   3904 1.R1040
Contig ID
5'-most EST
                   gsv7\overline{0}1051707.h1
                  BLASTX
Method
NCBI GI
                   g2688828
BLAST score
                   290
E value
                   5.0e-26
Match length
                   121
                   50
% identity
                   (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
NCBI Description
                  armeniaca]
                   4680
Seq. No.
                   3906 1.R1040
Contig ID
5'-most EST
                  LIB3073-006-Q1-K1-E7
                  BLASTN
Method
NCBI GI
                  g2982267
BLAST score
                   150
E value
                   2.0e-78
Match length
                   422
                   84
% identity
                  Picea mariana probable 40S ribosomal protein S15 (Sb23)
NCBI Description
                  mRNA, complete cds
                   4681
Seq. No.
                   3906 2.R1040
Contig ID
5'-most EST
                  LIB3093-027-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2982267
BLAST score
                  178
                  4.0e-95
E value
Match length
                   422
% identity
                  86
                  Picea mariana probable 40S ribosomal protein S15 (Sb23)
NCBI Description
                  mRNA, complete cds
```

4682

Seq. No.

```
Contig ID
                   3906 3.R1040
                   crh7\overline{0}0855117.h1
5'-most EST
                   BLASTN
Method
                   g2982267
NCBI GI
                   117
BLAST score
                   8.0e-59
E value
                   425
Match length
                   83
% identity
                   Picea mariana probable 40S ribosomal protein S15 (Sb23)
NCBI Description
                   mRNA, complete cds
                   4683
Seq. No.
Contig ID
                   3910 1.R1040
5'-most EST
                   LIB3049-027-Q1-E1-E3
                   BLASTX
Method
                   q4539422
NCBI GI
BLAST score
                   416
                   9.0e-41
E value
                   117
Match length
                   68
% identity
                   (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                   4684
Seq. No.
                   3914 1.R1040
Contig ID
5'-most EST
                   gsv701043825.h1
Method
                   BLASTX
NCBI GI
                   q114200
BLAST score
                   165
                   3.0e-11
E value
                   117
Match length
                   38
% identity
                   SHIKIMATE KINASE PRECURSOR >gi 100253 pir_S21584 shikimate
NCBI Description
                   kinase precursor - tomato >gi_19349_emb_CAA45121_ (X63560)
                   shikimate kinase precursor [Lycopersicon esculentum]
Seq. No.
                   4685
                   3914 2.R1040
Contig ID
5'-most EST
                   q4260282
Method
                   BLASTX
NCBI GI
                   q114200
BLAST score
                   443
E value
                   4.0e-60
Match length
                   256
% identity
                   49
                   SHIKIMATE KINASE PRECURSOR >gi_100253_pir__S21584 shikimate .kinase precursor - tomato >gi_19349_emb_CAA45121_ (X63560)
NCBI Description
                   shikimate kinase precursor [Lycopersicon esculentum]
                   4686
Seq. No.
                   3915 1.R1040
Contig ID
                   LIB3028-024-Q1-B1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3913437
BLAST score
                   822
                   2.0e-88
E value
Match length
                   162
```

96

% identity

```
NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
                   HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
            . .
                   RNA helicase [Arabidopsis thaliana]
                   4687
Seq. No.
Contig ID
                   3916 1.R1040
5'-most EST
                   jC-qmro02800031h12d1
Seq. No.
                   3917 1.R1040 1
Contig ID
5'-most EST
                   LIB3028-024-Q1-B1-B3
Method
                   BLASTX
                   q4056495
NCBI GI
BLAST score
                   176
E value
                   1.0e-12
                   88
Match length
% identity
                   51
NCBI Description
                   (AC005896) putative TKRP125 [Arabidopsis thaliana]
                   4689
Seq. No.
                   3918 1.R1040
Contig ID
                   LIB3028-024-Q1-B1-B4
5'-most EST
Method
                   BLASTX
                   g2829910
NCBI.GI
BLAST score
                   1025
                   1.0e-112
E value
                   295
Match length
% identity
                   40
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                   chromosome condensation motifs [Arabidopsis thaliana]
                   4690
Seq. No.
Contig ID
                   3921 1.R1040
                   zzp700833785.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3881976
BLAST score
                   530
E value
                   5.0e-54
Match length
                   155
% identity
NCBI Description
                   (AJ012409) hypothetical protein [Homo sapiens]
Seq. No.
Contig ID
                   3922 1.R1040
5'-most EST
                   LIB3049-042-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   g1353516
BLAST score
                   2150
E value
                   0.0e + 00
Match length
                   501
% identity
NCBI Description
                   (U38651) sugar transporter [Medicago truncatula]
                   4692
Seq. No.
```

3922 2.R1040

q4282909

Contig ID 5'-most EST

```
Method
                   BLASTN
                   g169717
NCBI GI
BLAST score
                   54
                   2.0e-21
E value
Match length
                   110
                   87
% identity
                  Ricinus communis (clone PST293) sugar carrier protein
NCBI Description
                   (RCSTC) mRNA, complete CDS
Seq. No.
                   4693
                   3922_3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy258d01b1
Method
                   BLASTX
NCBI GI
                   g3915039
BLAST score
                   270
E value
                   2.0e-23
Match length
                   60
                   90
% identity
                  SUGAR CARRIER PROTEIN C >gi_169718 (L08196) sugar carrier
NCBI Description
                  protein [Ricinus communis]
                   4694
Seq. No.
                   3922 4.R1040
Contig ID
5'-most EST
                   fC-gmse7000755922r1
Method
                  BLASTX
NCBI GI
                   q1083942
BLAST score
                   651
                   6.0e-68
E value
                   254
Match length
                   48
% identity
NCBI Description
                  rubber particle cytochrome P450 - guayule
                   >gi_791093_emb_CAA55025_ (X78166) rubber particle protein
                   [Parthenium argentatum]
                   4695
Seq. No.
Contig ID
                   3922 5.R1040
5'-most EST
                   uC-qmrominsoy140g06b1
Method
                  BLASTX
NCBI GI
                   q1353516
BLAST score
                   431
E value
                   2.0e-42
Match length
                   120
                   72
% identity
NCBI Description
                   (U38651) sugar transporter [Medicago truncatula]
Seq. No.
Contig ID
                   3922 6.R1040
                   zhf700959335.hl
5'-most EST
Seq. No.
                   4697
                   3922 8.R1040
Contig ID
5'-most EST
                  uC-qmronoir024d11b1
Method
                  BLASTN
NCBI GI
                  g1353515
BLAST score
                  63
                  5.0e-27
E value
Match length
                  123
```

% identity

```
% identity
NCBI Description
                  Medicago truncatula sugar tranporter mRNA, complete cds
Seq. No.
Contig ID
                   3922 10.R1040
                   vwf700674586.hl
5'-most EST
Seq. No.
Contig ID
                   3923 1.R1040
5'-most EST
                   LIB3028-024-Q1-B1-C10
                   4700
Seq. No.
Contig ID
                   3925 1.R1040
5'-most EST
                   LIB3050-001-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   1136
E value
                   1.0e-124
Match length
                   302
% identity
                   73
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   4701
                   3925 2.R1040
Contig ID
5'-most EST
                   LIB3107-004-Q1-K1-F3
Method
                   BLASTX '
                   g3759184
NCBI GI
BLAST score
                   728
E value
                   4.0e-77
Match length
                   222
% identity
                   68
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
Contig ID
                   3928 1.R1040
5'-most EST
                   leu701156935.hl
Method
                   BLASTX
NCBI GI
                   g3413322
BLAST score
                   688
E value
                   2.0e-72
                   191
Match length
% identity
                   68
                   (Y11118) polygalacturonase [Medicago sativa]
NCBI Description
                   4703
Seq. No.
Contig ID
                   3929 1.R1040
5'-most EST
                   LIB3028-023-Q1-B1-H5
                   4704
Seq. No.
                   3932 1.R1040
Contig ID
5'-most EST
                   LIB3092-017-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                   q1076288
BLAST score
                   393
E value
                   7.0e-38
Match length
                   149
```

```
NCBI Description amino acid permease AAP3 - Arabidopsis thaliana
                   4705
Seq. No.
Contig ID
                   3937 1.R1040
5'-most EST
                   hyd700730315.hl
Method
                   BLASTN
NCBI GI
                   g20872
BLAST score
                   217
E value
                   1.0e-118
Match length
                   525
% identity
                   85
                   Pea mRNA for plastid ribosomal protein CL24
NCBI Description
Seq. No.
Contig ID
                   3940 1.R1040
5'-most EST
                   LIB3170-042-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   q285741
BLAST score
                   1512
E value
                   1.0e-168
Match length
                   422
                   70
% identity
NCBI Description (D14550) EDGP precursor [Daucus carota]
                   4707
Seq. No.
Contig ID "
                   3941 1.R1040
5'-most EST
                   fua701042582.h1
Method
                   BLASTN
NCBI GI
                   q1620908
BLAST score
                   239
E value
                   1.0e-131
Match length
                   523
% identity
                   86
NCBI Description Carrot mRNA for DcARF1, complete cds
Seq. No.
                   4708
Contig ID
                   3941 2.R1040
5'-most EST
                   LIB3109-035-Q1-K1-D6
Method
                   BLASTN
NCBI GI
                   q1620908
BLAST score
                   235
E value
                   1.0e-129
Match length
                   531
% identity
                   86
NCBI Description Carrot mRNA for DcARF1, complete cds
Seq. No.
                   4709
                   3941 3.R1040
Contig ID
                   LIB3106-060-Q1-K1-G9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2281102
BLAST score
                   213
E value
                   1.0e-16
Match length
                   93
                   71
% identity
```

NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]

```
4710
Seq. No.
Contig ID
                   3941 4.R1040
5'-most EST
                   jex700910011.hl
Method
                  BLASTX
NCBI GI
                   q3819099
BLAST score
                   211
E value
                   6.0e-17
Match length
                  75
% identity
                   56
NCBI Description
                   (AJ009825) copper amine oxidase [Cicer arietinum]
Seq. No.
                   4711
Contig ID
                   3941 5.R1040
5'-most EST
                  LIB3109-035-Q1-K6-D12
Method
                  BLASTX
NCBI GI
                  q2501337
BLAST score
                   432
E value
                   6.0e-46
Match length
                  118
% identity
                   75
NCBI Description
                  AMINE OXIDASE PRECURSOR [COPPER-CONTAINING]
                  >gi_2129875_pir__C44239 amine oxidase (copper-containing)
                   (EC 1.4.3.6) precursor - garden pea >gi 685198 (L39931)
                  copper amine oxidase [Pisum sativum]
Seq. No.
                  4712
                   3941 6.R1040
Contig ID
5'-most EST
                  kl1701214261.h1
Seq. No.
                   4713
                   3941 7.R1040
Contig ID
                  LIB3074-011-Q1-E1-B4
5'-most EST
Seq. No.
                   4714
Contig ID
                   3941 9.R1040
5'-most EST
                  jC-qmst02400039f10a1
Method
                  BLASTN
NCBI GI
                  q1620908
BLAST score
                  42
                  3.0e-14
E value
Match length
                  70
% identity
                  90
                  Carrot mRNA for DcARF1, complete cds
NCBI Description
Seq. No.
                   4715
Contig ID
                  3941 10.R1040
5'-most EST
                  jC-gmst02400047a03d1
Method
                  BLASTN
                  q1620908
NCBI GI
BLAST score
                  59
E value
                  2.0e-24
Match length
                  135
                  86
% identity
                  Carrot mRNA for DcARF1, complete cds
NCBI Description
Seq. No.
                   4716
```

3941 12.R1040

Contig ID.

```
LIB3087-012-01-K1-A5
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1184986
BLAST score
                  . 76
E value
                  2.0e-34
Match length
                  160
% identity
                  87
                  Nicotiana tabacum GTP-binding protein NTGB1 mRNA, partial
NCBI Description
                  4717
Seq. No.
                  3942 1.R1040
Contig ID
5'-most EST
                  LIB3040-008-Q1-E1-G9
Method
                  BLASTN
                  q170919
NCBI GI
BLAST score
                  122
E value
                  8.0e-62
Match length
                  322
% identity
                  85
                  C.maltosa ribosomal protein L41 (LEL41) gene, complete cds
NCBI Description
Seq. No.
                 · 3943 1.R1040
Contig ID
                  pmv700895034.hl
5'-most EST
                  4719
Seq. No.
                  3944 1.R1040
Contig ID
                  pmv700893947.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3894194
BLAST score
                  479
E value
                  7.0e-48
Match length
                  158
% identity
                  56
NCBI Description
                  (AC005662) putative strictosidine synthase [Arabidopsis
                  thaliana]
                  4720
Seq. No.
                  3945 1.R1040
Contig ID
5'-most EST
                  LIB3039-042-Q1-E1-C11
                  4721
Seq. No.
                  3945 2.R1040
Contig ID
5'-most EST
                  smc700747713.h1
                  4722
Seq. No.
Contig ID
                  3946 1.R1040
                  LIB3049-002-Q1-E1-D7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3283893
BLAST score
                  143
E value
                  8.0e-12
Match length
                  87
% identity
                  43
NCBI Description
                 (AF070626) unknown [Homo sapiens]
```

4723

Seq. No.

% identity

```
3946_2.R1040
Contig ID
                  LIB3170-029-Q1-K1-D3
5'-most EST
Method
                  BLASTX
                  g3283893
NCBI GI
BLAST score
                  157
                  2.0e-10
E value
Match length
                  70
% identity
                  46
NCBI Description
                  (AF070626) unknown [Homo sapiens]
Seq. No.
                  4724
                  3946 3.R1040
Contig ID
5'-most EST
                  jC-gmf102220063h02a1
                  4725
Seq. No.
                  3946 4.R1040
Contig ID
                  LIB3073-006-Q1-K1-A12
5'-most EST
                  4726
Seq. No.
Contig ID
                  3947 1.R1040
                  LIB3028-023-Q1-B1-G10
5'-most EST
Method
                  BLASTX
                  g2832640
NCBI GI
BLAST score
                  592
                  2.0e-61
E value
Match length
                  159
% identity
                  69
                   (AL021710) neoxanthin cleavage enzyme - like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  4727
Contig ID
                  3949 1.R1040
5'-most EST
                  fua701038069.h1
                  BLASTX
Method
NCBI GI
                  g1174583
BLAST score
                  298
E value
                  1.0e-26
Match length
                  162
                  40
% identity
                  TRANSALDOLASE >gi_1074653_pir__D64167 hypothetical protein
NCBI Description
                  HI1125 - Haemophilus influenzae (strain Rd KW20)
                  >gi 1574680 (U32792) transaldolase B (talB) [Haemophilus
                  influenzae Rd]
Seq. No.
                  4728
Contig ID
                  3949 2.R1040
5'-most EST
                  asn701140690.h1
Seq. No.
                  4729
                  3951 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy048d09b1
Method
                  BLASTX
NCBI GI
                  q2499710
BLAST score
                  1620
E value
                  0.0e + 00
Match length
                  346
```

```
NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                   >qi 1438075 (L33686) phospholipase D [Ricinus communis]
                   4730
Seq. No.
                   3951 2.R1040
Contig ID
5'-most EST
                   LIB3\overline{0}51-105-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g3914359
BLAST score
                   1877
E value
                   0.0e + 00
Match length
                   382
                   90
% identity
                   PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
NCBI Description
                   >qi 1928979 (U92656) phospholipase D [Vigna unguiculata]
                   4731
Seq. No.
Contig ID
                   3952 1.R1040
5'-most EST
                   asn7\overline{0}1138149.h1
Method
                   BLASTX
NCBI GI
                   q3024706
BLAST score
                   280
E value
                   2.0e-24
Match length
                   94
% identity
                   60
                   TRANSCRIPTION INITIATION FACTOR TFIID 18 KD SUBUNIT
NCBI Description
                   (TAFII-18) (TAFII18) >gi_1362894_pir__S54782 PolII
                   transcription factor TFIID chain hTAFII18 - human
                   >gi 791053_emb_CAA58827_ (X84003) PolII transcription
                   factor TFIID [Homo sapiens]
                   4732
Seq. No.
Contig ID
                   3952 2.R1040
5'-most EST
                   LIB3051-034-Q1-K1-C10
                   4733
Seq. No.
                   3952 3.R1040
Contig ID
5'-most EST
                   LIB3028-023-Q1-B1-G5
                   4734
Seq. No.
                   3953 1.R1040
Contig ID
5'-most EST
                   LIB3028-023-Q1-B1-G6
Seq. No.
                   4735
Contig ID
                   3956 1.R1040
                   zhf700956881.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2494299
BLAST score
                   1032
E value
                   1.0e-112
Match length
                   269
% identity
                   76
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
NCBI Description
```

factor 2 beta [Malus domestica]

(EIF-2-BETA) >gi\_1732361 (U80269) translation initiation

```
4736
Seq. No.
                  3957 1.R1040
Contig ID
5'-most EST
                  LIB3139-055-P1-N1-E11
Method
                  BLASTN
                  g408793
NCBI GI
BLAST score
                  698
                  0.0e + 00
E value
Match length
                  801
                   98
% identity
                  Glycine soja chloroplast 3-omega faty acid desaturase
NCBI Description
                   (Fad3) mRNA, complete cds
Seq. No.
                   4737
                  3957 2.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy036a11b1
Method
                  BLASTN
NCBI GI
                  g408793
BLAST score
                  235
E value
                  1.0e-129
                  635
Match length
% identity
                  92
NCBI Description Glycine soja chloroplast 3-omega faty acid desaturase
                   (Fad3) mRNA, complete cds
                  4738
Seq. No.
                  3958 1.R1040
Contig ID
5'-most EST
                  LIB3028-023-Q1-B1-D4
Seq. No.
                  4739
Contig ID
                  3961 1.R1040
5'-most EST
                  zsg701120931.h1
                  BLASTX
Method
NCBI GI
                  q3184061
BLAST score
                  340
E value
                  1.0e-31
Match length
                  177
% identity
                  (AL023776) atp dependent helicase [Schizosaccharomyces
NCBI Description
                  pombe]
Seq. No.
                  4740
Contig ID
                  3962 1.R1040
5'-most EST
                  LIB3049-025-Q1-E1-H8
                  4741
Seq. No.
                  3964 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400020dg12d1
                  4742
Seq. No.
                  3968 1.R1040
Contig ID
5'-most EST
                  LIB3028-023-Q1-B1-E4
Seq. No.
                  4743
                  3970 1.R1040
Contig ID
5'-most EST
                  jC-gmro02800029h10a1
Method
                  BLASTX
NCBI GI
                  g3329368
```

5'-most EST

g5687826

```
735
BLAST score
                  1.0e-77
E value
Match length
                  377
% identity
                  43
NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]
                  4744
Seq. No.
                  3971 1.R1040
Contig ID
                  dpv7\overline{0}1102529.h1
5'-most EST
                  BLASTX
Method
                  g481896
NCBI GI
BLAST score
                  498
                  8.0e-50
E value
Match length
                  246
% identity
                  41
                  chitinase (EC 3.2.1.14) - rice
NCBI Description
Seq. No.
                  3971 2.R1040
Contig ID
5'-most EST
                  jC-gmf102220085d04d1
Seq. No.
                  3971 3.R1040
Contig ID
5'-most EST
                  pxt700945993.h1
Seq. No.
                  4747
                  3972 1.R1040
Contig ID
5'-most EST
                  bth700847151.h1
Method
                  BLASTX
NCBI GI
                  g2829751
BLAST score
                  205
                  8.0e-16
E value
                  114
Match length
                  37
% identity
                  MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF)
NCBI Description
                  >gi_1850559 (U88035) macrophage migration inhibitory factor
                  [Brugia malayi] >gi_2190976 (AF002699) macrophage migration
                 inhibitory factor [Brugia malayi]
                  4748
Seq. No.
                  3974 1.R1040
Contig ID
5'-most EST
                  LIB3028-023-Q1-B1-B7
                  4749
Seq. No.
                  3979 1.R1040
Contig ID
5'-most EST
                  LIB3028-023-Q1-B1-C3
Method
                  BLASTX
NCBI GI
                  q3702333
BLAST score
                  196
E value
                  4.0e-15
                  95
Match length
                  49
% identity
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  4750
Seq. No.
                  3983 1.R1040
Contig ID
```

Match length

```
BLASTX
Method
                   g4406772
NCBI GI
BLAST score
                   306
                   2.0e-27
E value
Match length
                   119
                   55
% identity
                   (AC006836) putative nitrilase-associated protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   4751
Contig ID
                   3983 2.R1040
5'-most EST
                   sat701003125.h1
Method
                   BLASTX
NCBI GI
                   g2765837
BLAST score
                   279
E value
                   2.0e-24
                   131
Match length
                   50
% identity
                   (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
                   4752
Seq. No.
Contig ID
                   3983 3.R1040
5'-most EST
                   jC-gmro02910061a08a1
Seq. No.
                   4753
                   3983 4.R1040
Contig ID
5'-most EST
                   LIB3053-006-Q1-N1-A8
                   BLASTX
Method
                   g2765837
NCBI GI
BLAST score
                   208
E value
                   4.0e-16
Match length
                   102
% identity
                   49
NCBI Description
                   (Z96936) NAP16kDa protein [Arabidopsis thaliana]
                   4754
Seq. No.
Contig ID
                   3987 1.R1040
                   pmv7\overline{0}0894858.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3860246
BLAST score
                   172
E value
                   1.0e-11
Match length
                   153
% identity
                   36
                   (AC005824) putative reverse-transcriptase protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4510429_gb_AAD21515.1_
                   (AC006929) putative reverse transcriptase [Arabidopsis
                   thaliana]
                   4755
Seq. No.
                   3988 1.R1040
Contig ID
5'-most EST
                   ssr700556516.hl
Method
                   BLASTX
NCBI GI
                   q2245012
BLAST score
                   172
                   4.0e-21
E value
```

E value

```
% identity
                   58
                   (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   4756
Seq. No.
                   3990 1.R1040
Contig ID
                  uC-gmropic018e11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4107276
BLAST score
                   1010
                   1.0e-137
E value
Match length
                   271
% identity
                   85
                  (X98506) acetyl-CoA synthetase [Solanum tuberosum]
NCBI Description
Seq. No.
                   4757
                   3991 1.R1040
Contig ID
5'-most EST
                   q4287582
Method
                   BLASTX
NCBI GI
                   g4335745
BLAST score
                   387
E value
                   4.0e-37
Match length
                  192
                   42
% identity
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   4758
Seq. No.
                   3992 1.R1040
Contig ID
                  uC-gmrominsoy216h02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2196466
BLAST score
                   256
E value
                   2.0e-21
                   267
Match length
% identity
                   44
NCBI Description
                   (Y13673) TATA binding protein-associated factor
                   [Arabidopsis thaliana]
                   4759
Seq. No.
                   3993 1.R1040
Contig ID
5'-most EST
                  LIB3028-023-Q1-B1-A2
Method
                  BLASTX
NCBI GI
                   g3510248
BLAST score
                  200
E value
                   2.0e-15
Match length
                   94
% identity
NCBI Description
                   (AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   4760
Contig ID
                   4001 1.R1040
5'-most EST
                  txt700732386.h1
Method
                  BLASTX
NCBI GI
                  g2911044
BLAST score
                  461
```

1.0e-46

```
225
Match length
% identity
                   49
NCBI Description
                   (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                   4761
                   4001 2.R1040
Contig ID
5'-most EST
                   LIB3170-074-Q1-J1-A6
                   4762
Seq. No.
Contig ID
                   4007 1.R1040
                   LIB3028-022-Q1-B1-G10
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3924611
BLAST score
                   584
E value
                   1.0e-70
Match length
                   207
% identity
                   67
NCBI Description
                   (AF069442) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   4763
Contig ID
                   4011 1.R1040
5'-most EST
                   LIB3073-024-Q1-K1-F6
Method
                   BLASTN
NCBI GI
                   q166421
BLAST score
                   163
E value
                   3.0e-86
Match length
                   459
% identity
                   84
NCBI Description
                  Medicago sativa ubiquitin carrier protein mRNA, complete
Seq. No.
                   4764
                   4011 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir062f10b1
Method
                   BLASTN
NCBI GI
                   q166421
BLAST score
                   171
E value
                   6.0e-91
Match length
                   459
% identity
                   84
NCBI Description
                  Medicago sativa ubiquitin carrier protein mRNA, complete
                   4765
Seq. No.
                   4011 3.R1040
Contig ID
5'-most EST
                   xpa700794105.h1
Method
                   BLASTN
NCBI GI
                   g166923
BLAST score
                   78
                   9.0e-36
E value
Match length
                   234
% identity
                   84
                  Arabidopsis thaliana ubiquitin carrier protein (UBC1) mRNA,
NCBI Description
                   complete cds
                   4766
Seq. No.
Contig ID
                   4011 6.R1040
```

```
5'-most EST
                   g5510194
Method
                   BLASTN
NCBI GI
                   g166421
BLAST score
                   38
                   5.0e-12
E value
Match length
                   86
% identity
                   86
                   Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                   4767
Seq. No.
                   4015_1.R1040
Contig ID
                   k117\overline{0}1211906.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3004556
BLAST score
                   363
E value
                   2.0e-34
Match length
                   130
% identity
                   67
NCBI Description
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
                   4768
Seq. No.
                   4019_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910021b09d1
Method
                   BLASTX
NCBI GI
                   g3021506
BLAST score
                   1639
                   0.0e + 00
E value
                   359
Match length
% identity
                   89
NCBI Description
                   (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
                   tabacum]
                   4769
Seq. No.
                   4019 2.R1040
Contig ID
5'-most EST
                   LIB3051-090-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g3021506
BLAST score
                   313
                   1.0e-28
E value
Match length
                   90
% identity
                   72
                   (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
NCBI Description
                   tabacum]
                   4770
Seq. No.
Contig ID
                   4019 3.R1040
5'-most EST
                   LIB3093-007-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   g3021506
BLAST score
                   273
E value
                   4.0e-24
Match length
                   80
% identity
NCBI Description
                   (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
                   tabacum]
```

% identity

```
4771
Seq. No.
                   4019 5.R1040
Contig ID
5'-most EST
                   jex700904639.h1
                   4772
Seq. No.
                   4020 1.R1040
Contig ID
5'-most EST
                   LIB3039-027-Q1-E1-B10
                   BLASTX
Method
NCBI GI
                   q2695711
BLAST score
                   619
E value
                   3.0e-64
Match length
                   134
                   84
% identity
NCBI Description
                   (AJ001370) cytochome b5 [Olea europaea]
                   4773
Seq. No.
Contig ID
                   4020 2.R1040
5'-most EST
                   fC-gmro700848840a1
Method
                   BLASTN
NCBI GI
                   g2647950
BLAST score
                   59
E value
                   2.0e-24
Match length
                   123
% identity
                   87
                  Olea europaea cytochrome b5 gene-2
NCBI Description
                   4774
Seq. No.
                   4020 3.R1040
Contig ID
5'-most EST
                   bth700848441.h1
                   BLASTX
Method
NCBI GI
                   g4240120
BLAST score
                   226
                   9.0e-19
E value
Match length
                   64
                   69
% identity
NCBI Description
                   (AB007801) cytochrome b5 [Arabidopsis thaliana]
                   4775
Seq. No.
Contig ID
                   4024 1.R1040
5'-most EST
                  LIB3028-022-Q1-B1-E10
Method
                   BLASTX
NCBI GI
                   q4558665
BLAST score
                   170
E value
                   5.0e-12
Match length
                   124
                   29
% identity
NCBI Description
                   (AC007063) putative white protein [Arabidopsis thaliana]
Seq. No.
                   4776
Contig ID
                   4026 1.R1040
5'-most EST
                   hyd700725705.h1
Method
                   BLASTX
NCBI GI
                   q2462753
BLAST score
                   306
E value
                   4.0e-32
Match length
                   129
```

5'-most EST

```
NCBI Description (AC002292) putative polygalacturonase [Arabidopsis
                   thaliana]
                  4777
Seq. No.
                   4028 1.R1040
Contig ID
                   jex700908404.hl
5'-most EST
                  BLASTX
Method
                  q4218120
NCBI GI
BLAST score
                   283
                   4.0e-25
E value
Match length
                   90
% identity
                   64
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   4778
Seq. No.
Contig ID
                   4028 2.R1040
5'-most EST
                  LIB3030-004-Q1-B1-G8
Method
                  BLASTX
NCBI GI
                  q4218120
BLAST score
                   444
E value
                   4.0e-44
Match length
                  109
                   78
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                  thaliana]
                  4779
Seq. No.
Contig ID
                  4031 1.R1040
5'-most EST
                  wrq7\overline{0}0788672.h1
Method
                  BLASTX
NCBI GI
                  g3702327
BLAST score
                  576
E value
                  3.0e-59
Match length
                  162
                  75
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
                  4780
Seq. No.
                  4031 3.R1040
Contig ID
                  LIB3056-010-Q1-N1-H8
5'-most EST
                  4781
Seq. No.
                  4037 1.R1040
Contig ID
                  LIB3049-042-Q1-E1-D9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3342800
BLAST score
                  848
E value
                  4.0e-91
Match length
                  211
% identity
                  78
NCBI Description
                  (AF061837) putative cytosolic 6-phosphogluconate
                  dehydrogenase [Zea mays]
                  4782
Seq. No.
                  4037 2.R1040
Contig ID
```

LIB3028-022-Q1-B1-D5

Contig ID

5'-most EST

```
BLASTX
Method
                   a3342802
NCBI GI
BLAST score
                   461
E value
                   1.0e-45
Match length
                   133
                   54
% identity
                   (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                   dehydrogenase [Zea mays]
Seq. No.
                   4783
                   4037 3.R1040
Contig ID
                   fua7\overline{0}1038701.h1
5'-most EST
Method
                   BLASTX
                   q3342802
NCBI GI
                   261
BLAST score
                   1.0e-22
E value
                   69
Match length
                   75
% identity
                   (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                   dehydrogenase [Zea mays]
                   4784
Seq. No.
                   4037 4.R1040
Contig ID
5'-most EST
                   uC-gmropic063f06b1
                   BLASTX
Method
NCBI GI
                   g2529229
BLAST score
                   751
                   6.0e-80
E value
                   195
Match length
% identity
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                   4785
Contig ID
                   4038 1.R1040
5'-most EST
                   LIB3139-014-P1-N1-E12
Method
                   BLASTX
NCBI GI
                   g1431629
BLAST score
                   1863
                   0.0e + 00
E value
                   399
Match length
% identity
                   (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                   4786
Seq. No.
                   4038 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy119e06b1
                   BLASTX
Method
                   g1431629
NCBI GI
BLAST score
                   754
E value
                   3.0e-80
Match length
                   203
% identity
                   (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                   4787
Seq. No.
```

4038 3.R1040

 $dpv7\overline{0}1102573.h1$ 

Method

BLASTX

```
Method
                  BLASTN
NCBI GI
                  g1431628
BLAST score
                  248
E value
                  1.0e-137
Match length
                  356
% identity
                  92
NCBI Description V.radiata mRNA for pectinacetylesterase
                  4788
Seq. No.
                  4038 4.R1040
Contig ID
5'-most EST
                  jC-gmro02910008e06a1
                  BLASTN
Method
                  a1431628
NCBI GI
BLAST score
                  89
E value
                  3.0e-42
Match length
                  196
                  90
% identity
                  V.radiata mRNA for pectinacetylesterase
NCBI Description
                  4789
Seq. No.
                  4040 1.R1040
Contig ID
5'-most EST
                  LIB3109-021-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q1170508
BLAST score
                  1957
E value
                  0.0e + 00
Match length
                  399
% identity
                  94
                  EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
NCBI Description
                  >gi 2119931_pir__S60244 translation initiation factor
                  eIF-4A.8, anther-specific - common tobacco
                  >gi 475219_emb_CAA55639_ (X79004) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
                  >gi 475221 emb CAA55640 (X79005) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
Seq. No.
                  4790
                  4040 2.R1040
Contig ID
                  g5606855
5'-most EST
Method
                  BLASTX
                  g1170508
NCBI GI
BLAST score
                  974
E value
                  1.0e-106
Match length
                  202
% identity
                  92
                  EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
NCBI Description
                  >qi 2119931 pir S60244 translation initiation factor
                  eIF-4A.8, anther-specific - common tobacco
                  >qi 475219 emb CAA55639 (X79004) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
                  >gi 475221 emb_CAA55640_ (X79005) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
                  4791
Seq. No.
Contig ID
                  4040 3.R1040
                  ncj7\overline{0}0986770.h1
5'-most EST
```

19.50

```
g2119933
NCBI GI
BLAST score
                   602.
E value
                   2.0e-62
Match length
                   125
% identity
                   92
                  translation initiation factor eIF-4A.11 - common tobacco
NCBI Description
Seq. No.
Contig ID
                   4040 4.R1040
5'-most EST
                   jC-qmst02400031b10d1
Method
                   BLASTX
NCBI GI
                   q1170508
BLAST score
                   424
E value
                   1.0e-41
Match length
                   92
% identity
                   92
                  EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
NCBI Description
                  >gi_2119931_pir__S60244 translation initiation factor
                  eIF-4A.8, anther-specific - common tobacco
                  >gi_475219_emb_CAA55639_ (X79004) translation initiation
                   factor (eIF-4A) [Nicotiana tabacum]
                  >gi_475221_emb_CAA55640_ (X79005) translation initiation
                   factor (eIF-4A) [Nicotiana tabacum]
Seq. No.
                   4793
                   4040 5.R1040
Contig ID
                  LIB3107-067-Q1-K1-C4
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2119933
BLAST score
                   456
E value
                  2.0e-45
Match length
                  94
                  93
% identity
NCBI Description
                  translation initiation factor eIF-4A.11 - common tobacco
                   4794
Seq. No.
                   4046 1.R1040
Contig ID
                  k117\overline{0}1206255.h1
5'-most EST
Method
                  BLASTX
                  g4406801
NCBI GI
BLAST score
                  309
E value
                  6.0e-29
                  121
Match length
                  52
% identity
NCBI Description (AC006304) unknown protein [Arabidopsis thaliana]
                  4795
Seq. No.
                  4047 1.R1040
Contig ID
5'-most EST
                  crh700851546.h1
Method
                  BLASTN
                  g22635
NCBI GI
BLAST score
                  349
                  0.0e+00
E value
Match length
                  617
% identity
                  90
```

NCBI Description P.vulgaris mRNA for 70 kD heat shock protein

```
4796
Seq. No.
                   4047_2.R1040
Contig ID
                   jC-gmf102220069b04d1
5'-most EST
Method
                   BLASTN
                   g22635
NCBI GI
BLAST score
                   73
                   7.0e-33
E value
                   160
Match length
% identity
                   87
NCBI Description
                  P.vulgaris mRNA for 70 kD heat shock protein
Seq. No.
Contig ID
                   4050 1.R1040
5'-most EST
                   wvk700683438.hl
                   4798
Seq. No.
                   4051 1.R1040
Contig ID
5'-most EST
                  LIB3028-022-Q1-B1-C6
Method
                  BLASTX
NCBI GI
                  q4388728
BLAST score
                   173
                   1.0e-13
E value
Match length
                  84
% identity
NCBI Description
                   (AC006413) putative grrl-like protein [Arabidopsis
                   thaliana]
                   4799
Seq. No.
Contig ID
                   4053 1.R1040
5'-most EST
                  LIB3030-003-Q1-B1-E5
Method
                  BLASTX
NCBI GI
                   g1199467
BLAST score
                   707
E value
                   8.0e-75
Match length
                  163
% identity
                   70
                   (D64155) possible aldehyde decarbonylase [Arabidopsis
NCBI Description
                  thaliana]
                   4800
Seq. No.
                   4054 1.R1040
Contig ID
5'-most EST
                   fC-gmle700683850f1
Method
                  BLASTX
NCBI GI
                  g2352812
BLAST score
                  516
E value
                  3.0e-52
                  179
Match length
                  56
% identity
                   (AF008597) desacetoxyvindoline-4-hydroxylase [Catharanthus
NCBI Description
                  roseus]
                   4801
Seq. No.
                   4055 1.R1040
Contig ID
                  hrw701058906.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2224732
BLAST score
                  109
```

Contig ID

```
E value
                   3.0e-54
Match length
                   356
% identity
                   87
NCBI Description
                  Vigna radiata mRNA for Aux22e, complete cds
Seq. No.
                   4055 2.R1040
Contig ID
5'-most EST
                   fjg700968470.hl
Method
                   BLASTN
NCBI GI
                   g2224732
BLAST score
                   112
E value
                   5.0e-56
Match length
                   331
% identity
                   89
NCBI Description
                  Vigna radiata mRNA for Aux22e, complete cds
Seq. No.
                   4803
                   4056 1.R1040
Contig ID
5'-most EST
                  bth700849157.h1
                   4804
Seq. No.
                   4056 2.R1040
Contig ID
5'-most EST
                   epx701108971.hl
                   4805
Seq. No.
Contig ID
                   4061 1.R1040
5'-most EST
                  LIB3109-011-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2443886
BLAST score
                   147
E value
                   5.0e-09
Match length
                   136
% identity
                   33
NCBI Description
                   (AC002294) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   4063 1.R1040
Contig ID
5'-most EST
                  LIB3049-042-Q1-E1-G12
Seq. No.
                   4807
                   4063 2.R1040
Contig ID
5'-most EST
                  LIB3049-006-Q1-E1-F2
                   4808
Seq. No.
                   4064 1.R1040
Contig ID
5'-most EST
                  LIB3139-016-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  g2924781
BLAST score
                  509
E value
                  7.0e-52
Match length
                  126
% identity
                   (AC002334) putative cellulose synthase [Arabidopsis
NCBI Description
                  thaliana]
                   4809
Seq. No.
```

4066 1.R1040

Match length

```
pmv700890148.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1747310
BLAST score
                  849
E value
                  5.0e-91
Match length
                  314
% identity
                  54
NCBI Description
                   (D58424) Myb-like DNA binding protein [Arabidopsis
                  thaliana]
                  4810
Seq. No.
                  4067 1.R1040
Contig ID
                  txt700732591.hl
5'-most EST
Method
                  BLASTX
                  q4454452
NCBI GI
BLAST score
                  313
E value
                  1.0e-28
Match length
                  100
% identity
                  62
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  4811
Seq. No.
Contig ID
                  4068 1.R1040
                  LIB3107-006-Q1-K1-G1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1781299
BLAST score
                  289
E value
                  1.0e-25
Match length
                  82
% identity
                  66
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  4812
Contig ID
                  4068 2.R1040
5'-most EST
                  LIB3170-054-Q1-K1-A1
Seq. No.
                  4813
                  4069 1.R1040
Contig ID
                  fC-qmle700685876f1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4432858
BLAST score
                  317
E value
                  6.0e-29
                  231
Match length
% identity
                   (AC006300) putative disease resistance protein [Arabidopsis
NCBI Description
                  thaliana]
                  4814
Seq. No.
                  4074 1.R1040
Contig ID
5'-most EST
                  LIB3138-045-Q1-N1-F6
Method
                  BLASTX
NCBI GI
                  g4512678
BLAST score
                  947
                  1.0e-102
E value
```

Seq. No.

```
73
% identity
                   (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                   4815
Seq. No.
                   4074 2.R1040
Contig ID
5'-most EST
                   LIB3138-074-P1-N1-H5
                   BLASTX
Method
NCBI GI
                   g4512678
BLAST score
                   474
                   2.0e-47
E value
Match length
                   158
% identity
                   61
                   (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4816
                   4074 3.R1040
Contig ID
5'-most EST
                   LIB3170-012-Q1-J1-F9
Seq. No.
                   4817
Contig ID
                   4075 1.R1040
                   zhf700951788.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1293835
BLAST score
                   486
                   2.0e-48
E value
Match length
                   286
% identity
                   38
                   (U56965) C15H9.5 gene product [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   4818
Contig ID
                   4075 3.R1040
5'-most EST
                   LIB3170-021-Q1-K1-B9
Seq. No.
                   4819
                   4075_4.R1040
Contig ID
5'-most EST
                   jC-gmst02400071d07d1
Method
                  BLASTN
NCBI GI
                   q3510343
BLAST score
                   45
                   6.0e-16
E value
Match length
                   141
% identity
                   83
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   4820
Contig ID
                   4076 1.R1040
5'-most EST
                  LIB3039-028-Q1-E1-A2
Method
                  BLASTX
NCBI GI
                  q4127456
BLAST score
                   321
E value
                   2.0e-29
Match length
                  149
% identity
NCBI Description
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
```

BLAST score

```
4076 2.R1040
Contig ID
5'-most EST
                   zhf700958459.h1
                   BLASTX
Method
NCBI GI
                  g4127456
BLAST score
                   222
                   5.0e-18
E value
                   87
Match length
                   43
% identity
NCBI Description
                   (AJ010818) Cpn21 protein [Arabidopsis thaliana]
                   4822
Seq. No.
                  4077 1.R1040
Contig ID
5'-most EST
                   fC-gmro700750047a2
Method
                   BLASTX
NCBI GI
                   q422337
BLAST score
                   154
                   6.0e-10
E value
                   55
Match length
                   28
% identity
                  protein disulfide-isomerase homolog precursor - fluke
NCBI Description
                   (Schistosoma mansoni) >gi_312018_emb_CAA80520_ (Z22933)
                  protein disulfide isomerase homologue [Schistosoma mansoni]
                  4823
Seq. No.
Contig ID
                   4077 2.R1040
5'-most EST
                  LIB3106-098-Q1-K1-G1
Method
                  BLASTX
                  g422337
NCBI GI
BLAST score
                   230
E value
                   6.0e-19
Match length
                   67
% identity
                   34
                  protein disulfide-isomerase homolog precursor - fluke
NCBI Description
                   (Schistosoma mansoni) >gi_312018_emb_CAA80520_ (Z22933)
                  protein disulfide isomerase homologue [Schistosoma mansoni]
Seq. No.
                   4824
Contig ID
                   4077 3.R1040
                  LIB3065-012-Q1-N1-G7
5'-most EST
                   4825
Seq. No.
Contig ID
                   4078 1.R1040
5'-most EST
                  uC-gmropic060a12b1
Method
                   BLASTX
NCBI GI
                  g3522961
BLAST score
                   1192
E value
                   1.0e-154
Match length
                   357
% identity
                   79
                   (ACO04411) putative pto kinase [Arabidopsis thaliana]
NCBI Description
                   4826
Seq. No.
Contig ID
                   4078_2.R1040
5'-most EST
                  uC-gmrominsoy153c05b1
Method
                  BLASTN
NCBI GI
                  g1216483
```

BLAST score

```
E value
                   2.0e-19
Match length
                   143
% identity
                   84
                   Arabidopsis thaliana dual specificity kinase 1 (ADK1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   4827
Contig ID
                   4078 3.R1040
                   uC-gmropic036f07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3522961
BLAST score
                   379
E value
                   2.0e-36
Match length
                   93
                   78
% identity
NCBI Description
                   (AC004411) putative pto kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                   4078 4.R1040
5'-most EST
                   LIB3107-010-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q3668069
BLAST score
                   378
E value
                   3.0e-36
Match length
                   109
% identity
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
Seq. No.
                   4829
Contig ID
                   4078 5.R1040
5'-most EST
                   LIB3074-018-Q1-E1-F7
Method
                   BLASTX
NCBI GI
                   g1586940
BLAST score
                   874
E value
                   5.0e-94
                   248
Match length
                   71
% identity
NCBI Description Ser/Thr kinase [Lycopersicon esculentum]
                   4830
Seq. No.
Contig ID
                   4078 6.R1040
5'-most EST
                   LIB3050-025-Q1-K1-D1
Method
                   BLASTX
NCBI GI
                   g3242705
BLAST score
                   1076
E value
                   1.0e-117
Match length
                   235
% identity
                   (ACO03040) putative nicotinate phosphoribosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   4831
                   4078 7.R1040
Contig ID
5'-most EST
                   LIB3107-037-Q1-K1-G11
                  BLASTX
Method
NCBI GI
                   g3668069
```

NCBI GI

```
4.0e-33
E value
Match length
                   121
                   60
% identity
NCBI Description
                   (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
Seq. No.
Contig ID
                   4078 8.R1040
5'-most EST
                   txt700731595.hl
Method
                   BLASTX
NCBI GI
                   q3668069
BLAST score
                   416
E value
                   9.0e-41
Match length
                   123
% identity
NCBI Description
                   (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
                   4833
Seq. No.
                   4078 9.R1040
Contig ID
5'-most EST
                   V4L-\overline{0}2-Q1-B1-B12
Method
                   BLASTX
NCBI GI
                   g2914700
BLAST score
                   700
E value
                   8.0e-74
Match length
                   169
% identity
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thalianal
Seq. No.
                   4834
Contig ID
                   4078 10.R1040
5'-most EST
                   LIB3051-077-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g2914700
BLAST score
                   918
E value
                   2.0e-99
Match length
                   259
% identity
                   73
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   4835
                   4078 11.R1040
Contig ID
5'-most EST
                  uC-gmropic068h01b1
Method
                  BLASTX
                   g3242705
NCBI GI
BLAST score
                   283
                   5.0e-25
E value
                   67
Match length
                   78
% identity
                   (AC003040) putative nicotinate phosphoribosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   4836
Seq. No.
                   4078 12.R1040
Contig ID
5'-most EST
                  LIB3139-099-P1-N1-H8
Method
                  BLASTX
```

g1586940

```
BLAST score
                   141
                   1.0e-08
E value
Match length
                   63
% identity
                   51
                   Ser/Thr kinase [Lycopersicon esculentum]
NCBI Description
                   4837
Seq. No.
                   4078_13.R1040
Contig ID
5'-most EST
                   LIB3051-049-Q1-K1-D6
                   4838
Seq. No.
                   4078 15.R1040
Contig ID
5'-most EST
                   eep700867417.h1
                   4839
Seq. No.
                   4080 1.R1040
Contig ID
5'-most EST
                   LIB3028-021-Q1-B1-F5
Seq. No.
                   4840
                   4081 1.R1040
Contig ID
                   LIB3138-083-P1-N1-F4
5'-most EST
Seq. No.
                   4841
                   4081 2.R1040
Contig ID
5'-most EST
                   LIB3109-053-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   g118561
BLAST score
                   217
                   7.0e-17
E value
Match length
                   204
% identity
                   31
                   GLUCOSE 1-DEHYDROGENASE B
NCBI Description
Seq. No.
                   4842
                   4081 3.R1040
Contig ID
5'-most EST
                   zzp700835451.h1
                   4843
Seq. No.
                   4082 1.R1040
Contig ID
                   rca701000512.h1
5'-most EST
                   4844
Seq. No.
                   4082 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy236h07b1
Seq. No.
                   4845
                   4083 1.R1040
Contig ID
5'-most EST
                   txt700734689.h1
Method
                   BLASTX
NCBI GI
                   q730526
BLAST score
                   909
E value
                   3.0e-98
                   193
Match length
                   88
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                   >gi_480787_pir _S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein
```

## [Arabidopsis thaliana]

```
Seq. No.
                   4846
                   4088 1.R1040
Contig ID
                   LIB3051-091-Q1-K1-F1
5'-most EST
                   4847
Seq. No.
                   4089 1.R1040
Contig ID
                   LIB3028-021-Q1-B1-G4
5'-most EST
Seq. No.
                   4848
                   4091 1.R1040
Contig ID
5'-most EST
                   LIB3028-021-Q1-B1-G6
Method
                   BLASTX
NCBI GI
                   q4490316
BLAST score
                   186
E value
                   6.0e-14
Match length
                   47
% identity
NCBI Description
                   (AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.
                   4093 1.R1040
Contig ID
5'-most EST
                   LIB3028-021-Q1-B1-G8
Seq. No.
                   4850
                   4096 1.R1040
Contig ID
                   LIB3039-034-Q1-E1-F11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1685005
BLAST score
                   1014
E value
                   1.0e-110
Match length
                   474
% identity
NCBI Description
                   (U32644) immediate-early salicylate-induced
                   glucosyltransferase [Nicotiana tabacum]
Seq. No.
                   4099 1.R1040
Contig ID
                   rca701001277.h1
5'-most EST
Method
                   BLASTX
                   g267131
NCBI GI
BLAST score
                   531
                   1.0e-53
E value
Match length
                   289
% identity
                   NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)
NCBI Description
                   >gi 423120 pir A46174 RNA-binding protein TIAR - human
                   >gi_189310 (M96954) nucleolysin TIAR [Homo sapiens]
>gi_4507499_ref_NP_003243.1_pTIAL1_ TIA1 cytotoxic
                   granule-associated RNA-binding protein-like
```

Seq. No. 4852

4100 1.R1040 Contig ID

5'-most EST uC-gmropic044h04b1

Method BLASTX NCBI GI q4508079

Method

```
279
BLAST score
                   9.0e-25
E value
Match length
                   107
% identity
                   57
                   (AC005882) 66284 [Arabidopsis thaliana]
NCBI Description
                   4853
Seq. No.
                   4100 2.R1040
Contig ID
5'-most EST
                   vzy700754417.hl
Method
                  BLASTX
NCBI GI
                   q4508079
BLAST score
                   258
E value
                   2.0e-22
Match length
                   96
% identity
                   61
NCBI Description
                   (AC005882) 66284 [Arabidopsis thaliana]
Seq. No.
                   4854
Contig ID
                   4101 1.R1040
5'-most EST
                  LIB3040-054-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                   q541968
BLAST score
                  267
E value
                   6.0e-23
Match length
                   91
% identity
                  HMG 1 protein - garden pea >gi_436424_emb_CAA54168_
NCBI Description
                   (X76774) HMG 1 protein [Pisum sativum]
                   4855
Seq. No.
Contig ID
                   4103 1.R1040
                  pmv700891270.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3128168
BLAST score
                   450
E value
                   2.0e-44
Match length
                   142
                   56
% identity
NCBI Description
                   (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
Seq. No.
                   4856
                   4103 2.R1040
Contig. ID
5'-most EST
                  LIB3109-034-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q3128168
BLAST score
                  318
E value
                   4.0e-29
Match length
                  105
% identity
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   4104 1.R1040
Contig ID
                  LIB3106-076-Q1-K1-G1
5'-most EST
```

BLASTX

Contig ID

. .

```
q1172874
NCBI GI
                   753
BLAST score
                   8.0e-80
E value
Match length
                   289
                   58
% identity
NCBI Description
                   DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
                   >gi_479589_pir__S34823 dehydration-induced protein RD22 -
                   Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
                    [Arabidopsis thaliana]
                   4858
Seq. No.
Contig ID
                   4104 2.R1040
5'-most EST
                   LIB3039-044-Q1-E1-A11
                   4859
Seq. No.
Contig ID
                   4108 1.R1040
5'-most EST
                   uC-gmflminsoy053c11b1
Method
                   BLASTX
NCBI GI
                   q4325371
BLAST score
                   914
                   1.0e-98
E value
Match length
                   321
% identity
                   (AF128396) contains similarity to Medicago truncatula N7
NCBI Description
                   protein (GB:Y17613) [Arabidopsis thaliana]
Seq. No.
Contig ID
                   4108 2.R1040
5'-most EST
                   LIB3139-007-P1-N1-F7
Method
                   BLASTX
NCBI GI
                   q4325371
BLAST score
                   243
E value
                   2.0e-20
Match length
                   56
% identity
                   77
                   (AF128396) contains similarity to Medicago truncatula N7
NCBI Description
                   protein (GB:Y17613) [Arabidopsis thaliana]
Seq. No.
Contig ID
                   4108 3.R1040
5'-most EST
                   zzp700836162.h1
Method
                   BLASTX
NCBI GI
                   q4325371
BLAST score
                   243
E value
                   2.0e-20
Match length
                   56
% identity
                   (AF128396) contains similarity to Medicago truncatula N7
NCBI Description
                   protein (GB:Y17613) [Arabidopsis thaliana]
Seq. No.
                   4108 7.R1040
Contig ID
5'-most EST
                   pxt700945268.hl
Seq. No.
                   4863
```

4110 1.R1040

Seq. No.

```
qsv701050106.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2342719
BLAST score
                   355
E value
                   2.0e-33
Match length
                   184
% identity
                   46
NCBI Description
                   (AC002341) SF16 protein isolog [Arabidopsis thaliana]
Seq. No.
                   4110 2.R1040
Contig ID
                   k11701211941.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2342719
BLAST score
                   315
E value
                   1.0e-28
Match length
                   93
% identity
NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]
Seq. No.
                   4865
Contig ID
                   4110 3.R1040
5'-most EST
                   LIB3093-051-Q1-K1-C12
Seq. No.
                   4866
                   4110 4.R1040
Contig ID
5'-most EST
                   LIB3139-009-P1-N1-A8
Seq. No.
                   4867
Contig ID
                   4112 1.R1040
                   k117\overline{0}1208153.h1
5'-most EST
Method
                   BLASTX
                   g3024022
NCBI GI
BLAST score
                   779
E value
                   6.0e-83
Match length
                   159
% identity
                   91
                   INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation
factor 5A5 [Solanum tuberosum]
                   4868
Seq. No.
                   4114 2.R1040
Contig.ID
5'-most EST
                   leu701150411.h1
Seq. No.
                   4869
                   4116 1.R1040
Contig ID
5'-most EST .
                   uC-gmropic064d12b1
Method
                   BLASTX
NCBI GI
                   g3287680
BLAST score
                   260
E value
                   3.0e-22
Match length
                   139
                   50
% identity
NCBI Description (AC003979) T22J18.4 [Arabidopsis thaliana]
```

E value

```
4117 1.R1040
Contig ID
5'-most EST
                   LIB3028-021-Q1-B1-C12
                   BLASTX
Method
NCBI GI
                   q1931655
BLAST score
                   360
                   4.0e-34
E value
Match length
                   95
                   74
% identity
NCBI Description
                   (U95973) receptor-kinase isolog [Arabidopsis thaliana]
Seq. No.
                   4871
                   4118 1.R1040
Contig ID
5'-most EST
                   LIB3028-021-Q1-B1-C2
Seq. No.
                   4872
                   4119 1.R1040
Contig ID
5'-most EST
                   epx701110372.h1
                   BLASTX
Method
NCBI GI
                   g3033375
BLAST score
                   268
                   2.0e-23
E value
                   92
Match length
% identity
                   57
NCBI Description
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
                   thaliana]
                   4873
Seq. No.
Contig ID
                   4121 1.R1040
5'-most EST
                   leu7\overline{0}1153802.h1
                   BLASTX
Method
NCBI GI
                   q4103324
BLAST score
                   1222
E value
                   1.0e-135
Match length
                   275
% identity
NCBI Description
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
                   tuberosum
                   4874
Seq. No.
                   4121 2.R1040
Contig ID
5'-most EST
                   leu701146422.hl
Method
                   BLASTX
NCBI GI
                   g4103324
BLAST score
                   506
E value
                   2.0e-51
Match length
                   105
% identity
                   94
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
                   4875
Seq. No.
Contiq ID
                   4121 4.R1040
                   zpv700761104.hl
5'-most EST
                   BLASTN
Method
                   g4151924
NCBI GI
BLAST score
                   83
```

9.0e-39

5'-most EST

```
239
Match length
% identity
                   84
NCBI Description Arabidopsis thaliana CYT1 protein (cyt1) mRNA, complete cds
Seq. No.
                   4876
Contig ID`
                   4121 5.R1040
                  vzy700751791.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4103324
BLAST score
                  406
E value
                  1.0e-39
Match length
                  86
% identity
                   94
NCBI Description
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
                  tuberosum]
Seq. No.
                   4877
                   4121 6.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy086a10b1
Method
                  BLASTX
NCBI GI
                  q2642159
BLAST score
                  261
E value
                   1.0e-22
Match length
                  55
% identity
NCBI Description
                   (AC003000) putative mannose-1-phosphate guanyltransferase
                   [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
Seq. No.
                  4878
                  4121 7.R1040
Contig ID
5'-most EST
                  zhf700959268.h1
Method
                  BLASTN
NCBI GI
                  q2642152
BLAST score
                  41
E value
                  8.0e-14
Match length
                  101
% identity
                  85
                  Arabidopsis thaliana chromosome II BAC T517 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  4879
Seq. No.
                  4123 1.R1040
Contig ID
                  awf700839701.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2129758
BLAST score
                  641
E value
                  8.0e-67
Match length
                  151
                  78
% identity
NCBI Description
                  ubiquitin conjugating enzyme E2 protein - Arabidopsis
                  thaliana >qi 992704 (U33757) UBC7 [Arabidopsis thaliana]
Seq. No.
                  4880
Contig ID
                  4123 2.R1040
```

LIB3049-041-Q1-E1-G12

% identity

```
BLASTX
Method
NCBI GI
                   a2129758
BLAST score
                   174
E value
                   3.0e-12
                   34
Match length
                   94
% identity
                   ubiquitin conjugating enzyme E2 protein - Arabidopsis
NCBI Description
                   thaliana >gi 992704 (U33757) UBC7 [Arabidopsis thaliana]
Seq. No.
                                                                            ر مرزي
Contig ID
                   4123 3.R1040
5'-most EST
                   qsv701056366.hl
Method
                   BLASTX
                   q2129758
NCBI GI
BLAST score
                   659
                   5.0e-69
E value
                   152
Match length
% identity
                   80
                   ubiquitin conjugating enzyme E2 protein - Arabidopsis
NCBI Description
                   thaliana >gi 992704 (U33757) UBC7 [Arabidopsis thaliana]
                   4882
Seq. No.
Contig ID
                   4123 4.R1040
5'-most EST
                   LIB3139-098-P1-N1-C5
Method
                   BLASTX
                   g2129758
NCBI GI
                   383
BLAST score
                   5.0e-37
E value
                   88
Match length
% identity
                   78
NCBI Description
                   ubiquitin conjugating enzyme E2 protein - Arabidopsis
                   thaliana >gi 992704 (U33757) UBC7 [Arabidopsis thaliana]
                   4883
Seq. No.
                   4123_6.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1157761.h1
                   BLASTX
Method
NCBI GI
                   q2624417
BLAST score
                   174
                   1.0e-12
E value
                   47
Match length
% identity
                   (AJ002959) Ubiquitin carrier protein [Zea mays]
NCBI Description
                   4884
Seq. No.
                   4123 8.R1040
Contig ID
5'-most EST
                   uxk700667391.hl
Seq. No.
                   4885
                   4124 1.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0981844.h1
Method
                   BLASTX
NCBI GI
                   a1040877
BLAST score
                   572
E value
                   6.0e-59
Match length
                   116
```

```
NCBI Description
                 (U30460) expansin S2 precursor [Cucumis sativus]
Seq. No.
                  4886
                  4124 2.R1040
Contig ID
                  jC-gmro02910046c02a1
5'-most EST
                  BLASTX
Method
                  q1040877
NCBI GI
BLAST score
                  464
                  2.0e-46
E value
Match length
                  115
                  72
% identity
                  (U30460) expansin S2 precursor [Cucumis sativus]
NCBI Description
                  4887
Seq. No.
Contig ID
                  4125 1.R1040
5'-most EST
                  LIB3028-021-Q1-B1-D12
                  BLASTX
Method
                  g4218991
NCBI GI
BLAST score
                  217
                  2.0e-17
E value
Match length
                  82
                  51
% identity
                  (AF098632) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                  4888
Seq. No.
                 4125 2.R1040
Contig ID
5'-most EST
                  pmv700889380.h1
Method
                  BLASTX
NCBI GI
                  q4218991
BLAST score
                  312
                  2.0e-28
E value
Match length
                  129
% identity
                  49
                  (AF098632) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                  4889
Seq. No.
                  4126 1.R1040
Contig ID
5'-most EST
                  LIB3040-003-Q1-E1-E4
Method
                  BLASTN
                  g407800
NCBI GI
BLAST score
                  60
                  6.0e-25
E value
Match length
                  80
                  94
% identity
                  G.hirsutum mRNA for ribosomal protein 41, large subunit
NCBI Description
                   (RL41)
                  4890
Seq. No.
                  4126 2.R1040
Contig ID
5'-most EST
                  LIB3170-013-Q1-J1-F4
Method
                  BLASTN
                  g407800
NCBI GI
BLAST score
                  60
E value
                  5.0e-25
Match length
                  80
                  94
% identity
NCBI Description G.hirsutum mRNA for ribosomal protein 41, large subunit
```

BLAST score

E value

343

0.0e + 00

```
(RL41)
                   4891
Seq. No.
Contig ID
                   4130 1.R1040
                  LIB3028-020-Q1-B1-H8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2098709
BLAST score
                   716
E value
                   7.0e-76
                   182
Match length
% identity
                   71
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
                   4892
Seq. No.
Contig ID
                   4133 1.R1040
                  LIB3028-021-Q1-B1-A5
5'-most EST
Method
                  BLASTX
                   g3242079
NCBI GI
BLAST score
                   223
E value
                   7.0e-18
                   67
Match length
% identity
                   66
NCBI Description
                  (AJ006984) proline-rich protein [Capsicum annuum]
                   4893
Seq. No.
Contig ID
                   4133 2.R1040
                  ncj700981439.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   q3242079
BLAST score
                   226
E value
                   1.0e-18
Match length
                   68
                   65
% identity
NCBI Description
                  (AJ006984) proline-rich protein [Capsicum annuum]
Seq. No.
                   4894
Contig ID
                   4135 1.R1040
5'-most EST
                  hyd700730983.h1
Method
                  BLASTX
NCBI GI
                   q1651904
BLAST score
                   172
E value
                   5.0e-12
Match length
                   93
                   40
% identity
NCBI Description
                  (D90901) hypothetical protein [Synechocystis sp.]
Seq. No.
                   4895
                   4137 1.R1040
Contig ID
                   zhf700964788.hl
5'-most EST
                   4896
Seq. No.
Contig ID
                   4141 1.R1040
                  leu701154311.h1
5'-most EST
Method
                  BLASTN
                  g396818
NCBI GI
```

```
935
Match length
                   86
% identity
NCBI Description P.sativum pspor1 mRNA encoding porin
                   4897
Seq. No.
                   4142 1.R1040
Contig ID
5'-most EST
                   ncj700981734.h1
                   BLASTX
Method
NCBI GI
                   q4006854
BLAST score.
                   235
E value
                   2.0e-19
Match length
                   102
                   49
% identity
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   4142 2.R1040
Contig ID
5'-most EST
                   leu701148704.h1
Seq. No.
                   4899
                   4147 1.R1040
Contig ID
5'-most EST
                   zhf7\overline{0}0953783.h1
                   BLASTX
Method
NCBI GI
                   q3287691
BLAST score
                   483
E value
                   4.0e-48
Match length
                   252
                   45
% identity
                  (AC003979) Contains similarity to RING zinc finger protein
NCBI Description
                   gb X95455 from Gallus gallus. [Arabidopsis thaliana]
Seq. No.
                   4147_2.R1040
Contig ID
5'-most EST
                   jC-gmle01810064h11a1
Method
                   BLASTX
NCBI GI
                   q3642014
BLAST score
                   173
E value
                   1.0e-11
Match length
                   49
% identity
                   61
NCBI Description
                   (AL031620) similar to Zinc finger, C3HC4 type (RING finger)
                   [Caenorhabditis elegans]
Seq. No.
                   4147 3.R1040
Contig ID
5'-most EST
                   LIB3138-012-Q1-N1-C12
Seq. No.
                   4902
Contig ID
                   4148 1.R1040
                   asn7\overline{0}1138390.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3377517
BLAST score
                   219
E value
                   2.0e-17
Match length
                   99
% identity
NCBI Description
                   (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
```

Method

```
4903
Seq. No.
                   4149 1.R1040
Contig ID
5'-most EST
                   leu701146016.h1
Method
                   BLASTX
                   g3184289
NCBI GI
                   334
BLAST score
E value
                   6.0e-31
Match length
                   160
% identity
                   51
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   4904
Seq. No.
Contig ID
                   4152 1.R1040
5'-most EST
                   txt700732376.h1
                   4905
Seq. No.
                   4153 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810022h01a1
                   4906
Seq. No.
                   4154_1.R1040
Contig ID
                   LIB3139-093-P1-N1-E3
5'-most EST
Method
                   BLASTX
                   q2982303
NCBI GI
BLAST score
                   568
                   2.0e-58
E value
                   204
Match length
                   58
% identity
                   (AF051236) hypothetical protein [Picea mariana]
NCBI Description
Seq. No.
                   4907
                   4154_2.R1040
Contig ID
                   dpv7\overline{0}1103307.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2982303
BLAST score
                   539
                   3.0e-55
E value
Match length
                   134
% identity
NCBI Description
                   (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                   4908
Contig ID
                   4160 1.R1040
5'-most EST
                   LIB3087-005-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   q4454026
BLAST score
                   903
E value
                   2.0e-97
Match length
                   323
% identity
                   60
NCBI Description
                   (AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                   4160 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy025a07b1
```

BLASTX

Contig ID

```
NCBI GI
                  q4454026
BLAST score
                  379
E value
                  2.0e-36
Match length
                  101
% identity
                  76
NCBI Description
                   (AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  4163 1.R1040
5'-most EST
                  sat701010905.hl
Method
                  BLASTX
NCBI GI
                  q3297891
BLAST score
                  934
E value
                  1.0e-101
Match length
                  194
% identity
                  89
NCBI Description
                   (AJ002990) nucleotide repair protein [Lilium longiflorum]
Seq. No.
                  4911
                  4166_1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy271c10b1
Method
                  BLASTX
NCBI GI
                  q1946355
BLAST score
                  191
E value
                  2.0e-14
Match length
                  119
% identity
                  39
NCBI Description
                   (U93215) maize transposon MuDR mudrA protein isolog
                   [Arabidopsis thaliana] >gi 2880040 (AC002340) maize
                  transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                  4912
                  4167 1.R1040
Contig ID
                  zpv700761920.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3763927
BLAST score
                  894
E value
                  3.0e-96
Match length
                  287
% identity
                  62
NCBI Description
                   (AC004450) putative carboxyphosphoenolpyruvate mutase
                   [Arabidopsis thaliana]
                  4913
Seq. No.
                  4167 2.R1040
Contig ID
5'-most EST
                  gsv701049034.h1
Method
                  BLASTX
NCBI GI
                  g3763927
BLAST score
                  353
E value
                  2.0e-33
Match length
                  108
% identity
                   (AC004450) putative carboxyphosphoenolpyruvate mutase
NCBI Description
                   [Arabidopsis thaliana]
                  4914
Seq. No.
```

4169 1.R1040

:::

Seq. No.

```
5'-most EST
                   LIB3040-033-01-E1-C8
                   4915
Seq. No.
Contig ID
                   4171 1.R1040
5'-most EST
                  LIB3138-031-Q1-N1-G6
                   4916
Seq. No.
Contig ID
                   4172 1.R1040
5'-most EST
                  LIB3039-005-Q1-E1-H8
Seq. No.
                   4917
Contig ID
                   4177 1.R1040
5'-most EST
                   dpv701103646.h1
Seq. No.
                   4918
                   4178 1.R1040
Contig ID
                   jex700909168.hl
5'-most EST
                   4919
Seq. No.
Contig ID
                   4180 1.R1040
5'-most EST
                   rlr700900441.h1
Seq. No.
                   4920
                   4182 1.R1040
Contig ID
                  LIB3109-006-Q1-K1-A6
5'-most EST
Method
                  BLASTX
                   q3328240
NCBI GI
BLAST score
                   597
                   1.0e-61
E value
Match length
                   255
% identity
                   47
NCBI Description
                   (AF064775) early nodule-specific protein [Medicago
                   truncatula]
                   4921
Seq. No.
Contig ID
                   4182 2.R1040
5'-most EST
                  LIB3094-055-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                   a1110502
BLAST score
                   307
E value
                   5.0e-28
Match length
                  118
                   53
% identity
NCBI Description
                  (U40387) coil protein [Medicago sativa]
                   4922
Seq. No.
Contig ID
                   4184_1.R1040
5'-most EST
                  rca701002018.hl
Method
                  BLASTX
NCBI GI
                  q2398521
BLAST score
                   526
E value
                  2.0e-53
Match length
                  209
% identity
                  (Y13720) transcription factor [Arabidopsis thaliana]
NCBI Description
```

```
4184 2.R1040
Contig ID
                   ssr700555336.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2398521
BLAST score
                   439
E value
                   5.0e-43
                   223
Match length
                   48
% identity
NCBI Description
                   (Y13720) transcription factor [Arabidopsis thaliana]
                   4924
Seq. No.
Contig ID
                   4186 1.R1040
                   fde7\overline{0}0873486.h1
5'-most EST
                   4925
Seq. No.
                   4187 1.R1040
Contig ID
                   taw700659693.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2695711
BLAST score
                   360
E value
                   7.0e-34
Match length
                   93
                   67
% identity
                   (AJ001370) cytochome b5 [Olea europaea]
NCBI Description
                   4926
Seq. No.
Contig ID
                   4187 2.R1040
5'-most EST
                   jsh701070289.h1
Method
                   BLASTX
NCBI GI
                   q2695711
BLAST score
                   372
E value
                   1.0e-35
Match length
                   113
                   59
% identity
                   (AJ001370) cytochome b5 [Olea europaea]
NCBI Description
Seq. No.
                   4927
                   4187_3.R1040
Contig ID
                   jC-gmro02800033d10a1
5'-most EST
Method
                   BLASTX
                   g729252
NCBI GI
BLAST score
                   270
                   5.0e-24
E value
Match length
                   64
                   73
% identity
                  CYTOCHROME B5 >gi 167140 (M87514) cytochrome b-5 [Brassica
NCBI Description
                   oleracea] >gi 384338_prf__1905426A cytochrome b5 [Brassica
                   oleracea]
                   4928
Seq. No.
                   4189 1.R1040
Contig ID
                   fua701042753.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4006932
BLAST score
                   180
                   5.0e-13
E value
                   135
Match length
```

Contig ID

·:`--·

```
% identity
                   (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit
NCBI Description
                   [Bos taurus]
3.
Seq. No.
                   4929
                   4189 3.R1040
Contig ID
5'-most EST
                   jC-qmf102220064b02a1
Method
                   BLASTX
NCBI GI
                   q4580395
BLAST score
                   283
E value
                   5.0e-25
Match length
                   88
% identity
NCBI Description
                   (AC007171) putative kinesin-related protein [Arabidopsis
                   thalianal
Seq. No.
                   4930
                   4190 1.R1040
Contig ID
5'-most EST
                   vzy7\overline{0}0753930.h1
Method
                   BLASTX
NCBI GI
                   q4049354
BLAST score
                   1999
E value
                   0.0e + 00
Match length
                   452
                   83
% identity
NCBI Description
                   (AL034567) glycine hydroxymethyltransferase (EC
                   2.1.2.1)-like protein [Arabidopsis thaliana]
Seq. No.
                   4931
                   4190 2.R1040
Contig ID
5'-most EST
                   LIB3107-056-Q1-K1-H10
Seq. No.
                   4932
                   4194 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy049d03b1
Method
                   BLASTX
NCBI GI
                   q282994
BLAST score
                   1032
E value
                   1.0e-113
                   226
Match length
% identity
                   81
                   Sip1 protein - barley >gi_167100 (M77475) seed imbibition
NCBI Description
                   protein [Hordeum vulgare]
Seq. No.
                   4933
Contig ID
                   4196 1.R1040
5'-most EST
                   LIB3039-047-Q1-E1-A3
Method
                   BLASTX
NCBI GI
                   g4468813
BLAST score
                   736
E value
                   7.0e-78
Match length
                   247
% identity
                   53
NCBI Description
                   (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                   4934
```

4196 2.R1040

NCBI GI

```
5'-most EST
                   fC-qmse7000751282d1
                   4935
Seq. No.
Contig ID
                   4196 3.R1040
                   LIB3039-028-Q1-E1-C4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4468813
BLAST score
                   369
E value
                   4.0e-35
                   119
Match length
% identity
                   55
                   (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   4936
Seq. No.
Contig ID
                   4201 1.R1040
5'-most EST
                   jC-qmst02400052e06a1
                   4937
Seq. No.
                   4203 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy091g11b1
Method
                   BLASTX
                   g3461821
NCBI GI
BLAST score
                   522
E value
                   2.0e-66
Match length
                   267
                   54
% identity
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   4938
Seq. No.
Contig ID
                   4203 3.R1040
5'-most EST
                   xpa700793151.hl
Method
                   BLASTX
NCBI GI
                   g3461821
BLAST score
                   576
E value
                   2.0e-59
Match length
                   173
% identity
                   62
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   4939
                   4204 1.R1040
Contig ID
5'-most EST
                   zhf700952486.hl
Method
                   BLASTX
NCBI GI
                   q1854581
BLAST score
                   886
E value
                   2.0e-95
Match length
                   276
% identity
NCBI Description
                  (L24120) peroxidase precursor [Linum usitatissimum]
Seq. No.
                   4940
                   4204 2.R1040
Contig ID
5'-most EST
                   LIB3106-022-Q1-K1-F10
Method
                   BLASTX
```

q1518388

Seq. No.

```
163
BLAST score
                   3.0e-11
E value
Match length
                   65
% identity
                   51
                  (X91172) korean-radish isoperoxidase [Raphanus sativus]
NCBI Description
                   4941
Seq. No.
Contig ID
                   4205 1.R1040
5'-most EST
                   leu7\overline{0}1146640.h1
Method
                  BLASTX
NCBI GI
                   q2129605
BLAST score
                   932
                   1.0e-104
E value
Match length
                   210
% identity
                   87
                  GTP-binding protein 2 - Arabidopsis thaliana
NCBI Description
                  >gi_2129702_pir__S71585 Rab2 homolog GTP-binding protein
                  ATGB2 - Arabidopsis thaliana >gi_1184983 (U46925) ATGB2
                   [Arabidopsis thaliana] >gi_3805852_emb_CAA21472_ (AL031986)
                  GTP-binding protein GB2 [Arabidopsis thaliana]
                   4942
Seq. No.
Contig ID
                   4207 1.R1040
5'-most EST
                  leu701149522.h1
Method ·
                  BLASTN
NCBI GI
                   a603218
BLAST score
                   504
                  0.0e + 00
E value
Match length
                  884
                  89
% identity
NCBI Description
                  Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
                   complete cds
                   4943
Seq. No.
                   4207 2.R1040
Contig ID
5'-most EST
                   k11701215133.h1
Method
                  BLASTX
NCBI GI
                   q3617770
BLAST score
                   752
E value
                   1.0e-79
Match length
                  183
% identity
NCBI Description
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                   4944
Contig ID
                   4207 3.R1040
5'-most EST
                   jC-qmro02910062c06a1
Method
                  BLASTN
NCBI GI
                  q603218
BLAST score
                  113
E value
                   1.0e-56
Match length
                  261
% identity.
                  86
                  Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
NCBI Description
                  complete cds
```

Seq. No.

```
Contig ID
                   4207 4.R1040
                   zsg701128628.hl
5'-most EST
Method
                   BLASTX
                   g3617770
NCBI GI
BLAST score
                   2232
                   0.0e+00
E value
                   505
Match length
% identity
                   80
NCBI Description
                   (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
                   4946
Seq. No.
                   4207 5.R1040
Contig ID
                   LIB3170-061-Q1-K2-F9
5'-most EST
Method
                   BLASTN
                   g603218
NCBI GI
BLAST score
                   56
E value
                   1.0e-22
Match length
                   116
% identity
                   88
NCBI Description
                   Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
                   complete cds
Seq. No.
                   4947
Contig ID
                   4207 7.R1040
                   leu7\overline{0}1157358.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g603218
BLAST score
                   53
E value
                   5.0e-21
                   77
Match length
% identity
                   92
                   Medicago sativa glucose-6-phosphate dehydrogenase mRNA,
NCBI Description
                   complete cds
                   4948
Seq. No.
Contig ID
                   4208 1.R1040
5'-most EST
                   hyd7\overline{0}0730986.h1
Method
                   BLASTX
NCBI GI
                   q4091806
BLAST score
                   331
                   6.0e-34
E value
Match length
                   92
                   53
% identity
NCBI Description
                   (AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.
                   4949
Contig ID
                   4210 1.R1040
5'-most EST
                   LIB3049-001-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   q3599968
BLAST score
                   1008
E value
                   1.0e-110
Match length
                   250
% identity
NCBI Description
                   (AF032123) clp protease [Arabidopsis thaliana]
```

```
Contig ID
                  4212 1.R1040
5'-most EST
                  LIB3050-016-Q1-E1-C3
Method
                  BLASTX
NCBI GI
                  q4572674
BLAST score
                  209
                  2.0e-16
E value
                  91
Match length
                  56
% identity
NCBI Description
                  (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                  4951
                  4212 2.R1040
Contig ID
5'-most EST
                  LIB3050-015-Q1-E1-B8
                  4952
Seq. No.
                  4214 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400031f01a1
Method
                  BLASTX
NCBI GI
                  g2982465
                  200
BLAST score
E value
                  5.0e-15
Match length
                  209
                  26
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                  4953
Seq. No.
Contig ID
                  4215 1.R1040
                  LIB3028-019-Q1-B1-F1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4558678
BLAST score
                  233
                  2.0e-19
E value
Match length
                  92
                  47
% identity
                  (AC006586) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4954
                  4215_2.R1040
Contig ID
                  gsf700698478.hl
5'-most EST
Method
                  BLASTX
                  g4558678
NCBI GI
BLAST score
                  141
                  9.0e-09
E value
                  74
Match length
% identity
                  42
                  (AC006586) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  4955
                  4216_1.R1040
Contig ID
5'-most EST
                  LIB3028-019-Q1-B1-F10
                  4956
Seq. No.
                  4223_1.R1040
Contig ID
5'-most EST
                  LIB3028-019-Q1-B1-F8
Seq. No.
                  4957
```

4224 1.R1040

Contig ID

Match length

```
5'-most EST
                   pxt700945114.h1
Method
                   BLASTX
                   g3193306
NCBI GI
BLAST score
                   366
E value
                   9.0e-35
                   104
Match length
                   69
% identity
                   (AF069300) contains similarity to Arabidopsis
NCBI Description
                   membrane-associated salt-inducible-like protein
                   (GB:AL021637) [Arabidopsis thaliana]
                   4958
Seq. No.
                   4225 1.R1040
Contig ID ·
5'-most EST
                   LIB3170-035-Q1-K1-D6
Method
                   BLASTN
NCBI GI
                   g1230613
BLAST score
                   116
                   2.0e-58
E value
                   428
Match length
                   86
% identity
                   Lupinus albus isoflavone reductase-like protein mRNA,
NCBI Description
                   complete cds
                   4959
Seq. No.
Contig ID
                   4227 1.R1040
                   leu701157591.h1
5'-most EST
Method
                   BLASTN
                   g512399
NCBI GI
                   399
BLAST score
                   0.0e+00
E value
                   923
Match length
% identity
                   86
NCBI Description
                  M.sativa mRNA for annexin
                   4960
Seq. No.
Contig ID
                   4227 2.R1040
5'-most EST
                   smc7\overline{0}0747149.h1
                   4961
Seq. No.
                   4228 1.R1040
Contig ID
                   LIB3109-054-Q1-K1-F1
5'-most EST
Method
                   BLASTX
                   g4455232
NCBI GI
BLAST score
                   1938
                   0.0e+00
E value
                   609
Match length
                   62
% identity
NCBI Description
                   (AL035523) putative protein [Arabidopsis thaliana]
                   4962
Seq. No.
                   4229 1.R1040
Contig ID
                   g5753542
5'-most EST
Method
                   BLASTX
                  g2191138
NCBI GI
BLAST score
                   529
E value
                   1.0e-53
```

```
% identity
                   69
NCBI Description
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
                   thaliana]
                   4963
Seq. No.
                   4229 2.R1040
Contig ID
5'-most EST
                   LIB3106-013-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   g2191138
BLAST score
                   439
E value
                   2.0e-43
Match length
                   131
% identity
                   66
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   4964
Seq. No.
                   4229 3.R1040
Contig ID
                   LIB3106-051-Q1-K1-E1
5'-most EST
Seq. No.
                   4965
Contig ID
                   4230 1.R1040
5'-most EST
                   leu701146067.hl
Method
                   BLASTX
                   g2702281
NCBI GI
BLAST score
                   1132.
                   1.0e-124
E value
Match length
                   276
% identity
                   77
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   4966
Seq. No.
                   4234 1.R1040
Contig ID
                   fde700877068.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1651651
BLAST score
                   241
                   5.0e-41
E value
Match length
                   179
% identity
                   53
NCBI Description
                   (D90899) prenyltransferase [Synechocystis sp.]
Seq. No.
                   4967
Contig ID
                   4234 2.R1040
5'-most EST
                   LIB3055-013-Q1-N1-E3
Seq. No.
                   4968
Contig ID
                   4237 1.R1040
5'-most EST
                   LIB3056-014-Q1-N1-A11
Method
                   BLASTX
NCBI GI
                   q3367534
BLAST score
                   1798
E value
                   0.0e + 00
Match length
                   500
% identity
                   71
                   (ACO04392) Strong similarity to coatamer alpha subunit
NCBI Description
```

5'-most EST

```
Seq. No.
                   4969
                   4240 1.R1040
Contig ID
5'-most EST
                   LIB3170-082-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   g4490332
BLAST score
                   380
                   2.0e-36
E value
Match length
                   124
% identity
                   54
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4970
                   4240 2.R1040
Contig ID
5'-most EST
                   LIB3028-019-Q1-B1-D9
Method
                   BLASTX
NCBI GI
                   g4490332
BLAST score
                   331
                   3.0e-37
E value
Match length
                   121
% identity
                   60
NCBI Description
                   (AL035656) putative protein [Arabidopsis thaliana]
                   4971
Seq. No.
                   4241 1.R1040
Contig ID
                   hyd7\overline{0}0730638.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2257531
BLAST score
                   166
                   8.0e-11
E value
Match length
                   165
% identity
                   28
                   (AB004537) WEB1 PROTEIN [Schizosaccharomyces pombe]
NCBI Description
                   >gi_2950507_emb_CAA17835_ (AL022072) web1 homolog; protein
                   transport protein; WD-repeat protein [Schizosaccharomyces
                   pombe]
                   4972
Seq. No.
Contig ID
                   4241 2.R1040
5'-most EST
                   LIB3049-015-Q1-E1-G6
Seq. No.
                   4973
                   4241_3.R1040
Contig ID
5'-most EST
                   leu701155661.h1
Method
                   BLASTX
NCBI GI
                   g3845237
BLAST score
                   181
E value
                   3.0e-13
Match length
                   102
% identity
NCBI Description
                  (AE001407) WEB-1 ortholog, WD40 [Plasmodium falciparum]
Seq. No.
                   4974
Contig ID
                   4244 1.R1040
```

thaliana]

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

LIB3028-019-Q1-B1-E3

Match length

```
Seq. No.
                   4975
                   4244 2.R1040
Contig ID
5'-most EST
                   leu701157087.h1
                   4976
Seq. No.
                   4245 1.R1040
Contig ID
                   LIB3050-011-Q1-E1-B9
5'-most EST
Method
                   BLASTN
                   q287810
NCBI GI
BLAST score
                   162
E value
                   1.0e-85
                   241
Match length
                   94
% identity
NCBI Description M.sativa mRNA for phosphoprotein phosphatase type 2A
                   4977
Seq. No.
                   4245 2.R1040
Contig ID
                   uxk700671425.hl
5'-most EST
Method
                   BLASTN
                   g287810
NCBI GI
BLAST score
                   316
E value
                   1.0e-177
Match length
                   558
                   91
% identity
NCBI Description
                  M.sativa mRNA for phosphoprotein phosphatase type 2A
                   4978
Seq. No.
                   4245 3.R1040
Contig ID
                   r1r7\overline{0}0900452.h1
5'-most EST
Method
                  BLASTN
                   g287810
NCBI GI
BLAST score
                   449
                   0.0e+00
E value
Match length
                  705
% identity
                  91
NCBI Description M.sativa mRNA for phosphoprotein phosphatase type 2A
                   4979
Seq. No.
                   4245 4.R1040
Contig ID
5'-most EST
                  LIB3087-012-Q1-K1-F4
Method
                  BLASTN
NCBI GI
                  q287810
BLAST score
                  123
E value
                   1.0e-62
Match length
                  221
% identity
                  90
NCBI Description
                  M.sativa mRNA for phosphoprotein phosphatase type 2A
                   4980
Seq. No.
Contig ID
                   4245 5.R1040
5'-most EST
                  LIB3170-075-Q1-K2-A8
Method
                  BLASTN
NCBI GI
                  g287810
BLAST score
                  174
E value
                   5.0e-93
```

% identity

```
89
% identity
                  M.sativa mRNA for phosphoprotein phosphatase type 2A
NCBI Description
Seq. No.
                   4245 6.R1040
Contig ID
                   LIB3109-011-Q1-K1-G1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g287810
BLAST score
                   143
E value
                   1.0e-74
Match length
                   238
% identity
                   91
                  M.sativa mRNA for phosphoprotein phosphatase type 2A
NCBI Description
Seq. No.
                   4982
Contig ID
                   4246 1.R1040
5'-most EST
                   LIB3028-019-Q1-B1-C9
Method
                   BLASTX
NCBI GI
                   q4191791
BLAST score
                   356
E value
                   6.0e-34
Match length
                   82
% identity
                   77
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   4983
                   4251 1.R1040
Contig ID
5'-most EST
                   epx701107616.hl
Method
                   BLASTX
NCBI GI
                   q2052383
BLAST score
                   1559
E value
                   1.0e-174
Match length
                   347
% identity
NCBI Description
                   (U66345) calreticulin [Arabidopsis thaliana]
                   4984
Seq. No.
                   4251 2.R1040
Contig ID
5'-most EST
                   LIB3107-015-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2052383
BLAST score
                   256
E value
                   4.0e-22
Match length
                   54
% identity
NCBI Description
                  (U66345) calreticulin [Arabidopsis thaliana]
Seq. No.
                   4985
                   4253 1.R1040
Contig ID
                   jex700905636.hl
5'-most EST
Method
                   BLASTN
                   q2970653
NCBI GI
BLAST score
                   199
E value
                   1.0e-107
Match length
                   575
```

Contig ID

```
Vigna unquiculata ferritin subunit cowpea2 precursor, mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
Seq. No.
Contig ID
                  4253 3.R1040
                  fde700875371.h1
5'-most EST
Method
                  BLASTN
                  g2970653
NCBI GI
BLAST score
                  37
E value
                  2.0e-11
Match length
                  97
% identity
                  Vigna unquiculata ferritin subunit cowpea2 precursor, mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                  4987
Contig ID
                  4260 1.R1040
                  LIB3028-019-Q1-B1-C2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1055130
BLAST score
                  179
E value
                  4.0e-13
Match length
                  85
% identity
                  (U39998) coded for by C. elegans cDNA yk92b11.3; coded for
NCBI Description.
                  by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA
                  yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by
                  C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA
                  yk78c2.3
Seq. No.
                  4988
Contig ID
                  4269 1.R1040
5'-most EST
                  uC-gmronoir018f07b1
                  4989
Seq. No.
Contig ID
                  4269 2.R1040
5'-most EST
                  fde7\overline{0}0874154.h1
                  4990
Seq. No.
                  4275 1.R1040
Contig ID
5'-most EST
                  sat701003283.hl
Method
                  BLASTX
NCBI GI
                  q2129933
BLAST score
                  699
E value
                  9.0e-74
Match length
                  130
% identity
                  96
NCBI Description
                  myb-related transcription factor TMH27 - tomato
                  >gi_1167484_emb_CAA64614_ (X95296) transcription factor
                  [Lycopersicon esculentum]
Seq. No.
Contig ID
                  4276 1.R1040
5'-most EST
                  crh700854095.h1
                  4992
Seq. No.
```

4278\_1.R1040

```
fua701042058.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3877252
BLAST score
                   306
                   7.0e-28
E value
Match length
                   137
% identity
                   47
NCBI Description
                   (Z93382) F45G2.10 [Caenorhabditis elegans]
Seq. No.
                   4993
Contig ID
                   4282 1.R1040
5'-most EST
                   gsv701045871.h1
Method
                   BLASTX
                   q3152660
NCBI GI
BLAST score
                   361
                   1.0e-33
E value
Match length
                   322
% identity
                   29
NCBI Description
                   (AF064603) GA17 protein [Homo sapiens]
Seq. No.
                   4994
Contig ID
                   4282 2.R1040
5'-most EST
                   pcp700995151.hl
Seq. No.
                   4995
Contig ID
                   4282 4.R1040
5'-most EST
                   zsq701121632.h1
Seq. No.
                   4996
                   4287 1.R1040
Contig ID
5'-most EST
                   eep7\overline{0}0868521.h1
                   4997
Seq. No.
Contig ID
                   4291 1.R1040
5'-most EST
                   LIB3028-010-Q1-B1-H2
Method
                   BLASTX
NCBI GI
                   q2129858
BLAST score
                   465
E value
                   1.0e-46
Match length
                   110
                   75
% identity
NCBI Description
                   trypsin inhibitor precursor (clone ATI18) - alfalfa
                   >gi_509372_emb_CAA56253_ (X79879) serine proteinase
                   inhibitor [Medicago sativa]
                   4998
Seq. No.
Contig ID
                   4298 1.R1040
5'-most EST
                   LIB3073-004-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   q2500345
BLAST score
                   444
E value
                   7.0e-44
Match length
                   128
% identity
NCBI Description
                   NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY
```

>gi\_2618578\_dbj\_BAA23363\_ (D50420) OTK27 [Homo sapiens]

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)

```
4999
Seq. No.
                   4299 1.R1040
Contig ID
5'-most EST
                   LIB3030-010-Q1-B1-E4
                   BLASTX
Method
NCBI GI
                   g619747
BLAST score
                   649
                   7.0e-68
E value
Match length
                   182
% identity
                   65
                   (U18968) phosphoribosylanthranilate isomerase [Arabidopsis
NCBI Description
                   thaliana]
                   5000
Seq. No.
                   4300 1.R1040
Contig ID
                   LIB3028-018-Q1-B1-E2
5'-most EST
                   5001
Seq. No.
                   4300 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220098b05d1
                   5002
Seq. No.
                   4301 1.R1040
Contig ID
5'-most EST
                   LIB3170-076-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q4325282
BLAST score
                   609
E value
                   3.0e-63
Match length
                   146
                   74
% identity
NCBI Description
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   5003
Seq. No.
Contig ID
                   4302 1.R1040
                   pcp7\overline{0}0994416.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4519263
BLAST .score
                   267
E value
                   1.0e-148
                   583
Match length
% identity
NCBI Description
                   Citrus unshiu mRNA for vacuolar H+-ATPase B subunit,
                   complete cds
                   5004
Seq. No.
Contig ID
                   4302 2.R1040
5'-most EST
                   zzp7\overline{0}0836191.h1
Method
                   BLASTX
NCBI GI
                   q2493129
BLAST score
                   2395
E value
                   0.0e+00
Match length
                   489
```

>gi\_3859990 (AF091076) OTK27 [Homo sapiens]

[Homo sapiens]

>gi\_1589072\_prf\_\_2210268A nuclear protein-NHP2-like protein

Method

BLASTX

```
96
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi 459198 (U07052) vacuolar H+-ATPase subunit B
                   [Gossypium hirsutum]
                   5005
Seq. No.
                   4302 3.R1040
Contig ID
                  LIB3040-044-Q1-E1-A7
5'-most EST
                  BLASTN
Method
NCBI GI
                   g459197
BLAST score
                  152
                   7.0e-80
E value
Match length
                   348
% identity
                   86
                  Gossypium hirsutum vacuolar H+-ATPase subunit B mRNA,
NCBI Description
                   complete cds
                   5006
Seq. No.
                   4302 4.R1040
Contig ID
5'-most EST
                   g575<u>2</u>591
Method
                   BLASTN
                   g4519263
NCBI GI
                   92
BLAST score
                   4.0e-44
E value
Match length
                   244
% identity
                   84
                  Citrus unshiu mRNA for vacuolar H+-ATPase B subunit,
NCBI Description
                   complete cds
                   5007
Seq. No.
                   4302 5.R1040
Contig ID
                   hyd700729925.h1
5'-most EST
Method
                   BLASTN
                   g459197
NCBI GI
                   72
BLAST score
                   3.0e-32
E value
Match length
                   184
% identity
                   85
                   Gossypium hirsutum vacuolar H+-ATPase subunit B mRNA,
NCBI Description
                   complete cds
                   5008
Seq. No.
                   4302 8.R1040
Contig ID
                   zhf700960468.h1
5'-most EST
                   BLASTN
Method
                   g459197
NCBI GI
BLAST score
                   44
E value
                   1.0e-15
Match length
                   60
% identity
                   Gossypium hirsutum vacuolar H+-ATPase subunit B mRNA,
NCBI Description
                   complete cds
                   5009
Seq. No.
                   4310 1.R1040
Contig ID
                   leu701145010.hl
5'-most EST
```

Method

BLASTX

```
q4038044
NCBI GI
BLAST score
                   222
                   6.0e-18
E value
                   83
Match length
                   55
% identity
                   (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4406788 gb AAD20098_ (AC006532) unknown protein
                   [Arabidopsis thaliana]
                   5010
Seq. No.
                   4318 1.R1040
Contig ID
                   LIB3028-018-Q1-B1-C4
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2245125
BLAST score
                   145
                   5.0e-09
E value
Match length
                   56
                   55
% identity
                   (297343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5011
Seq. No.
                   4321 1.R1040
Contig ID
5'-most EST
                   gsv701050109.hl
                   BLASTX
Method
NCBI GI
                   g3184282
BLAST score
                   391
E value
                   7.0e-38
                   134
Match length
% identity
                   62
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5012
Seq. No.
Contig ID
                   4321 2.R1040
                   rrt700646046.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3184282
BLAST score
                   145
E value
                   2.0e-09
Match length
                   50
                   64
% identity
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5013
                   4322 1.R1040
Contig ID
5'-most EST
                  LIB3028-016-Q1-B1-E5
Method
                  BLASTX
NCBI GI
                   g2633727
                   232
BLAST score
E value
                   7.0e-19
Match length
                   124
% identity
                   44
NCBI Description
                  (Z99111) ykrT [Bacillus subtilis]
Seq. No.
                   5014
Contig ID
                   4325 1.R1040
5'-most EST
                  LIB3109-013-Q1-K1-D9
```

Seq. No.

```
g2618705
NCBI GI
BLAST score
                   1273
                   1.0e-141
E value.
Match length
                   308
% identity
                   60
NCBI Description
                   (AC002510) putative ABC transporter, 5' partial
                   [Arabidopsis thaliana]
Seq. No.
                   5015
Contig ID
                   4326_1.R1040
5'-most EST
                   LIB3028-018-Q1-B1-B7
Method
                   BLASTN
                   g3702734
NCBI GI
BLAST score
                   35
E value
                   7.0e-10
Match length
                   147
                   86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNB8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   5016
                   4327 1.R1040
Contig ID
                   rlr700896704.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2688824
BLAST score
                   410
E value
                   9.0e-40
Match length
                   124
                   69
% identity
                   (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
                   5017
Seq. No.
                   4327_2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy260b07b1
Method
                   BLASTX
                   g2688824
NCBI GI
BLAST score
                   168
                   1.0e-11
E value
                   40
Match length
% identity
                   78
NCBI Description
                   (U93273) putative auxin-repressed protein [Prunus
                   armeniaca]
                   5018
Seq. No.
                   4327_3.R1040
Contig ID
5'-most EST
                   q430\overline{5}006
Method
                   BLASTX
NCBI GI
                   q2688824
BLAST score
                   283
                   3.0e-31
E value
Match length
                   121
% identity
                   60
                   (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
```

NCBI GI

```
4327 4.R1040
Contig ID
5'-most EST
                   rca700996376.hl
                   5020 🐠
Seq. No.
                   4327 5.R1040
Contig ID
                   q429<del>5</del>801
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2688824
BLAST score
                   367
E value
                   6.0e-35
Match length
                   92
                   78
% identity
                   (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniacal
Seq. No.
                   5021
                   4327 6.R1040
Contig ID
5'-most EST
                   pxt7\overline{0}0943152.h1
Method
                   BLASTX
NCBI GI
                   q2688824
BLAST score
                   226
E value
                   2.0e-18
Match length
                   61
% identity
                   79
NCBI Description
                   (U93273) putative auxin-repressed protein [Prunus
                   armeniaca]
                   5022
Seq. No.
Contig ID
                   4330 1.R1040
5'-most EST
                   LIB3049-005-Q1-E1-B8
Method
                   BLASTX
NCBI GI
                   q2791806
BLAST score
                   523
E value
                   5.0e-53
Match length
                   165
% identity
NCBI Description
                   (AF041433) bet3 [Mus musculus]
Seq. No.
                   5023
Contig ID
                   4331 1.R1040
5'-most EST
                   LIB3138-020-Q1-N1-A9
Method
                   BLASTX
NCBI GI
                   q731672
BLAST score
                   318
E value
                   2.0e-29
Match length
                   124
% identity
                   48
                   HYPOTHETICAL 56.5 KD PROTEIN IN DYS1-ERG7 INTERGENIC REGION
NCBI Description
                   >gi_626628_pir__S46697 hypothetical protein YHR070w - yeast
                   (Saccharomyces cerevisiae) >gi 487945 (U00061) Yhr070wp
                   [Saccharomyces cerevisiae]
Seq. No.
                   5024
                   4335 1.R1040
Contig ID
                   ncj700977406.hl
5'-most EST
Method
                   BLASTN
```

g2330565

5'-most EST

```
BLAST score
                   37
                   5.0e-11
E value
Match length
                   141
                   86
% identity
                  Arabidopsis thaliana rpoMt gene
NCBI Description
                   5025
Seq. No.
                   4335 2.R1040
Contig ID
                   zhf700953673.hl
5'-most EST
                   5026
Seq. No.
                   4340 1.R1040
Contig ID
                   leu7\overline{0}1150583.h1
5'-most EST
                   BLASTX
Method
                   g3559805
NCBI GI
BLAST score
                   363
                   2.0e-34
E value
Match length
                   79
                   80
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   5027
                   4340 2.R1040
Contig ID
                   zzp700834154.h1
5'-most EST
                   5028
Seq. No.
Contig ID
                   4346 1.R1040
                   hrw701059215.h1
5'-most EST
                   BLASTX
Method
                   q1657855
NCBI GI
                   502
BLAST score
                   2.0e-50
E value
Match length
                   201
                   50
% identity
                   (U73216) cold acclimation protein WCOR413 [Triticum
NCBI Description
                   aestivum]
Seq. No.
                   5029
                   4346 2.R1040
Contig ID
5'-most EST
                   g5607172
                   5030
Seq. No.
                   4346 3.R1040
Contig ID
                   LIB3170-086-Q1-K1-C7
5'-most EST
                   BLASTX
Method
                   g1657855
NCBI GI
BLAST score
                   221
                   1.0e-17
E value.
Match length
                   54
                   70
% identity
                   (U73216) cold acclimation protein WCOR413 [Triticum
NCBI Description
                   aestivum]
                   5031
Seq. No.
                   4346 4.R1040
Contig ID
```

LIB3093-048-Q1-K1-F5

```
Method
                   BLASTX
NCBI GI
                   g1657855
BLAST score
                   129
                   2.0e-20
E value
Match length
                   80
% identity
                   66
                   (U73216) cold acclimation protein WCOR413 [Triticum
NCBI Description
                   aestivum]
                   5032
Seq. No.
                   4347 2.R1040
Contig ID
5'-most EST
                   LIB3028-017-Q1-B1-G7
                   5033
Seq. No.
                   4348 1.R1040
Contig ID
5'-most EST
                   LIB3049-046-Q1-E1-A3
Method
                   BLASTN
NCBI GI
                   g3821292
BLAST score
                   65
E value
                   7.0e-28
                   196
Match length
                   84
% identity
                  Pisum sativum cDNA fragment generated by DDRT-Alu
NCBI Description
                   5034
Seq. No.
Contig ID
                  4351 1.R1040
5'-most EST
                   LIB3040-059-Q1-E1-E6
Method
                   BLASTN
NCBI GI
                   q2565416
BLAST score
                   147
                   2.0e-76
E value
                   511
Match length
                   83
% identity
                  Onobrychis viciifolia oxygen-evolving enhancer protein 3
NCBI Description
                   precursor, mRNA, complete cds
                   5035
Seq. No.
Contig ID
                   4351 2.R1040
                   asn7\overline{0}1133531.h2
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2565416
BLAST score
                   42
                   2.0e-14
E value
Match length
                   126
                   83
% identity
                   Onobrychis viciifolia oxygen-evolving enhancer protein 3
NCBI Description
                   precursor, mRNA, complete cds
                   5036
Seq. No.
Contig ID
                   4353 1.R1040
                   jC-gmle01810044d07d1
5'-most EST
                   BLASTX
Method
                   g2262165
NCBI GI
BLAST score
                   436
E value
                   6.0e-43
Match length
                   98
```

87

% identity

% identity

```
(AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   5037
Seq. No.
                   4353 2.R1040
Contig ID
                   LIB3051-003-Q1-E1-D9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2262165
BLAST score
                   528
                   2.0e-55
E value
                   174
Match length
                   70
% identity
NCBI Description
                   (AC002329) predicted protein of unknown function
                   [Arabidopsis thaliana]
                   5038
Seq. No.
Contig ID
                   4354 1.R1040
                   jex7\overline{0}0908542.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4099092
BLAST score
                   475
E value
                   8.0e-48
                   115
Match length
% identity
                   77
                   (U83179) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5039
Contig ID
                   4355 1.R1040
                   uC-gmrominsoy202c05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2924792
BLAST score
                   417
E value
                   1.0e-40
Match length
                   112
                   71
% identity
                   (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5040
                   4355 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy135e12b1
Method
                   BLASTX
NCBI GI
                   g2914706
BLAST score
                   863
                   8.0e-93
E value .
Match length
                   195
                   81
% identity
NCBI Description
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
                   5041
Seq. No.
Contig ID
                   4355 3.R1040
                   pxt700944245.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2914706
BLAST score
                   336
                   2.0e-31
E value
Match length
                   78
```

NCBI GI

```
NCBI Description
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
                   5042
Seq. No.
Contig ID
                   4355 5.R1040
                   jC-gmro02910027h02d1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1174498
BLAST score
                   303
E value
                   1.0e-27
                   91
Match length
% identity
                   68
NCBI Description
                  SYNAPTOBREVIN-RELATED PROTEIN >gi 600710 (M90418) formerly
                   called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                   5043
Seq. No.
                   4355 6.R1040
Contig ID
                  uC-gmrominsoy170g03b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2914706
BLAST score
                   430
                  2.0e-42
E value
Match length
                  98
% identity
                  79
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                  5044
Seq. No.
                   4357 1.R1040
Contig ID
5'-most EST
                  rca701001244.h1
Seq. No.
                  5045
                   4358 1.R1040
Contig ID
                  k11701205513.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2677829
BLAST score
                  198
E value
                  1.0e-107
Match length
                  -498
                  85
% identity
NCBI Description
                  Prunus armeniaca ribosomal protein L12 mRNA, complete cds
Seq. No.
                  5046
Contig ID
                  4358 2.R1040
5'-most EST
                  LIB3093-028-Q1-K1-E5
Method
                  BLASTN
NCBI GI
                  q2677829
BLAST score
                  181
E value
                  5.0e-97
Match length
                  505
% identity
NCBI Description Prunus armeniaca ribosomal protein L12 mRNA, complete cds
Seq. No.
                  5047
Contig ID
                  4358 3.R1040
5'-most EST
                  LIB3073-004-Q1-K1-B11
Method
                  BLASTX
```

g2677830

```
÷. .
BLAST score
                   181
                   3.0e-13
E value
                   37
Match length
% identity
                   89
                  (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                   5048
Seq. No.
                   4361 1.R1040
Contig ID
5'-most EST
                   txt700735883.h1
                   BLASTN
Method
NCBI GI
                   q1617035
BLAST score
                   250
                   1.0e-138
E value
                   385
Match length
% identity
                   92
                   V.unguiculata mRNA for Ted2 protein
NCBI Description
                   5049
Seq. No.
                   4363 1.R1040
Contig ID
5'-most EST
                   rca700997990.h1
                   5050
Seq. No.
Contig ID
                   4368 1.R1040
5'-most EST
                   sat7\overline{0}1007339.h2
Method
                   BLASTX
NCBI GI
                   q1724114 ·
BLAST score
                   320
                   6.0e-29
E value
                   285
Match length
                   41
% identity
NCBI Description
                   (U80041) Af10-protein [Avena fatua]
                   5051
Seq. No.
                   4368_2.R1040
Contig ID
5'-most EST
                   jC-gmf102220073a05d1
Seq. No.
                   5052
                   4369 1.R1040
Contig ID
                   dpv7\overline{0}1097973.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1407705
BLAST score
                   533
E value
                   1.0e-54
Match length
                   150
                   67
% identity
NCBI Description
                   (U60202) lipoxygenase [Solanum tuberosum]
Seq. No.
                   5053
Contig ID
                   4370 1.R1040
5'-most EST
                   uC-gmrominsoy029f01b1
Method
                   BLASTX
NCBI GI
                   g1899050
BLAST score
                   464
E value
                   2.0e-46
Match length
                   141
                   72
% identity
                   (U62773) ripening-associated protein [Lycopersicon
NCBI Description
```

Method

NCBI GI

E value

BLAST score

Match length

BLASTX

464 4.0e-46

162

q4455250

## esculentum] 5054 Seq. No. Contig ID 4370 2.R1040 LIB3056-012-Q1-N1-B7 5'-most EST BLASTX Method g1899050 NCBI GI 972 BLAST score E value 1.0e-105 Match length 256 72 % identity (U62773) ripening-associated protein [Lycopersicon NCBI Description esculentum] 5055 Seq. No. 4371 1.R1040 Contig ID 5'-most EST LIB3049-004-Q1-E1-D10 5056 Seq. No. 4374 1.R1040 Contig ID 5'-most EST uC-gmropic028a08b1 5057 Seq. No. 4375 1.R1040 Contig ID 5'-most EST jC-gmf102220137c08a1 BLASTX Method NCBI GI g99809 BLAST score 1209 E value 1.0e-133 Match length 326 71 % identity gene Bp10 protein - rape >gi 17795 emb CAA47177 (X66608) NCBI Description Bplo [Brassica napus] 5058 Seq. No. 4376 1.R1040 Contig ID 5'-most EST LIB3028-017-Q1-B1-D1 Method BLASTX NCBI GI g2642157 223 BLAST score E value 3.0e-18 Match length 68 % identity 57 (AC003000) ankyrin-like protein [Arabidopsis thaliana] NCBI Description 5059 Seq. No. Contig ID 4377 1.R1040 kmv700742027.h1 5'-most EST Seq. No. 5060 Contig ID 4379 1.R1040 5'-most EST uC-gmrominsoy208f01b1

NCBI Description

```
% identity
                   48
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   5061
Seq. No.
                   4379 2.R1040
Contig ID
                  LIB3051-026-Q1-K1-F4
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4455250
BLAST score
                   394
E value
                   3.0e-38
Match length
                  121
% identity
                   50
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5062
                   4385 1.R1040
Contig ID
                   ssr700559413.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                  g433608
BLAST score
                  268
E value
                  1.0e-148
Match length
                  851
% identity
                  83
NCBI Description R.communis mRNA for enolase
                  5063
Seq. No.
Contig ID
                  4385 2.R1040
                  LIB3028-009-Q1-B1-B2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1041244
BLAST score
                  41
E value
                  1.0e-13
                  89
Match length
                  87
% identity
NCBI Description A.glutinosa mRNA for enolase
Seq. No.
                  5064
                  4385 3.R1040
Contig ID
                  zsq701118769.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2673918
BLAST score
                  197
                  6.0e-15
E value
Match length
                  150
                  37
% identity
NCBI Description
                  (AC002561) unknwon protein [Arabidopsis thaliana]
Seq. No.
                  5065
Contig ID
                  4389 1.R1040
5'-most EST
                  asn701143195.hl
Method
                  BLASTX
NCBI GI
                  q4522008
BLAST score
                  463
E value
                  2.0e-46
Match length
                  149
                  59
% identity
```

(AC007069) hypothetical protein [Arabidopsis thaliana]

```
5066
Seq. No.
                  4392 1.R1040
Contig ID
5'-most EST
                  LIB3170-019-Q1-K1-G2
Method
                  BLASTX
                  g3046693
NCBI GI
BLAST score
                   722
                  2.0e-76
E value
Match length
                  137
% identity
                  92
NCBI Description
                  (AL022140) receptor like protein (fragment) [Arabidopsis
                  thaliana]
                  5067
Seq. No.
Contig ID
                  4392 2.R1040
5'-most EST
                   jC-gmle01810006h04a1
Method
                  BLASTX
                  g3046693
NCBI GI
BLAST score
                  220
                  7.0e-18
E value
Match length
                  50
                  80
% identity
                  (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  5068
Seq. No.
                  4392_3.R1040
Contig ID
                  LIB3049-019-Q1-E1-A11
5'-most EST
Method
                  BLASTX
                  q3046693
NCBI GI
BLAST score
                  150
                  8.0e-10
E value
Match length
                  32
                  84
% identity
                  (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                 . 5069
Seq. No.
                  4396_1.R1040 `
Contig ID
                  LIB3138-033-Q1-N1-D5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3360289
BLAST score
                  1017
                  1.0e-146
E value
                  373
Match length
% identity
NCBI Description
                  (AF023164) leucine-rich repeat transmembrane protein kinase
                  1 [Zea mays]
                  5070
Seq. No.
                  4396_2.R1040
Contig ID
5'-most EST
                  fC-qmle700685276b1
Method
                  BLASTX
NCBI GI
                  q3360291
BLAST score
                  313
E value
                  1.0e-28
Match length
                  81
```

```
% identity
NCBI Description
                   (AF023165) leucine-rich repeat transmembrane protein kinase
                  2 [Zea mays]
                  5071
Seq. No.
                  4398 1.R1040
Contig ID
5'-most EST
                  dpv701099682.hl
Method
                  BLASTX
NCBI GI
                  q544075
BLAST score
                  563
E value
                  6.0e-58
Match length
                  135
% identity
                  28
NCBI Description
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
                  (P102) >gi_486768_pir__S35312 coatomer complex chain beta'
                  - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop
                  [Bos taurus]
Seq. No.
                  5072
Contig ID
                  4398 2.R1040
5'-most EST
                  uC-gmropic074d04b1
Method
                  BLASTX
NCBI GI
                  q544075
BLAST score
                  540
E value
                  3.0e-55
Match length
                  129
% identity
                  30
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                  (P102) >gi_486768_pir__S35312 coatomer complex chain beta'
                  - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop
                  [Bos taurus]
Seq. No.
                  5073
Contig ID
                  4398 3.R1040
5'-most EST
                  jex700905015.h1
Method
                  BLASTX
NCBI GI
                  q3023522
BLAST score
                  2067
E value
                  0.0e + 00
Match length
                  660
% identity
                  53
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                  (P102) >gi_2454309 (AF002705) beta prime COP [Rattus
                  norvegicus]
Seq. No.
                  5074
Contig ID
                  4398 4.R1040
                  fua701037018.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g544075
BLAST score
                  503
E value
                  6.0e-51
Match length
                  130
% identity
                  28
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                  (P102) >gi 486768 pir S35312 coatomer complex chain beta'
```

- bovine >gi\_312732\_emb\_CAA51285\_ (X72756) beta prime cop

Seq. No.

```
[Bos taurus]
                    5075
Seq. No.
Contig ID
                    4398 5.R1040
                    jC-gmst02400059b04a1
5'-most EST
                    BLASTN
Method
                    q3046855
NCBI GI
BLAST score
                    36
E value
                    1.0e-10
                    96
Match length
% identity
                    84
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                    MSL1, complete sequence [Arabidopsis thaliana]
Seq. No.
                    5076
                    4400 1.R1040
Contig ID
                    LIB3028-017-Q1-B1-C12
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3885329
BLAST score
                    458
E value
                    5.0e-53
Match length
                    131
% identity
                    84
NCBI Description
                    (AC005623) alien-like protein [Arabidopsis thaliana]
Seq. No.
                    4408 1.R1040
Contig ID
5'-most EST
                    jC-gmst02400060g09a1
Method
                    BLASTX
NCBI GI
                    q417256
BLAST score
                    159
E value
                    6.0e-10
Match length
                    164
                    32
% identity
NCBI Description
                    LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)
Seq. No.
                    5078
Contig ID
                    4408 3.R1040
5'-most EST
                    ncj700987853.hl
Seq. No.
                    5079
Contig ID
                    4410 1.R1040
5'-most EST
                    taw700657037.hl
Method
                    BLASTX
NCBI GI
                    g140739
BLAST score
                    283
E value
                    6.0e-25
Match length
                    169
% identity
                    36
                    HYPOTHETICAL 31.0 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION
NCBI Description
                    (ORF 2) >gi_78519_pir__JQ0613 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli
                    >gi_216632_dbj_BAA14238_ (D90212) ORF2 [Escherichia coli]
>gi_606065 (U18997) ORF_f299 [Escherichia coli] >gi_1789513
                    (AE000394) putative dehydrogenase [Escherichia coli]
```

NCBI Description

```
4411 1.R1040
Contig ID
                  LIB3028-017-Q1-B1-A2
5'-most EST
                  5081
Seq. No.
                  4413 1.R1040
Contig ID
                  asn701132849.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4567255
BLAST score
                  512
E value
                  5.Qe-56
Match length
                  183
% identity
                  66
                  (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  5082
Seq. No.
                  4413 2.R1040
Contig ID
5'-most EST
                  LIB3106-115-Q1-K1-H2
Method
                  BLASTN
                  g1177368
NCBI GI
BLAST score
                  86
E value
                  2.0e-40
Match length
                  158
                  89
% identity
NCBI Description
                  Z.mays mRNA for ribosomal protein L39
                  5083
Seq. No.
Contig ID
                  4413 3.R1040
5'-most EST
                  jC-gmst02400053c10d1
Method
                  BLASTN
NCBI GI
                  q1177368
BLAST score
                  86
E value
                  1.0e-40
Match length
                  158
                 89
% identity
NCBI Description Z.mays mRNA for ribosomal protein L39
Seq. No.
                  5084
Contig ID
                  4413 5.R1040
5'-most EST
                  g4292679
Method
                  BLASTN
NCBI GI
                  g1177368
BLAST score
                  67
                  3.0e-29
E value
Match length
                  159
                  86
% identity
                  Z.mays mRNA for ribosomal protein L39
NCBI Description
Seq. No.
                  5085
Contig ID
                  4415 1.R1040
5'-most EST
                  LIB3109-048-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q1170606
BLAST. score
                  302
                  7.0e-34
E value
Match length
                  120
                  59
% identity
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
```

```
>gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,
Adenylate Kinase From Maize In Complex With The Inhibitor
P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)
>gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize
In Complex With The Inhibitor
P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)
```

Contig ID 4416 1.R1040 kmv700738152.hl 5'-most EST Method BLASTX NCBI GI q2505879 BLAST score 373 E value 2.0e-35 Match length 251 % identity 42

5086

NCBI Description (Y12776) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5087

Seq. No.

Contig ID 4416\_2.R1040 5'-most EST leu701147855.h1

Seq. No. 5088

Contig ID 4416\_3.R1040 5'-most EST uxk700669004.h1

Seq. No. 5089

Contig ID 4418 1.R1040

5'-most EST LIB3051-114-Q1-K1-A1

Method BLASTX
NCBI GI g136140
BLAST score 374
E value 2.0e-35
Match length 195
% identity 38

NCBI Description PUTATIVE AC9 TRANSPOSASE >gi\_72973\_pir\_\_TQZMCA probable

transposase - maize transposon Ac9

Seq. No. 5090

Contig ID 4419\_1.R1040

5'-most EST LIB3109-022-Q1-K1-G4

Method BLASTX
NCBI GI g2760325
BLAST score 671
E value 1.0e-134
Match length 360
% identity 66

NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No. 5091

Contig ID 4419 2.R1040

5'-most EST LIB3139-074-P1-N1-B5

Method BLASTX
NCBI GI g2760325
BLAST score 249
E value 2.0e-21

```
Match length
                   67
                   72
% identity
                   (AC002130) F1N21.10 [Arabidopsis thaliana]
NCBI Description
                   5092
Seq. No.
                   4419 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy316c12b1
                   BLASTX
Method
                   g2760325
NCBI GI
                   366
BLAST score
                   8.0e-51
E value
Match length
                   137
                   77
% identity
NCBI Description
                   (AC002130) F1N21.10 [Arabidopsis thaliana]
Seq. No.
                   5093
                   4420 1.R1040
Contig ID
5'-most EST
                   LIB3107-002-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g3218467
                   154
BLAST score
                   7.0e-10
E value
Match length
                   149
% identity
                   31
                   (AJ006529) putative phosphatase [Gallus gallus]
NCBI Description
Seq. No.
                   5094
Contig ID
                   4422 1.R1040
                   zhf700957434.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q166379
                   565
BLAST score
E value
                   0.0e+00
                   1241
Match length
                   83
% identity
                   Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                   mRNA, complete cds
                   5095
Seq. No.
                   4422 2.R1040
Contig ID
                   kmv700739677.h1
5'-most EST
                   BLASTN
Method
                   g166379
NCBI GI
BLAST score
                   66
E value
                   1.0e-28
                   180
Match length
                   84
% identity
                   Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                   mRNA, complete cds
Seq. No.
                   5096
                   4422 3.R1040
Contig ID
5'-most EST
                   LIB3051-010-Q1-E1-E7
Method
                   BLASTN
                   g166379
NCBI GI
BLAST score
                   83
E value
                   8.0e-39
```

Contig ID

```
164
Match length
                   92
% identity
                   Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                   mRNA, complete cds
                   5097
Seq. No.
                   4422 4.R1040
Contig ID
5'-most EST
                   jC-gmle01810070g05a1
Method
                   BLASTN
NCBI GI
                   g166379
BLAST score
                   43
E value
                   9.0e-15
Match length
                   164
                   87
% identity
                   Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                   mRNA, complete cds
                   5098
Seq. No.
                   4427 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400058c09d1
Method
                   BLASTX
NCBI GI
                   g4033735
BLAST score
                   209
E value
                   6.0e-29
Match length
                   86
% identity
                   65
NCBI Description
                   (AF054284) spliceosomal protein SAP 155 [Homo sapiens]
                   5099
Seq. No.
                   4433 1.R1040
Contig ID
5'-most EST
                   LIB3139-071-P1-N1-C7
Method
                   BLASTX
NCBI GI
                   g2129473
BLAST score
                   282
E value
                   1.0e-24
Match length
                   145
% identity
                   43
NCBI Description
                   arabinogalactan-like protein - loblolly pine >gi_607774
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                   5100
Seq. No.
Contig ID
                   4433 2.R1040
5'-most EST
                   jC-gmst02400002c01d1
Seq. No.
                   5101
                   4436 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{0}28-016-Q1-B1-G9
Method
                   BLASTX
NCBI GI
                   q3415113
BLAST score
                   300
E value
                   1.0e-34
Match length
                   133
% identity
                   39
NCBI Description
                   (AF081201) villin 1 [Arabidopsis thaliana]
Seq. No.
```

4438\_1.R1040

NCBI GI

```
sat701003234.hl
5'-most EST
Method
                  BLASTX
                  g401621
NCBI GI
BLAST score
                  245
                  1.0e-20
E value
                  137
Match length
                  42
% identity
                  HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION
NCBI Description
                  >gi 290561 (L10328) o188 [Escherichia coli] >gi_1790149
                  (AE000448) orf, hypothetical protein [Escherichia coli]
                  5103
Seq. No.
Contig ID
                  4440 1.R1040
                  LIB3039-021-Q1-E1-E4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3650368
BLAST score
                  687
                  3.0e-72
E value
                  190
Match length
% identity
                  69
                  (AJ011398) profucosidase [Pisum sativum]
NCBI Description
                  5104
Seq. No.
                  4442 1.R1040
Contig ID
5'-most EST
                  zzp700834319.hl
Seq. No.
                  5105
                  4447 1.R1040
Contig ID
                  uC-gmropic009a06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3522950
BLAST score
                  354
E value
                  2.0e-33
Match length
                  115
                  58
% identity
NCBI Description
                  (AC004411) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  5106
                  4448 1.R1040
Contig ID
                  leu701157807.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3402282
BLAST score
                  442
E value
                  1.0e-43
Match length
                  155
                  55
% identity
NCBI Description
                  (AJ000997) proline-rich protein [Solanum tuberosum]
Seq. No.
                  5107
                  4450 1.R1040
Contig ID
5'-most EST
                  g4302030
Seq. No.
                  5108
                  4450 2.R1040
Contig ID
5'-most EST
                  LIB3107-055-Q1-K1-C11
Method
                  BLASTN
```

g170067

BLAST score

```
540
BLAST score
                   0.0e+00
E value
                   559
Match length
                   99
% identity
NCBI Description
                   Soybean (G.max) proline-rich cell wall protein (SbPRP3)
                   gene, complete cds
                   5109
Seq. No.
                   4450 3.R1040
Contig ID
                   uC-gmrominsoy086e07b1
5'-most EST
Method
                   BLASTX
                   g2760330
NCBI GI
BLAST score
                   541
                   3.0e-55
E value
Match length
                   139
% identity
                   71
                   (AC002130) F1N21.15 [Arabidopsis thaliana]
NCBI Description
                   5110
Seq. No.
                   4452 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810061c04a1
Method
                   BLASTX
                   g3292814
NCBI GI
BLAST score
                   446
E value
                   5.0e-44
Match length
                   101
% identity
                   80
                   (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5111
Contig ID
                   4453 1.R1040
                   uC-gmrominsoy204h12b1
5'-most EST
Method
                   BLASTX
                   g4239845
NCBI GI
                   695
BLAST score
E value
                   7.0e-73
Match length
                   336
% identity
                   46
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
Seq. No.
                   5112
Contig ID
                   4453 3.R1040
5'-most EST
                   fC-gmro700869769f3
                   BLASTX
Method
NCBI GI
                   g4239845
BLAST score
                   468
E value
                   8.0e-47
Match length
                   171
% identity
                   53
                   (AB015855) transcription factor TEIL [Nicotiana tabacum]
NCBI Description
Seq. No.
                   5113
Contig ID
                   4455 1.R1040
5'-most EST
                   LIB3028-016-Q1-B1-E6
Method
                   BLASTN
NCBI GI
                   q4165340
```

```
5.0e-11
E value
Match length
                  170
                  86
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F11M15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  5114
Seq. No.
Contig ID
                  4456_1.R1040
5'-most EST
                  LIB3039-040-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  g417148
BLAST score
                  743
E value
                  9.0e-79
Match length
                  226
                  63
% identity
NCBI Description
                  PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
                  (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                  soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.
                  5115
Contig ID
                  4458 1.R1040
5'-most EST
                  kmv700743063.hl
                  BLASTX
Method
NCBI GI
                  g3482967 -
BLAST score
                  785
                  1.0e-83
E value
Match length
                  185
                  75
% identity
                  (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
                  5116
Seq. No.
Contig ID
                  4459_1.R1040
5'-most EST
                  LIB3106-087-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2498732
BLAST score
                  603
E value
                  2.0e-62
Match length
                  169
                  68
% identity
NCBI Description
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2
                  >gi_1362014_pir__S57612 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268)
                  zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  5117
Contig ID
                  4459 2.R1040
5'-most EST
                  uC-gmropic010d10b1
Method
                  BLASTX
NCBI GI
                  g2498732
BLAST score
                  1064
E value
                  1.0e-116
Match length
                  276
% identity
                  72
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2
NCBI Description
                  >gi 1362014 pir S57612 zeta-crystallin homolog -
```

NCBI GI

E value

. 15. ...

BLAST score

Match length

```
Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268)
                    zeta-crystallin homologue [Arabidopsis thaliana]
                    5118
Seq. No.
                    4459 3.R1040
Contig ID
                    LIB3092-053-Q1-K1-B8
5'-most EST
Method
                    BLASTX
NCBI GI
                    g2498731
BLAST score
                    541
E value
                    2.0e-55
Match length
                    153
                    65
% identity
                    PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                    >gi_1362013_pir__S57611 zeta-crystallin homolog -
Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                    zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
Contig ID
                    4459 4.R1040
                    LIB3051-108-Q1-K1-H10
5'-most EST
Method
                    BLASTX
NCBI GI
                    q2498731
BLAST score
                    692
                    6.0e-73
E value
Match length
                    173
% identity
                    PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                    >gi_1362013_pir__S57611 zeta-crystallin homolog -
                    Arabidopsis thaliana >gi 886428 emb CAA89838 (Z49768)
                    zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                    4459 5.R1040
Contig ID
                    LIB3050-018-Q1-E1-A3
5'-most EST
Seq. No.
                    4459 6.R1040
Contig ID
                    ssr7\overline{0}0553955.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g2498731
BLAST score
                    535
E value
                    1.0e-54
                    150
Match length
                    67
% identity
NCBI Description
                    PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
                    >gi_1362013_pir__S57611 zeta-crystallin homolog -
Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                    zeta-crystallin homologue [Arabidopsis thaliana]
                    5122
Seq. No.
                    4466 2.R1040
Contig ID
                    ssr700554843.hl
5'-most EST
Method
                    BLASTX
```

g2905893

1.0e-59 173

```
68
% identity
NCBI Description
                   (U66424) fimbrin-like protein [Arabidopsis thaliana]
                   5123
Seq. No.
Contig ID
                   4467 1.R1040
                   uaw700661776.hl
5'-most EST
                   5124
Seq. No.
Contig ID
                   4467 2.R1040
5'-most EST
                   uC-gmflminsoy019c05b1
                   5125
Seq. No.
Contig ID
                   4467 3.R1040
5'-most EST
                   LIB3\overline{1}07-030-Q1-K1-B2
                   5126
Seq. No.
                   4467 4.R1040
Contig ID
5'-most EST
                   hyd700727362.h1
                   5127
Seq. No.
Contig ID
                   4469 1.R1040
                   sat701009455.hl
5'-most EST
                   5128
Seq. No.
Contig ID
                   4471 1.R1040
                  LIB3028-016-Q1-B1-C10
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2815897
BLAST score
                  177
                   9.0e-13
E value
Match length
                   64
% identity
                   59
                   (AF043279) protein kinase 1 [Toxoplasma gondii]
NCBI Description
                   >gi 4325070 gb AAD17245 (AF118099) PITSLRE-like protein
                   kinase [Toxoplasma gondii]
Seq. No.
                   5129
Contig ID
                   4476 1.R1040
5'-most EST
                  uC-gmrominsoy093d12b1
Method
                  BLASTX
                  g967125
NCBI GI
BLAST score
                   2482
E value
                   0.0e+00
Match length
                   487
                   98
% identity
NCBI Description
                   (U08140) calcium dependent protein kinase [Vigna radiata]
                  5130
Seq. No.
Contig ID
                   4476 2.R1040
5'-most EST
                  LIB3093-018-Q1-K1-C1
Method
                  BLASTN
NCBI GI
                  q967124
BLAST score
                   465
                  0.0e+00
E value
Match length
                  819
% identity
NCBI Description
                  Vigna radiata Rwilcz calcium dependent protein kinase
```

E value

Match length

% identity

4.0e-68

276 87

## (CDPK) mRNA, complete cds 5131 Seq. No. 4476 3.R1040 Contig ID 5'-most EST LIB3109-010-Q1-K1-B6 Method BLASTN g967124. NCBI GI 101 BLAST score 2.0e-49 E value Match length 137 93 % identity Vigna radiata Rwilcz calcium dependent protein kinase NCBI Description (CDPK) mRNA, complete cds 5132 Seq. No. 4476 4.R1040 Contig ID $ssr7\overline{0}0555278.h1$ 5'-most EST 5133 Seq. No. 4478 1.R1040 Contig ID 5'-most EST LIB3029-010-Q1-B1-B10 5134 Seq. No. 4479 1.R1040 Contig ID 5'-most EST gsv701049440.hl Method -BLASTN g3204100 NCBI GI BLAST score 103 3.0e-50 E value 407 Match length 85 % identity NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can107 5135 Seq. No. 4480 1.R1040 Contig ID 5'-most EST leu701151508.hl Method BLASTX g2739279 NCBI GI BLAST score 302 2.0e-27 E value Match length 110 % identity 57 NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi\_2791348\_emb\_CAA11154\_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum] Seq. No. 5136 Contig ID 4486\_1.R1040 5'-most EST zzp700832950.hl Method BLASTN NCBI GI g1556445 BLAST score 132

NCBI Description Hordeum vulgare alpha tubulin (tubA) mRNA, complete cds

```
5137
 Seq. No.
 Contig ID
                    4487 1.R1040
 5'-most EST
                    asn701133308.h1
                    BLASTX
 Method
 NCBI GI
                    q3193316
 BLAST score
                    1488
                    1.0e-166
 E value
 Match length
                    419
                    70
 % identity
 NCBI Description
                    (AF069299) contains similarity to nucleotide sugar
                    epimerases [Arabidopsis thaliana]
                    5138
 Seq. No.
 Contig ID
                    4487 2.R1040
 5'-most EST
                    trc7\overline{0}0568419.h1
 Method
                    BLASTX
 NCBI GI
                    q2583123
 BLAST score
                    415
 E value
                    2.0e-40
 Match length
                    116
 % identity
                    72
                    (AC002387) putative nucleotide sugar epimerase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    5139
                    4487 3.R1040
 Contig ID
 5'-most EST
                    LIB3049-041-Q1-E1-E5
                    BLASTX
 Method
                    g3193316
 NCBI GI
 BLAST score
                    242
 E value
                    5.0e-23
 Match length
                    151
                    48
 % identity
 NCBI Description
                    (AF069299) contains similarity to nucleotide sugar
                    epimerases [Arabidopsis thaliana]
Seq. No.
                    5140
 Contig ID
                    4487 4.R1040
 5'-most EST
                    LIB3028-015-Q1-B1-H7
 Method
                    BLASTN
 NCBI GI
                    g2583106
 BLAST score.
                    38
 E value.
                    6.0e-12
 Match length
                    70
                    90
 % identity
                    Arabidopsis thaliana chromosome II BAC F4L23 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    5141
                    4489 1.R1040
 Contig ID
 5'-most EST
                    LIB3170-030-Q1-K1-G5
 Seq. No.
                    5142
                    4495 1.R1040
 Contig ID
                    jC-gmst02400020dg11d1
 5'-most EST
Method
                    BLASTX
 NCBI GI
                    g4539321
```

5'-most EST

```
BLAST score
                   328
                   2.0e-30
E value
Match length
                   88
                   69
% identity
                   (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                   5143
Seq. No.
Contig ID
                   4498_1.R1040
5'-most EST
                   eep700866223.hl
Method
                  BLASTX
NCBI GI
                   g4204277
BLAST score
                   698
E value
                   3.0e-73
Match length
                   295
                   56
% identity
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5144
Seq. No.
                   4498 2.R1040
Contig ID
5'-most EST
                  LIB3139-020-P1-N1-G11
Seq. No.
                   5145
                   4498 3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy231a03b1
Method
                  BLASTX
NCBI GI
                   g4204277
BLAST score
                   310
E value
                   3.0e-28
Match length
                  133
                  53
% identity
NCBI Description
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
                  5146
Seq. No.
                   4498 4.R1040
Contig ID
5'-most EST
                  ssr700556564.h1
Method
                  BLASTX
NCBI GI
                  g4204277
BLAST score
                   623
E value
                  1.0e-64
Match length
                  259
                  57
% identity
NCBI Description
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  5147
                  4498 5.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy097b09b1
Method
                  BLASTX
NCBI GI
                  q4204277
BLAST score
                  410
E value
                  3.0e-40
Match length
                  82
% identity
NCBI Description
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  5148
Contig ID
                  4498 6.R1040
```

uC-gmrominsoy215d03b1

```
Method
                   BLASTX
                   g4204277
NCBI GI
                   274
BLAST score
E value
                   3.0e-24
Match length
                   55
% identity
                   93
NCBI Description
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
                   5149
Seq. No.
                   4500 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400011g06a1
Seq. No.
                   5150
                   4500 2.R1040
Contig ID
5'-most EST
                   LIB3107-010-Q1-K1-E8
                   5151
Seq. No.
                   4500 3.R1040
Contig ID
                   vwf700673739.hl
5'-most EST
Seq. No.
                   5152
Contig ID
                   4504_1.R1040
5'-most EST
                   uC-gmropic021c06b1
Method
                   BLASTN
NCBI GI
                   g1237085
BLAST score
                   480
E value
                   0.0e + 00
Match length
                   1016
                   87
% identity
NCBI Description
                   P.sativum mRNA for ADP-glucose pyrophosphorylase (agpl1)
                   >gi_1599261_gb_I18906_I18906 Sequence 1 from patent US
                   5498831 >gi 3972107 gb AR014653 AR014653 Sequence 1 from
                   patent US
Seq. No.
                   5153
Contig ID
                   4504 2.R1040
5'-most EST
                   r1r7\overline{0}0896089.h1
Method
                   BLASTN
                   g1237085
NCBI GI
BLAST score
                   68
                   9.0e-30
E value
Match length
                   96
                   93
% identity
NCBI Description
                   P.sativum mRNA for ADP-glucose pyrophosphorylase (agpl1)
                   >gi_1599261_gb_I18906_I18906 Sequence 1 from patent US
                   5498831 >gi_3972107_gb_AR014653_AR014653 Sequence 1 from
                   patent US
Seq. No.
                   5154
                   4504_3.R1040
Contig ID
5'-most EST
                   uaw700663791.hl
Method
                   BLASTX
NCBI GI
                   g2625086
BLAST score
                   333
E value
                   1.0e-55
Match length
                   137
```

78

% identity

BLAST score

```
NCBI Description
                   (AF030383) ADP-glucose pyrophosphorylase large subunit
                   [Cucumis melo var. markuwa Markino]
Seq. No.
                  5155
                  4506 1.R1040
Contig ID
5'-most EST
                  LIB3028-015-Q1-B1-G12
                  BLASTX
Method
NCBI GI
                  g4406777
BLAST score
                  198
                  2.0e-15
E value
Match length
                  53
                  79
% identity
                  (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  5156
Seq. No.
                  4507 1.R1040
Contig ID
5'-most EST
                  LIB3028-015-Q1-B1-F1
Method
                  BLASTX
NCBI GI
                  q3128186
BLAST score
                  159
                  1.0e-10
E value
Match length
                  49
% identity
                  69
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5157
                  4508 1.R1040
Contig ID
5'-most EST
                  LIB3028-015-Q1-B1-G2
Method
                  BLASTX
NCBI GI
                  q3287688
BLAST score
                  160
                  7.0e-11
E value
Match length
                  52
% identity
                  62
NCBI Description
                  (AC003979) Contains similarity to ycf37 gene product
                  gb_1001425 from Synechocystis sp. genome gb_D63999. ESTs
                  gb_T43026, gb_R64902, gb_Z18169 and gb_N37374 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  5158
                  4511 1.R1040
Contig ID
                  uC-gmrominsoy156g06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2335108
BLAST score
                  520
E value
                  5.0e-53
Match length
                  142
% identity
                  71
NCBI Description
                  (AC002339) putative isulinase [Arabidopsis thaliana]
Seq. No.
                  5159
Contig ID
                  4513 1.R1040
5'-most EST
                  LIB3107-070-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q4204265
```

Match length

```
E value
                   1.0e-137
Match length
                  403
% identity
                   61
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
                  5160
Seq. No.
                  4513 2.R1040
Contig ID
5'-most EST
                  LIB3107-033-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q4204265
BLAST score
                  289
E value
                  2.0e-25
Match length
                  250
% identity
                  33
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  5161
                  4513 3.R1040
Contig ID
5'-most EST
                  LIB3049-001-Q1-E1-E6
Seq. No.
                  5162
                  4514 1.R1040
Contig ID
5'-most EST
                  zhf700958333.h1
Method
                  BLASTX
NCBI GI
                  q2398679
BLAST score
                  2001
E value
                  0.0e + 00
Match length
                  408
% identity
                  93
NCBI Description
                  (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                  synthase [Morinda citrifolia]
Seq. No.
                  5163
Contig ID
                  4514_2.R1040
5'-most EST
                  LIB3139-055-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  q114193
BLAST score
                  496
E value
                  5.0e-50
Match length
                  167
% identity
                  60
NCBI Description
                  PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR
                  (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP
                  SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
                  SYNTHASE 1) >gi_170225 (M64261)
                  3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
                  [Nicotiana tabacum] >gi_228697_prf__1808327A
                  deoxyheptulosonate phosphate synthase [Nicotiana tabacum]
Seq. No.
                  5164
                  4516 1.R1040
Contig ID
5'-most EST
                  kl1701211336.hl
Method
                  BLASTX
NCBI GI
                  g3790100
BLAST score
                  2440
E value
                  0.0e + 00
```

Contig ID

```
% identity
                   (AF095520) pyrophosphate-dependent phosphofructokinase beta
NCBI Description
                  subunit [Citrus X paradisi]
Seq. No.
                  5165
                  4516 2.R1040
Contig ID
5'-most EST
                   zsg701129503.hl
Method
                  BLASTX
NCBI GI
                  g3618343
BLAST score
                  655
E value
                  4.0e-68
                  379
Match length
                  37
% identity
                   (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]
NCBI Description
                  >gi_4506223 ref. NP 002808.1_pPSMD13_ proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
Seq. No.
                  5166
                  4516 3.R1040
Contig ID
5'-most EST
                  fC-gmro700747787a2
Method
                  BLASTX
NCBI GI
                  g3790100
BLAST score
                  205
E value
                  5.0e-16
                  65
Match length
% identity
                   (AF095520) pyrophosphate-dependent phosphofructokinase beta
NCBI Description
                  subunit [Citrus X paradisi]
                  5167
Seq. No.
Contig ID
                  4516 4.R1040
5'-most EST
                  epx701110260.hl
                  BLASTX
Method
NCBI GI
                  g3790100
BLAST score
                  710
E value
                  4.0e-75
Match length
                  176
% identity
                   (AF095520) pyrophosphate-dependent phosphofructokinase beta
NCBI Description
                  subunit [Citrus X paradisi]
Seq. No.
                  5168
Contig ID
                  4516 5.R1040
5'-most EST
                  LIB3170-062-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q3157931
BLAST score
                  322
E value
                  1.0e-29
Match length
                  64
% identity
NCBI Description
                   (AC002131) Similar to pyrophosphate-dependent
                  phosphofuctokinase beta subunit gb_Z32850 from Ricinus
                  communis. ESTs gb_N65773, gb_N64925 and gb F15232 come
                  from this gene. [Arabidopsis thaliana]
                  5169
Seq. No.
```

4516\_6.R1040

```
5'-most EST
                   fC-gmro700747787d3
                   5170
Seq. No.
                   4516 7.R1040
Contig ID
                  LIB3170-033-Q1-K1-D11
5'-most EST
Method
                  BLASTN
                   q2832611
NCBI GI
BLAST score
                   59
E value
                   3.0e-24
                   205
Match length
% identity
                   87
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
NCBI Description
                   (ESSAII project)
Seq. No.
                   5171
                   4516 10.R1040
Contig ID
                  LIB3170-033-Q1-J1-D11
5'-most EST
Seq. No.
                  5172
Contig ID
                   4516 11.R1040
5'-most EST
                   gsv701056017.hl
Method
                  BLASTN
NCBI GI
                  q3790099
BLAST score
                  79
E value
                  1.0e-36
Match length
                  107
                  93
% identity
                  Citrus X paradisi pyrophosphate-dependent
NCBI Description
                  phosphofructokinase beta subunit (PPi-PFKb) mRNA, complete
                  cds
                   5173
Seq. No.
                  4516 12.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy271d04b1
Method
                  BLASTX
NCBI GI
                  g3790100
BLAST score
                  278
                   6.0e-25
E value
Match length
                  71
                   75
% identity
NCBI Description
                   (AF095520) pyrophosphate-dependent phosphofructokinase beta
                   subunit [Citrus X paradisi]
Seq. No.
                   5174
Contig ID
                   4518 1.R1040
5'-most EST
                  kwa701015659.h1
Method
                  BLASTX
NCBI GI
                  q4204265
BLAST score
                  459
E value
                  2.0e-91
Match length
                  294
% identity
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  5175
```

4520 1.R1040

leu701147564.h1

Contig ID 5'-most EST

% identity

NCBI Description

49



```
Method
                   BLASTX
NCBI GI
                   q2191177
                   194
BLAST score
                   7.0e-15
E value
Match length
                   67
                   61
% identity
                   (AF007270) belongs to the SPOU family of rRNA methylases.
NCBI Description
                   [Arabidopsis thaliana]
                  5176
Seq. No.
Contig ID
                   4521 1.R1040
5'-most EST
                   leu701155507.hl
Method
                   BLASTX
                   g445612
NCBI GI
BLAST score
                   600
E value
                   4.0e-62
Match length
                   122
                   93
% identity
NCBI Description
                  ribosomal protein S19 [Solanum tuberosum]
                   5177
Seq. No.
                   4521 4.R1040
Contig ID
                   jC-gmro02910067a06d1
5'-most EST
                   BLASTX
Method
                   g445612
NCBI GI
BLAST score
                   252
E value
                   1.0e-21
Match length
                   53
                   92
% identity
                  ribosomal protein S19 [Solanum tuberosum]
NCBI Description
Seq. No.
                   5178
                   4530 1.R1040
Contig ID
5'-most EST
                   LIB3170-039-Q1-K2-B7
                   5179
Seq. No.
Contig ID
                   4530 2.R1040
5'-most EST
                   LIB3107-018-Q1-K1-C3
                   BLASTX
Method
NCBI GI
                   q4467158
BLAST score
                   168
E value
                   2.0e-11
Match length
                   127
% identity
NCBI Description
                   (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                   5180
Contig ID
                   4530 3.R1040
5'-most EST
                   LIB3170-045-Q1-J1-G10
Method
                   BLASTX
NCBI GI
                   q4467158
BLAST score
                   646
E value
                   3.0e-67
Match length
                   351
```

(AL035540) putative protein [Arabidopsis thaliana]

Match length

```
Seq. No.
                   5181
Contig ID
                   4530 5.R1040
5'-most EST
                   awf700839714.h1
Method
                   BLASTX
NCBI GI
                   q4467158
BLAST score
                   147
E value
                   1.0e-09
Match length
                   69
% identity
                   49
NCBI Description
                   (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   4531 1.R1040
5'-most EST
                   seb700650590.hl
Method
                   BLASTX
NCBI GI
                   g1354849
BLAST score
                   501
E value
                   1.0e-50
Match length
                   154
% identity
                   61
NCBI Description
                  (U57350) epoxide hydrolase [Nicotiana tabacum]
Seq. No.
                   5183
                   4531 3.R1040
Contig ID
5'-most EST
                   bth700849189.h1
Method
                   BLASTX
NCBI GI
                   a1354849
BLAST score
                   194
E value
                   5.0e-15
Match length
                   62
% identity
                   61
NCBI Description
                  (U57350) epoxide hydrolase [Nicotiana tabacum]
Seq. No.
                   5184
Contig ID
                   4533 1.R1040
5'-most EST
                   wvk700686367.h1
Method
                  BLASTX
NCBI GI
                   q4455256
BLAST score
                   875
E value
                   4.0e-94
Match length
                   228
% identity
                   71
NCBI Description
                   (AL035523) protein-methionine-S-oxide reductase
                   [Arabidopsis thaliana]
Seq. No.
                   4533 2.R1040
Contig ID
5'-most EST
                  LIB3170-073-Q1-K1-D2
Seq. No.
                   5186
                   4533 3.R1040
Contig ID
5'-most EST
                   jC-qmle01810027e12d1
Method
                  BLASTX
NCBI GI
                  g1709690
BLAST score
                  318
                   3.0e-29
E value
```

Method

NCBI GI

**BLASTX** 

q4454472

```
80
% identity
NCBI Description
                  PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)
                   REDUCTASE) >gi_1076454_pir__S55365 probable peptide
                  methionine sulfoxide reductase - rape
                   >gi_853739_emb_CAA88538_ (Z48619) peptide methionine
                   sulfoxide reductase [Brassica napus]
                   >gi_1143406_emb_CAA63919_ (X94225) methionine sulfoxide
                   reductase [Brassica napus]
Seq. No.
                   5187
Contig ID
                   4533_4.R1040
                   jC-gmf102220070e08a1
5'-most EST
                  5188
Seq. No.
Contig ID
                   4533 6.R1040
5'-most EST
                  pxt700943002.hl
                  5189
Seq. No.
Contig ID
                  4537 1.R1040
5'-most EST
                  LIB3053-007-Q1-N1-G10
Method
                  BLASTX
NCBI GI
                  g1652057
BLAST score
                  187
E value
                  1.0e-13
Match length
                  116
                   35
% identity
NCBI Description
                  (D90902) hypothetical protein [Synechocystis sp.]
                  5190
Seq. No.
Contig ID
                  4542 1.R1040
5'-most EST
                  epx701106433.h1
Method
                  BLASTX
                  g1717975
NCBI GI
BLAST score
                   353
E value
                   4.0e-33
Match length
                  123
% identity
                  54
                  14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114
NCBI Description
                  ANTIGEN HOMOLOG) >gi_1177435_emb_CAA64670_ (X95384) 14.5
                  kDa translational inhibitor protein, p14.5 [Homo sapiens]
Seq. No.
                  5191
                   4552 1.R1040
Contig ID
5'-most EST
                  LIB3139-116-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  g4454472
BLAST score
                  227
E value
                  2.0e-18
Match length
                  118
% identity
                  43
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5192
                  4552 2.R1040
Contig ID
5'-most EST
                  zzp700831916.h1
```

5'-most EST Method

BLAST score

NCBI GI



```
421
BLAST score
                   8.0e-41
E value
                   228
Match length
                   46
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5193
Seq. No.
                   4552 3.R1040
Contig ID
                   jC-gmro02800034c03a1
5'-most EST
                   5194
Seq. No.
                   4552 4.R1040
Contig ID
5'-most EST
                   LIB3049-033-Q1-E1-E5
                   5195
Seq. No.
                   4552 5.R1040
Contig ID
5'-most EST
                   LIB3139-025-P1-N1-H6
                   5196
Seq. No.
                   4554 1.R1040
Contig ID
5'-most EST
                   hyd7\overline{0}0728918.h1
Method
                   BLASTN
                   g2502086
NCBI GI
BLAST score
                   53
                   1.0e-20
E value
                   118
Match length
% identity
                   93
                  Vigna radiata adenosine triphosphatase mRNA, complete cds
NCBI Description
                   5197
Seq. No.
                   4554_2.R1040
Contig ID
5'-most EST
                   g5057934
Method
                   BLASTN
NCBI GI
                   g2502086
BLAST score
                   370
E value
                   0.0e + 00
Match length
                   552
% identity
                   93
NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds
                   5198
Seq. No.
                   4554 3.R1040
Contig ID
5'-most EST
                   eep7\overline{0}0868421.h1
Method
                   BLASTN
                   g2502086
NCBI GI
BLAST score
                   298
E value
                   1.0e-167
Match length
                   382
                   95
% identity
                  Vigna radiata adenosine triphosphatase mRNA, complete cds
NCBI Description
Seq. No.
                   5199
Contig ID
                   4554 4.R1040
                   LIB3170-058-Q1-J1-F2
```

180

BLASTN

g2502086



```
E value 1.0e-96
Match length 392
% identity 87
NCBI Description Vigna ra
```

NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 5200

Contig ID 4554\_5.R1040

5'-most EST LIB3087-010-Q1-K1-H3

Method BLASTN
NCBI GI g2502086
BLAST score 274
E value 1.0e-153
Match length 346
% identity 95

NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 5201

Contig ID 4556 1.R1040

5'-most EST LIB3051-016-Q1-E1-A3

Method BLASTX
NCBI GI 94097579
BLAST score 947
E value 1.0e-102
Match length 199
% identity 90

NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 5202

Contig ID 4558 1.R1040 5'-most EST pmv700891157.h1

Seq. No. 5203

Contig ID 4559 1.R1040

5'-most EST LIB3051-091-Q1-K1-H10

Method BLASTX
NCBI GI g2811066
BLAST score 337
E value 5.0e-31
Match length 125

% identity 50
NCBI Description PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN

MULTIPLE ADVANCED CANCERS 1) >gi\_1916330 (U92437) MMAC1

[Mus musculus]

Seq. No. 5204

Contig ID 4560 1.R1040

5'-most EST uC-gmronoir008e01b1

Method BLASTX
NCBI GI g3335378
BLAST score 251
E value 2.0e-21
Match length 136
% identity 40

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 5205

```
4560 2.R1040
Contig ID
                   kl1701214579.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4309734
BLAST score
                   163
E value
                   4.0e-11
                   63
Match length
                   51
% identity
                   (AC006439) putative 26S proteosome regulatory subunit 8
NCBI Description
                   [Arabidopsis thaliana]
                   5206
Seq. No.
                   4565 1.R1040
Contig ID
                   LIB3170-039-Q1-K2-D5
5'-most EST
                   5207
Seq. No.
Contig ID
                   4565 2.R1040
                   uC-gmrominsoy164h05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q422029
BLAST score
                   831
E value
                   8.0e-90
Match length
                   239
                   73
% identity
                  transcription factor OBF3.2, ocs element-binding - maize
NCBI Description
       >gi_297018_emb_CAA48904_ (X69152) ocs-element binding
                   factor 3.2 [Zea mays]
                   5208
Seq. No.
                   4565 3.R1040
Contig ID
5'-most EST
                   jC-gmro02910031a03a1
Method
                   BLASTX
                  g1076782
NCBI GI
BLAST score
                   717
E value
                   1.0e-75
Match length
                  277
                   57
% identity
NCBI Description transcription factor HBP-1b(c1) - wheat (fragment)
                  5209
Seq. No.
                   4565 4.R1040
Contig ID
5'-most EST
                  wrg7\overline{0}0787787.h2
                  5210
Seq. No.
                   4565 6.R1040
Contig ID
                  LIB3051-012-Q1-E1-E5
5'-most EST
Seq. No.
                  5211
Contig ID
                  4567 1.R1040
5'-most EST
                  LIB3106-099-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q2384671
BLAST score
                  845
E value
                  2.0e-97
Match length
                  244
                  73
% identity
```

NCBI Description (AF012657) putative potassium transporter AtKT2p



```
[Arabidopsis thaliana]
Seq. No.
                   5212
                   4569 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy099c05b1
                   BLASTX
Method .
                   q1076755
NCBI GI
                   302
BLAST score
                   2.0e-27
E value
                   140
Match length
                   46
% identity
                   protein kinase - rice >gi_450300 (L27821) protein kinase
NCBI Description
                   [Oryza sativa]
                   5213
Seq. No.
```

4569 2.R1040 Contig ID

5'-most EST uC-gmropic075a12b1

5214 Seq. No.

4570 1.R1040 Contig ID

 $LIB3\overline{0}28-014-Q1-B1-G6$ 5'-most EST

5215 Seq. No.

4572 1.R1040 Contig ID 5'-most EST k11701214909.h1

BLASTX Method NCBI GI g2673904 BLAST score 283 5.0e-25 E value 85 Match length

.75 % identity

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

5216 Seq. No.

4575 1.R1040 Contig ID

5'-most EST uC-gmropic066e04b1

Method BLASTN NCBI GI g3264766 BLAST score 90 E value 9.0e-43 Match length 206 % identity

NCBI Description Prunus armeniaca AP2 domain containing protein (AP2DCP)

mRNA, partial cds

5217 Seq. No.

Contig ID 4575 3.R1040 5'-most EST hrw701058671.h1 Method BLASTN

g2443456 NCBI GI 53 BLAST score 7.0e-21 E value Match length 69 % identity

Oryza sativa ethylene responsive element binding protein NCBI Description

(Os-EREBP1) mRNA, complete cds

BLAST score

```
5218
Seq. No.
                   4575 4.R1040
Contig ID
                   g5753147
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3122602
BLAST score
                   443
                   1.0e-43
E value
                   168
Match length
% identity
                   17
                   PEROXISOMAL TARGETING SIGNAL 2 RECEPTOR (PTS2 RECEPTOR)
NCBI Description
                   (PEROXIN-7) >gi_1890657 (U69171) peroxisomal PTS2 receptor
                   [Mus musculus]
                   5219
Seq. No.
Contig ID
                   4577 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-G11
Method
                   BLASTN
                   g3202041
NCBI GI
BLAST score
                   219
E value
                   1.0e-119
Match length
                   759 -
% identity
                   Mesembryanthemum crystallinum 26S proteasome regulatory
NCBI Description
                   subunit S5A mRNA, complete cds
Seq. No.
                   5220
                   4577 2.R1040
Contig ID
                   k117\overline{0}1213417.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3550985
BLAST score
                   295
                   8.0e-27
E value
Match length
                   61
% identity
                   92
                   (AB010740) OsS5a [Oryza sativa]
NCBI Description
                   5221
Seq. No.
                   4580 1.R1040
Contig ID
5'-most EST
                   LIB3106-056-Q1-K1-H8
                   5222
Seq. No.
                   4583 1.R1040
Contig ID
                   LIB3\overline{1}38-010-Q1-N1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4324495
BLAST score
                   1730
                   0.0e+00
E value
                   404
Match length
% identity
                   (AF105221) glutamyl-tRNA reductase precursor [Glycine max]
NCBI Description
Seq. No.
                   4586 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400023g07a1
Method
                   BLASTX
NCBI GI
                   q3142296
```

5'-most EST

```
9.0e-22
E value
                   75
Match length
                   63
% identity
                   (AC002411) Contains similarity to hypothetical
NCBI Description
                  mitochondrial import receptor subunit gb_Z98597 from S.
                   pombe. ESTs gb T45575 and gb Z26435 and gb AA394576 come
                   from this gene. [Arabidopsis thaliana]
                   5224
Seq. No.
                   4587 1.R1040
Contig ID
                  uxk700668616.h1
5'-most EST
                  BLASTX
Method
                   g2497281
NCBI GI
BLAST score
                   1069
                   1.0e-117
E value
Match length
                   386
                   55
% identity
                  TRANSLATION INITIATION FACTOR IF-2
NCBI Description
                   >gi 1651769 dbj BAA16696 (D90900) initiation factor IF-2
                   [Synechocystis sp.]
                   5225
Seq. No.
                   4589 1.R1040
Contig ID
                  LIB3028-014-Q1-B1-F1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2982301
BLAST score
                   509
E value
                   1.0e-51
Match length
                  169
                   59
% identity
                  (AF051235) YGL010w-like protein [Picea mariana]
NCBI Description
                   5226
Seq. No.
Contig ID
                  4592 1.R1040
                  LIB3107-013-Q1-K1-D9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2894603
BLAST score
                   182 -
E value
                   3.0e-13
Match length
                   66
                   36
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5227
                  4594 1.R1040
Contig ID
5'-most EST
                  k11701205740.h1
Method
                  BLASTX
NCBI GI
                   g4539310
BLAST score
                   536
                  4.0e-54
E value
                  309
Match length
                   42
% identity
                  (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                  5228
Seq. No.
                  4594 2.R1040
Contig ID
```

LIB3107-058-Q1-K1-D9

% identity

```
5229
Seq. No.
Contig ID
                   4594 3.R1040
5'-most EST
                   LIB3109-052-Q1-K1-F8
                   5230
Seq. No.
Contig ID
                   4594 4.R1040
5'-most EST
                   jex700910063.h1
                   5231
Seq. No.
                   4594 5.R1040
Contig ID
5'-most EST
                   jC-gmf102220068g03d1
                   5232
Seq. No.
                   4595 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220088f03a1
Method
                   BLASTX
NCBI GI
                   q4406801
BLAST score
                   314
                   6.0e-29
E value
Match length
                   92
% identity
NCBI Description
                   (AC006304) unknown protein [Arabidopsis thaliana]
                   5233
Seq. No.
Contig ID
                   4596 1.R1040
5'-most EST
                   sat7\overline{0}1014394.h1
Method
                   BLASTX
NCBI GI
                   g1658193
BLAST score
                   905
                   1.0e-97
E value
Match length
                   238
                   72
% identity
NCBI Description
                   (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
                   bicolor]
                   5234
Seq. No.
                   4596 2.R1040
Contig ID
5'-most EST
                   jex700907751.h1
Method
                   BLASTX
NCBI GI
                   g2262164
BLAST score
                   183
                   2.0e-13
E value
Match length
                   79
% identity
                   51
                   (AC002329) putative obtusifoliol 14-alpha demethylase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   5235
Contig ID
                   4598 1.R1040
                   k117\overline{0}1205289.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3912953
BLAST score
                   224
E value
                   5.0e-18
Match length
                   126
```

5'-most EST

```
NCBI Description PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC
                  DEAMINASE)
                  5236
Seq. No.
                  4601 1.R1040
Contig ID
5'-most EST
                  LIB3028-014-Q1-B1-D2
Method
                  BLASTX
                  g1350680
NCBI GI
                  186
BLAST score
                  8.0e-25
E value
Match length
                  133
% identity
                  57
                  60S RIBOSOMAL PROTEIN L1
NCBI Description
Seq. No.
                  5237
                  4607 1.R1040
Contig ID
5'-most EST
                  uC-gmropic103h01b1
Method
                  BLASTX
                  g4039155
NCBI GI
BLAST score
                  178
E value
                  2.0e-12
Match length
                  90
% identity
                  41
                  (AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                  [Festuca rubra]
Seq. No.
                  5238
Contig ID
                  4611 1.R1040
                  LIB3028-014-Q1-B1-A8
5'-most EST
                  5239
Seq. No.
                  4612 1.R1040
Contig ID
                  LIB3170-026-Q1-K1-C11
5'-most EST
Method
                  BLASTX
                  g1707981
NCBI GI
BLAST score
                  414
E value
                  2.0e-40
Match length
                  102
% identity
                  75
                  GLUTAREDOXIN >qi 1076561 pir S54825 glutaredoxin - castor
NCBI Description
                  bean
Seq. No.
                  5240
                  4615 1.R1040
Contig ID
                  leu701149172.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4163997
BLAST score
                  1927
                  0.0e+00
E value
Match length
                  476
% identity
                  72
                  (AF087483) alpha-xylosidase precursor [Arabidopsis
NCBI Description
                  thaliana]
                  5241
Seq. No.
                  4618 1.R1040
Contig ID
```

uC-gmrominsoy308a10b1

BLAST score

```
5242
Seq. No.
Contig ID
                   4619 1.R1040
5'-most EST
                   qsv7\overline{0}1046306.h1
Method
                   BLASTX
                   g1498053
NCBI GI
                   775
BLAST score
                   2.0e-82
E value
Match length
                   208
% identity
                   74
NCBI Description
                   (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                   5243
                   4620 1.R1040
Contig ID
5'-most EST
                   eep7\overline{0}0863857.h1
Method
                   BLASTX
                   q1710780
NCBI GI
BLAST score
                   663 -
E value
                   2.0e-69
Match length
                   173
% identity
                   72
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   5244
Seq. No.
Contig ID
                   4620 2.R1040
                   leu7\overline{0}1149795.h1
5'-most EST
                   BLASTX
Method
                   g1710780
NCBI GI
BLAST score
                   669
                   3.0e-70
E value
                   173
Match length
% identity
                   73
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   5245
Seq. No.
                   4620 3.R1040
Contig ID
5'-most EST
                   xpa700793723.h1
Method
                   BLASTX
NCBI GI
                   q1710780
BLAST score
                   337
E value
                   2.0e-31
Match length
                   77
% identity
                   81
NCBI Description
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb_CAA65433_
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   5246
Seq. No.
Contig ID
                   4620 4.R1040
5'-most EST
                   LIB3106-058-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   g131770
```

```
E value
                  5.0e-12
Match length
                  75
% identity
                  56
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                  (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880 pir R3DO24
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi 7353 emb CAA29844 (X06636) rp1024 protein
                  [Dictyostelium discoideum]
                  5247
Seq. No.
                  4625 1.R1040
Contig ID
5'-most EST
                  txt700737518.hl
                  BLASTX
Method
                  g4049632
NCBI GI
BLAST score
                  759
E value
                  1.0e-80
                  180
Match length
% identity
                  85
                  (AF039406) pyruvate dehydrogenase kinase [Arabidopsis
NCBI Description
                  thaliana]
                  5248
Seq. No.
Contig ID
                  4626 1.R1040
                  LIB3051-042-Q1-K1-B9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1706551
BLAST score
                  269
E value
                  2.0e-23
Match length
                  115
                  57
% identity
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                  ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                  (BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta
                  1,3-qlucanase [Triticum aestivum]
                  5249
Seq. No.
                  4626 2.R1040
Contig ID
5'-most EST
                  LIB3092-029-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1706551
                  926
BLAST score
                  1.0e-100
E value
                  351
Match length
% identity
                  52
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                  ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                  (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                  1,3-glucanase [Triticum aestīvum]
                  5250
Seq. No.
                  4626_3.R1040
Contig ID
5'-most EST
                  fC-gmro7000749504a1
Method
                  BLASTX
NCBI GI
                  g1706551
BLAST score
                  230
                  6.0e-19
E value
Match length
                  50
```

177.

```
80
% identity
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                   1,3-glucanase [Triticum aestivum]
                   5251
Seq. No.
                   4626 4.R1040
Contig ID
5'-most EST
                   LIB3028-013-Q1-B1-D4
                   5252
Seq. No.
                   4630 1.R1040
Contig ID
                   fC-qmf1700906093j1
5'-most EST
                   BLASTX
Method
                   g4415916
NCBI GI
BLAST score
                   448
E value
                   4.0e-44
                   238
Match length
                   40
% identity
NCBI Description
                   (AC006282) putative pectin methylesterase [Arabidopsis
                   thaliana]
                   5253
Seq. No.
                   4631 1.R1040
Contig ID
                   seb7\overline{0}0653612.h1
5'-most EST
                   BLASTX
Method
                   q3702328
NCBI GI
BLAST score
                   1832
                   0.0e + 00
E value
Match length
                   443
                   72
% identity
                   (AC005397) putative cytochrome b5 [Arabidopsis thaliana]
NCBI Description
                   5254
Seq. No.
                   4631_2.R1040
Contig ID
                   jC-gmf102220085g03a1
5'-most EST
Method
                   BLASTX
                   g3819710
NCBI GI
                   462
BLAST score
                   6.0e-46
E value
                   113
Match length
% identity
                   (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                   thaliana]
                   5255
Seq. No.
Contig ID
                   4638 1.R1040
5'-most EST
                   LIB3028-013-Q1-B1-E8
Method
                   BLASTX
                   g1931652
NCBI GI
BLAST score
                   712
E value
                   1.0e-121
Match length
                   377
% identity
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
NCBI Description
```

[Arabidopsis thaliana]

5'-most EST

q4313953

```
5256
Seq. No.
                   4638 2.R1040
Contig ID
5'-most EST
                   jC-qmf102220093g07a1
Method
                  BLASTX
NCBI GI
                  g1931652
BLAST score
                   336
E value
                   3.0e-31
Match length
                  113
% identity
                   58
NCBI Description
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
                   [Arabidopsis thaliana]
                  5257
Seq. No.
                  4638 3.R1040
Contig ID
5'-most EST
                  LIB3065-013-Q1-N1-G11
Method
                  BLASTX
NCBI GI
                  q2739367
BLAST score
                  490
E value
                  3.0e-49
Match length
                  142
% identity
                  63
                  (AC002505) putative phosphatidylinositol-4-phosphate
NCBI Description
                  5-kinase [Arabidopsis thaliana]
                  5258
Seq. No.
Contig ID
                  4641 1.R1040
5'-most EST
                  LIB3028-013-Q1-B1-F10
                  5259
Seq. No.
                  4642 1.R1040
Contig ID
5'-most EST
                  LIB3138-045-Q1-N1-D6
Method
                  BLASTX
NCBI GI
                  q3860272
BLAST score
                  1296
                  1.0e-143
E value
Match length
                  270
% identity
                  90
                  (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
Seq. No.
                  5260
Contig ID
                  4642 2.R1040
5'-most EST
                  uC-gmrominsoy307f06b1
Method
                  BLASTX
NCBI GI
                  q3860272
BLAST score
                  1219
E value
                  1.0e-134
Match length
                  280
% identity
                  (ACO05824) putative suppressor protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
                  5261
Seq. No.
Contig ID
                  4642 3.R1040
```

```
Method
                   BLASTX
. NCBI GI
                   q3860272
BLAST score
                   1132
E value
                   1.0e-124
Match length
                   256
 % identity
                   88
NCBI Description
                   (AC005824) putative suppressor protein [Arabidopsis
                   thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
                   protein [Arabidopsis thaliana]
                   5262
Seq. No.
Contig ID
                   4642_4.R1040
 5'-most EST
                   q4314039
Method
                   BLASTX
NCBI GI
                   q3860272
BLAST score
                   478
E value
                   9.0e-48
Match length
                   103
                   83
% identity
                   (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
                   protein [Arabidopsis thaliana]
                   5263
Seq. No.
Contig ID
                   4642 9.R1040
5'-most EST
                   pmv700893510.hl
Method
                   BLASTX
                   g3860272
NCBI GI
BLAST score
                   203
E value
                   4.0e-16
Match length
                   82
% identity
                   68
NCBI Description
                   (AC005824) putative suppressor protein [Arabidopsis
                   thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
                   protein [Arabidopsis thaliana]
Seq. No.
                   5264
Contig ID
                   4645 1.R1040
                   LIB3170-057-Q1-K1-C8
5'-most EST
Method
                   BLASTX
                   q3293547
NCBI GI
BLAST score
                   174
E value
                   3.0e-12
Match length
                   141
% identity
                   34
                   (AF072709) putative oxidoreductase [Streptomyces lividans]
NCBI Description
Seq. No.
                   5265
Contig ID
                   4645 2.R1040
5'-most EST
                   LIB3028-013-Q1-B1-F4
Method
                   BLASTX
NCBI GI
                   q117549
BLAST score
                   188
                   6.0e-14
E value
Match length
                   173
% identity
                   34
                   QUINONE OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE)
NCBI Description
```

```
quinone reductase (NADPH) (EC 1.6.-.-) - guinea pig
                   >gi 305333 (M26936) zeta-crystallin [Cavia porcellus]
                   5266
Seq. No.
Contig ID
                   4646 1.R1040
5'-most EST
                   kl1701208545.hl
Method
                   BLASTX
NCBI GI
                   g4079809
BLAST score
                   350
                   7.0e-33
E value
Match length
                   190
% identity
                   3
NCBI Description
                   (AF071172) HERC2 [Homo sapiens]
Seq. No.
                   5267
                   4649 1.R1040
Contig ID
                   asn7\overline{0}1137915.h1
5'-most EST
                   5268
Seq. No.
                   4649 2.R1040
Contig ID
5'-most EST
                   LIB3050-001-Q1-E1-F7
Method
                   BLASTX
NCBI GI
                   g416650
BLAST score
                   509
                   3.0e-51
E value
Match length
                   210
% identity
                   48
                   PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
NCBI Description
                   PGNT35/PCNT111) >gi_100304_pir__S16268 auxin-induced
                   protein (clone pGNT35) - common tobacco
                   >gi_19797_emb_CAA39706_ (X56265) auxin-induced protein [Nicotiana tabacum] >gi_19801_emb_CAA39710_ (X56269)
                   auxin-induced protein [Nicotiana tabacum]
                   5269
Seq. No.
                   4651 1.R1040
Contig ID
5'-most EST
                   LIB3028-013-Q1-B1-C7
                   5270
Seq. No.
                   4652 1.R1040
Contig ID
5'-most EST
                   LIB3139-052-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   q3204134
                   2063
BLAST score
                   0.0e+00
E value
                   677
Match length
% identity
                   (AJ006771) beta-galactosidase [Cicer arietinum]
NCBI Description
                   5271
Seq. No.
Contig ID
                   4655 1.R1040
5'-most EST
                   uC-gmronoir039g01b1
Seq. No.
                   5272
```

(ZETA-CRYSTALLIN) >gi 65895\_pir\_\_CYGPZ zeta-crystallin /

4659 1.R1040

LIB3028-013-Q1-B1-D7

Contig ID

5'-most EST

Seq. No.

```
BLASTX
Method
NCBI GI
                   a4107099
                   247
BLAST score
E value
                   2.0e-20
                   149
Match length
                   56
% identity
                   (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                  thaliana]
Seq. No.
                   5273
Contig ID
                   4662 1.R1040
                  wvk700681920.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q951449
BLAST score
                  1796
                   0.0e+00
E value
                  507
Match length
% identity
                   67
                   (L46681) aspartic protease precursor [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  5274
Contig ID
                   4662 2.R1040
                  LIB3028-009-Q1-B1-B10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q951449
BLAST score
                  933
                  1.0e-101
E value
                  249
Match length
% identity
                   66
NCBI Description
                   (L46681) aspartic protease precursor [Lycopersicon
                  esculentum]
                  5275
Seq. No.
Contig ID
                   4663 1.R1040
5'-most EST
                  LIB3093-051-Q1-K1-A12
                  BLASTX -
Method
NCBI GI
                  q4454467
BLAST score
                   414
E value
                   3.0e-40
Match length
                  84
                  85
% identity
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                  5276
Seq. No.
Contig ID
                  4664 1.R1040
5'-most EST
                  leu701154408.h1
Method
                  BLASTX
NCBI GI
                  q2244732
BLAST score
                  840
E value
                  3.0e-90
Match length
                  182
% identity
NCBI Description
                  (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
```

NCBI GI

```
4668 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir013a07b1
                   5278
Seq. No.
                   4668 2.R1040
Contig ID
                   qsv7\overline{0}1056644.h1
5'-most EST
                   5279
Seq. No.
                   4672 1.R1040
Contig ID
                   leu701153884.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   ġ4105097
                   342
BLAST score
                   2.0e-32
E value
                   79
Match length
                   82
% identity
                   (AF043255) MADS box protein 26 [Cucumis sativus]
NCBI Description
                   5280
Seq. No.
                   4674 1.R1040
Contig ID
                   leu701149025.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245109
                   589
BLAST score
                   5.0e-61
E value
Match length
                   145
                   77
% identity
                   (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis
NCBI Description
                   thaliana]
                   5281
Seq. No.
                   4675 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy083c10b1
Method
                   BLASTX
NCBI GI
                   g3219271
                   886
BLAST score
                   2.0e-95
E value
Match length
                   224
% identity
                   76
                   (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
NCBI Description
                   5282
Seq. No.
                   4675 2.R1040
Contig ID
5'-most EST
                   LIB3051-015-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   g3219271
BLAST score
                   762
E value
                   6.0e-81
                   222
Match length
                   71
% identity
                   (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
NCBI Description
                   5283
Seq. No.
Contig ID
                   4675 3.R1040
5'-most EST
                   jC-gmro02800039d05a1
Method
                   BLASTX
```

g3219271

```
BLAST score
                  185
E value
                   3.0e-15
                  97
Match length
                  60
% identity
                   (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
NCBI Description
                  5284
Seq. No.
                  4675 4.R1040
Contig ID
                  jC-gmf102220052d10d1
5'-most EST
                  BLASTX
Method
                  g1523800
NCBI GI
BLAST score
                  162
                  4.0e-11
E value
Match length
                  51
% identity
                  57
                  (Y07694) MAP kinase kinase alpha protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  5285
Seq. No.
                  4676 1.R1040
Contig ID
                  cf1700863656.h1
5'-most EST
Method
                  BLASTX
                  g2392895
NCBI GI
BLAST score
                  1512
                  1.0e-169
E value
Match length
                  333
                  87
% identity
NCBI Description
                  (AF017056) brassinosteroid insensitive 1 [Arabidopsis
                  thaliana]
                  5286
Seq. No.
                  4677 1.R1040
Contig ID
5'-most EST
                  ssr7\overline{0}0557419.h1
Method
                  BLASTX
                  g2072986
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
Match length
                  67
% identity
                  57
                  (U95142) putative G-protein-coupled receptor [Arabidopsis
NCBI Description
                  thaliana] >gi 2072988 (U95143) putative G-protein-coupled
                  receptor [Arabidopsis thaliana]
                  5287
Seq. No.
                  4677 2.R1040
Contig ID
5'-most EST
                  LIB3109-034-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2072986
BLAST score
                  462
                  3.0e-46
E value
Match length
                  118
                  74
% identity
                  (U95142) putative G-protein-coupled receptor [Arabidopsis
NCBI Description
                  thaliana] >gi 2072988 (U95143) putative G-protein-coupled
                  receptor [Arabidopsis thaliana]
```

5288

Seq. No.

5'-most EST

```
Contig ID
                   4679 1.R1040
                   leu701148521.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4099833
BLAST score
                   559
                   2.0e-57
E value
Match length
                   186
                   56
% identity
NCBI Description
                   (U90265) bifunctional nuclease [Zinnia elegans]
                   5289
Seq. No.
Contig ID
                   4680 1.R1040
                   fC-gmse700674289f1
5'-most EST
                   5290
Seq. No.
Contig ID
                   4680 2.R1040
5'-most EST
                   uC-gmrominsoy227f07b1
                   5291
Seq. No.
                   4680 4.R1040
Contig ID
5'-most EST
                   zsg701117722.h2
                   5292
Seq. No.
                   4682 1.R1040
Contig ID
5'-most EST
                   LIB3028-012-Q1-B1-H1
Seq. No.
                   5293
Contig ID
                   4696 1.R1040
                   hyd7\overline{0}0727117.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4519194
BLAST score
                   63
E value
                   1.0e-26
Match length
                   227
% identity
                   82
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHM17, complete sequence
                   5294
Seq. No.
                   4696 2.R1040
Contig ID
                   LIB3051-004-Q1-E1-E3
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4519194
BLAST score
                   48
                   1.0e-17
E value
Match length
                   176
% identity
                   82
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MHM17, complete sequence
Seq. No.
                   5295
Contig ID
                   4697 1.R1040
5'-most EST
                   LIB3028-010-Q1-B1-F2
Seq. No.
                   5296
Contig ID
                   4700 1.R1040
```

LIB3074-019-Q1-E1-C2

```
Method
                   BLASTX
NCBI GI
                   g4325369
BLAST score
                   251
                   2.0e-21
E value
Match length
                   81
                   58
% identity
                   (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5297
Contig ID
                   4701 1.R1040
5'-most EST
                   g4395911
                   BLASTX
Method
NCBI GI
                   g730542
BLAST score
                   245
                   2.0e-20
E value
Match length
                   98
                   54
% identity
                   60S RIBOSOMAL PROTEIN L22 (HEPARIN BINDING PROTEIN HBP15)
NCBI Description
                   >gi_543098_pir__JC2121 heparin-binding protein 15 - pig
                   >gi 627874 pir JC2119 heparin-binding protein 15 - mouse
                   >gi_409072_dbj_BAA04546_ (D17653) HBp15/L22 [Mus musculus]
>gi_409074_dbj_BAA04547_ (D17654) HBp15/L22 [Sus scrofa]
                   5298
Seq. No.
Contig ID
                   4701 2.R1040
5'-most EST
                   LIB3073-025-Q1-K1-G2
Method
                   BLASTX
                   g1172995
NCBI GI
BLAST score
                   249
                   4.0e-21
E value
Match length
                   101
% identity
                   52
                   60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
NCBI Description
                   protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
                   ribosomal protein L22 [Rattus norvegicus]
                   >gi 1093952 prf 2105193A ribosomal protein L22 [Rattus
                   norvegicus]
Seq. No.
                   5299
Contig ID
                   4703_1.R1040
5'-most EST
                   uaw700666912.h1
Method
                   BLASTX
NCBI GI
                   q2522534.
BLAST score
                   519
E value
                   1.0e-105
Match length
                   415
% identity
                   29
NCBI Description
                   (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]
Seq. No.
                   5300
Contig ID
                   4704 1.R1040
5'-most EST
                   LIB3106-037-Q1-K1-D6
Method
                   BLASTX
                   q4371280
NCBI GI
BLAST score
                   426
                   9.0e-42
E value
```

112

Match length

NCBI Description

```
% identity
                   76
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5301
Seq. No.
                   4710 2.R1040
Contig ID
                   LIB3028-012-Q1-B1-E7
5'-most EST
Method
                   BLASTX
                   g3877951
NCBI GI
BLAST score
                   246
                   1.0e-20
E value
Match length
                   133
% identity
                   36
                   (Z81555) predicted using Genefinder [Caenorhabditis
NCBI Description
                   elegans]
                   5302
Seq. No.
Contig ID
                   4712 1.R1040
                   LIB3051-017-Q1-E1-A4
5'-most EST
                   5303
Seq. No.
                   4714 1.R1040
Contig ID
                   LIB3109-035-Q1-K6-H10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3892058
BLAST score
                   490
E value
                   9.0e-49
Match length
                   226
% identity
                   47
NCBI Description
                   (AC002330) putative glutamate-/aspartate-binding peptide
                   [Arabidopsis thaliana]
                   5304
Seq. No.
                   4714 2.R1040
Contig ID
5'-most EST
                   LIB3139-030-P1-N1-B7
                   BLASTX
Method
NCBI GI
                   g2244904
BLAST score.
                   181
E value
                   3.0e-13
Match length
                   85
                   62
% identity
                   (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
NCBI Description
                   [Arabidopsis thaliana]
                   5305
Seq. No.
                   4714 3.R1040
Contig ID
5'-most EST
                   uC-gmronoir030b08b1
Seq. No.
                   5306
Contig ID
                   4716 1.R1040
5'-most EST
                   leu701154646.h1
                   BLASTX
Method
NCBI GI
                   g4262183
BLAST score
                   386
E value
                   3.0e-37
Match length
                   83
                   87
% identity
```

(AC005508) 51434 [Arabidopsis thaliana]

NCBI Description

```
5307
Seq. No.
                   4718 1.R1040
Contig ID
                  LIB3028-012-Q1-B1-D5
5'-most EST
Method
                  BLASTX
                  g4220480
NCBI GI
BLAST score
                  242
                  3.0e-20
E value
Match length
                  101
% identity
                   51
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  5308
Seq. No.
                   4721 1.R1040
Contig ID
5'-most EST
                  txt700734653.h1
Method
                  BLASTX
NCBI GI
                  g4454051
BLAST score
                  581
                   6.0e-60
E value
                  208
Match length
% identity
                   55
                   (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  5309
Seq. No.
                   4724 1.R1040
Contig ID
                   jC-gmf102220115f09a1
5'-most EST
                  BLASTX
Method
                  g2739370
NCBI GI
                   333
BLAST score
E value
                   4.0e-31
Match length
                  128
% identity
                   51
                   (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  5310
Seq. No.
Contig ID
                   4725 1.R1040
5'-most EST
                  LIB3028-007-Q1-B1-G3
Method
                  BLASTX
NCBI GI
                  g602292
BLAST score
                   507
E value
                   3.0e-51
Match length
                  208
                   49
% identity
NCBI Description
                  (U17987) RCH2 protein [Brassica napus]
Seq. No.
                  5311
                   4729 1.R1040
Contig ID
                  crh700852073.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4406759
BLAST score
                  542
E value
                   4.0e-55
Match length
                  291
% identity
                   44
```

(AC006836) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                   5312
                   4729 2.R1040
Contig ID
5'-most EST
                   kl1701212931.h1
Method
                   BLASTX
                   g4406759
NCBI GI
BLAST score
                   362
E value
                   6.0e - 34
                   239
Match length
                   36
% identity
                   (AC006836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   4733 1.R1040
Contig ID
5'-most EST
                   uC-gmropic019c04b1
Method
                   BLASTX
NCBI GI
                   g1350983
BLAST score
                   1092
                   1.0e-119
E value
                   234
Match length
                   88
% identity
                   40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                   5314
Seq. No.
                   4737 1.R1040
Contig ID
                   LIB3028-012-Q1-B1-B12
5'-most EST
                   5315
Seq. No.
Contig ID
                   4739 1.R1040
                   LIB3170-025-Q1-K1-H1
5'-most EST
                   BLASTX
Method
                   q3892058
NCBI GI
BLAST score
                   832
E value
                   4.0e-89
Match length
                   238
% identity
                   66
                   (AC002330) putative glutamate-/aspartate-binding peptide
NCBI Description
                   [Arabidopsis thaliana]
                   5316
Seq. No.
                   4740 1.R1040
Contig ID
                   zzp700834267.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2392021
BLAST score
                   628
E value
                   3.0e-65
Match length
                   168
                   68
% identity
NCBI Description
                   (D63425) phopholipid hydroperoxide glutathione
                   peroxidase-like protein [Spinacia oleracea]
                   5317
Seq. No.
Contig ID
                   4743 1.R1040
5'-most EST
                   LIB3109-019-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   g2460203
BLAST score
                   268
```

1.0e-23

E value

Contig ID

```
Match length
                   116
                   47
% identity
NCBI Description
                   (AF021244) coronatine-induced protein 1 [Arabidopsis
                   thaliana]
                   5318
Seq. No.
                   4744 1.R1040
Contig ID
5'-most EST
                   zhf700956861.h1
Method
                   BLASTX
                   g3193286
NCBI GI
BLAST score
                   199
E value
                   3.0e-15
Match length
                   54
                   63
% identity
                   (AF069298) T14P8.22 gene product [Arabidopsis thaliana]
NCBI Description
                   5319
Seq. No.
                   4744 2.R1040
Contig ID
5'-most EST
                   LIB3074-012-Q1-E1-E10
Seq. No.
                   5320
                   4744 3.R1040
Contig ID
                   LIB3\overline{1}38-007-Q1-N1-D10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3193286
BLAST score
                   587
E value
                   2.0e-60
Match length
                   255
                   51
% identity
                   (AF069298) T14P8.22 gene product [Arabidopsis thaliana]
NCBI Description
                   5321
Seq. No.
                   4745_1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy011h05b1
                   5322
Seq. No.
Contig ID
                   4746_1.R1040
5'-most EST
                   uC-gmrominsoy040e05b1
                   5323
Seq. No.
Contig ID
                   4746 2.R1040
5'-most EST
                   k117\overline{0}1202777.h1
                   5324
Seq. No.
Contig ID
                   4747 1.R1040
5'-most EST
                   jsh7\overline{0}1064513.h1
Method
                   BLASTX
NCBI GI
                   q2088643
BLAST score
                   509
                   1.0e-84
E value
Match length
                   197
% identity
                   45
NCBI Description
                   (AF002109) transcription factor SF3 isolog [Arabidopsis
                   thaliana]
Seq. No.
```

4747 2.R1040

5'-most EST

```
5'-most EST
                  LIB3139-076-P1-N1-C2
Method
                  BLASTX
NCBI GI
                   g1841464
BLAST score
                   334
E value
                   5.0e-31
Match length
                  75
                   42
% identity
NCBI Description. (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
                 . 5326
Seq. No.
Contig ID
                   4747 4.R1040
                   sat701015226.hl
5'-most EST
                   5327
Seq. No.
                   4747 5.R1040
Contig ID
5'-most EST
                  pmv700892040.h1
                   5328
Seq. No.
                   4749 1.R1040
Contig ID
5'-most EST
                  crh700852401.hl
Method
                  BLASTX
NCBI GI
                  g480618
                  724
BLAST score
                  2.0e-76
E value
                  216
Match length
% identity
                   69
NCBI Description
                  ATAF1 protein - Arabidopsis thaliana (fragment)
                  >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis
                  thaliana]
                  5329
Seq. No.
                   4749 2.R1040
Contig ID
                  uC-gmrominsoy245e10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g480618
BLAST score
                   677
E value
                   6.0e-71
Match length
                  206
% identity
                   68
                  ATAF1 protein - Arabidopsis thaliana (fragment)
NCBI Description
                  >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis
                  thaliana]
                  5330
Seq. No.
                  4749 3.R1040
Contig ID
5'-most EST
                  uC-gmronoir076d10b1
Method
                  BLASTX
NCBI GI
                  g4218535
BLAST score
                  446
E value
                  2.0e-44
Match length
                  126
% identity
                  64
                  (AJ010829) GRAB1 protein [Triticum sp.]
NCBI Description
                  5331
Seq. No.
Contig ID
                  4753 1.R1040
```

LIB3109-046-Q1-K1-D11

```
BLASTX
Method
                   q4455363
NCBI GI
BLAST score
                   471
E value
                   5.0e-47
Match length
                   216
% identity
                   46
                   (AL035524) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   5332
Seq. No.
Contig ID
                   4754 1.R1040
5'-most EST
                   LIB3039-009-Q1-E1-B7
                   5333
Seq. No.
Contig ID
                   4758 1.R1040
                   LIB3072-056-Q1-K1-E2
5'-most EST
Method
                   BLASTN
                   g3687405
NCBI GI
BLAST score
                   72
E value
                   4.0e-32
                   148
Match length
                   87
% identity
                   Lycopersicon esculentum mRNA for hypothetical protein
NCBI Description
                   5334
Seq. No.
                                                      . .
                   4758 2.R1040
Contig ID
                   q4290065
5'-most EST
Method
                   BLASTN
                   q3687405
NCBI GI
BLAST score
                   82
E value
                   4.0e-38
Match length
                   146
                   89
% identity
                   Lycopersicon esculentum mRNA for hypothetical protein
NCBI Description
                   5335
Seq. No.
Contig ID
                   4758 3.R1040
                   jsh7\overline{0}1063726.h1
5'-most EST
                   BLASTN
Method
                   g3687405
NCBI GI
BLAST score
                   79
E value
                   2.0e-36
                   139
Match length
                   89
% identity
                   Lycopersicon esculentum mRNA for hypothetical protein
NCBI Description
Seq. No.
                   5336
Contig ID
                   4758 4.R1040
5'-most EST
                   zhf700962928.hl
                   BLASTN
Method
NCBI GI
                   q3297806
BLAST score
                   34
E value
                   1.0e-09
Match length
                   66
                   47
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5
NCBI Description
```

(ESSAII project)

```
5337
Seq. No.
Contig ID
                   4763 1.R1040
5'-most EST
                   k11701214127.h1
                   5338
Seq. No.
Contig ID
                   4763 2.R1040
5'-most EST
                  pxt700945468.hl
                  5339
Seq. No.
                   4766 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir042a03b1
Method
                  BLASTX
NCBI GI
                   g4406809
BLAST score
                   245
E value
                   3.0e-20
                                                          • • • •
Match length
                   295
% identity
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5340
Seq. No.
                   4766 2.R1040
Contig ID
5'-most EST
                   awf700837035.h1
Method
                  BLASTN
                  g4097879
NCBI GI
                  35
BLAST score
                  2.0e-10
E value
Match length
                  51
% identity
                   92
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  5341
Seq. No.
Contig ID
                   4770 1.R1040
                   jC-gmle01810064h08a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1086225
BLAST score
                  949
E value
                  0.0e+00
Match length
                  534
% identity
                  76
                  RING-finger protein (C-terminal) - Lotus japonicus
NCBI Description
                  >gi 558545 emb CAA85321 (Z36750) protein containing
                  C-terminal RING-finger [Lotus japonicus]
                  >gi 1771195 emb CAA70734 (Y09539) RING-finger protein
                   [Lotus japonicus]
                  5342
Seq. No.
Contig ID
                  4775 1.R1040
5'-most EST
                  pxt700943412.hl
Seq. No.
                  5343
Contig ID
                  4777 1.R1040
5'-most EST
                  LIB3109-021-Q1-K2-E3
Method
                  BLASTX
NCBI GI
                  q1531758
                  750
BLAST score
```

```
E value
                   5.0e-80
Match length
                   147
% identity
                   92
                   (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   5344
Seq. No.
                   4782 1.R1040
Contig ID
                   LIB3028-011-Q1-B1-E6
5'-most EST
                   5345
Seq. No.
                   4782 2.R1040
Contig ID
                   LIB3\overline{0}55-005-Q1-N1-F10
5'-most EST
Seq. No.
                   5346
Contig ID
                   4783 1.R1040
                   leu701157320.hl
5'-most EST
                   5347
Seq. No.
                   4783 2.R1040
Contig ID
                   jC-qmle01810011d10a1
5'-most EST
Seq. No.
                   5348
                   4786 1.R1040
Contig ID
5'-most EST
                   LIB3139-064-P1-N1-H5
                   5349
Seq. No.
                   4787 1.R1040
Contig ID
5'-most EST
                   LIB3028-011-Q1-B1-B12
Method
                   BLASTX
NCBI GI
                   g1914845
BLAST score
                   383
                   1.0e-36
E value
Match length
                   135
                   59
% identity
NCBI Description
                   (U89496) liguleless1 protein [Zea mays]
                   5350
Seq. No.
Contig ID
                   4788 1.R1040
5'-most EST
                   jC-gmle01810042c06a1
Method
                   BLASTX
NCBI GI
                   g2244971
                   365
BLAST score
                   1.0e-34
E value
                   131
Match length
% identity
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5351
Contig ID
                   4788 2.R1040
5'-most EST
                   uC-gmflminsoy058c06b1
Method
                   BLASTX
NCBI GI
                   g2244971
BLAST score
                   508
E value
                   1.0e-51
Match length
                   154
```

64

% identity

% identity

```
NCBI Description
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
                   5352
Seq. No.
                   4791 1.R1040
Contig ID
                   LIB3138-030-Q1-N1-H11
5'-most EST
Seq. No.
                   5353
                   4792 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220050e08a1
                   BLASTX
Method
NCBI GI
                   g2827552
BLAST score
                   804
                   3.0e-86
E value
Match length
                   173
% identity
                   41
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5354
Contig ID
                   4799 1.R1040
5'-most EST
                   LIB3073-020-Q1-K1-C6
Method
                   BLASTX
NCBI GI
                   g4406772
BLAST score
                   156
E value
                   4.0e-10
Match length
                   63
                   60
% identity
NCBI Description
                   (AC006836) putative nitrilase-associated protein
                   [Arabidopsis thaliana]
Seq. No.
                   5355
Contig ID
                   4799 2.R1040
5'-most EST
                   LIB3049-003-Q1-E1-E9
                   5356
Seq. No.
Contig ID
                   4801 1.R1040
5'-most EST
                   fde7\overline{0}0873950.h1
Seq. No.
                   5357
                   4802 1.R1040
Contig ID
5'-most EST
                   LIB3107-080-Q1-K1-C1
Method
                   BLASTN
NCBI GI
                   q1813328
BLAST score
                   212
E value
                   1.0e-115
Match length
                   671
                   84
% identity
NCBI Description
                   Canavalia gladiata mRNA for HMG-1, complete cds
Seq. No.
                   5358
Contig ID
                   4802 2.R1040
5'-most EST
                   pcp700991734.hl
Method
                  BLASTN
NCBI GI
                   g1813328
BLAST score
                   126
E value
                   2.0e-64
Match length
                   286
```

Method

NCBI GI

BLASTX

g4220521

```
NCBI Description Canavalia gladiata mRNA for HMG-1, complete cds
                  5359
Seq. No.
Contig ID
                  4803 1.R1040
5'-most EST
                  LIB3028-010-Q1-B1-H6
Method
                  BLASTX
                  g100347
NCBI GI
BLAST score
                  498
                  1.0e-77
E value
Match length
                  220
                  66
% identity
NCBI Description
                  monosaccharide transport protein MST1 - common tobacco
                  >gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter
                   [Nicotiana tabacum]
                  5360
Seq. No.
                  4803 2.R1040
Contig ID
5'-most EST
                  jC-gmf102220138h04d1
Method
                  BLASTX
NCBI GI
                  g99758
BLAST score
                  344
                  2.0e-32
E value
                  92
Match length
                  65
% identity
NCBI Description
                  monosaccharid transport protein STP4 - Arabidopsis thaliana
                  >gi_16524_emb_CAA47325_ (X66857) sugar transport protein
                  [Arabidopsis thaliana]
                  5361
Seq. No.
Contig ID
                  4805 1.R1040
5'-most EST
                  uC-gmrominsoy053f06b1
Method
                  BLASTX
NCBI GI
                  g3914359
BLAST score
                  1743
E value
                  0.0e + 00
Match length
                  362
% identity
                  90
NCBI Description
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1928979 (U92656) phospholipase D [Vigna unguiculata]
                  5362
Seq. No.
                  4805 2.R1040
Contig ID
5'-most EST
                  leu701151758.h1
Method
                  BLASTN
                  g1928978
NCBI GI
BLAST score
                  181
                  3.0e-97
E value
Match length
                  282
% identity
                  93
                  Vigna unguiculata phospholipase D mRNA, complete cds
NCBI Description
Seq. No.
                  5363
Contig ID
                  4806 1.R1040
5'-most EST
                  zsq7\overline{0}1118351.h1
```

```
BLAST score
                   780
E value
                   8.0e-83
Match length
                   345
                   57
% identity
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                   5364
Seq. No.
                   4806 4.R1040
Contig ID
5'-most EST
                   zsg701118740.hl
Seq. No.
                   5365
                   4809 1.R1040
Contig ID
                   LIB3028-011-Q1-B1-A5
5'-most EST
                   BLASTX
Method
                   g1769895
NCBI GI
                   803
BLAST score
                   6.0e-86
E value
Match length
                   228
                   68
% identity
                   (X96598) CaLB protein [Arabidopsis thaliana]
NCBI Description
                   5366
Seq. No.
Contig ID
                   4811_1.R1040
5'-most EST
                   uC-gmrominsoy114g12b1
Method
                   BLASTX
NCBI GI
                   g1361979
BLAST score
                   310
E value
                   5.0e-30
                   108
Match length
                   70
% identity
                   serine O-acetyltransferase (EC 2.3.1.30) - watermelon
NCBI Description
                   >gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase
                   [Citrullus lanatus] >gi 1841312 dbj BAA08479 (D49535)
                   serine acetyltransferase. [Citrullus lanatus]
                   >gi_2337772_dbj_BAA21827_ (AB006530) serine
                   acetyltransferase [Citrullus lanatus]
Seq. No.
                   5367
Contig ID
                   4814 1.R1040
                   zhf700954244.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3377820
BLAST score
                   265
E value
                   8.0e-37
                   132
Match length
% identity
                   (AF076275) contains similarity to coatomer zeta chains
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   5368
Contig ID
                   4815 1.R1040
5'-most EST
                  LIB3109-034-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2454184
BLAST score
                  1235
                   1.0e-136
E value
                   405
Match length
```

Contig ID

```
% identity
                   67
NCBI Description
                   (U80186) pyruvate dehydrogenase El beta subunit
                   [Arabidopsis thaliana]
Seq. No.
                   5369
                   4815 2.R1040
Contig ID
                   seb700650890.hl
5'-most EST
                   5370
Seq. No.
Contig ID
                   4815 3.R1040
5'-most EST
                   jC-gmro02910071g01d1
                   5371
Seq. No.
                   4816 1.R1040
Contig ID
                   LIB3028-010-Q1-B1-F9
5'-most EST
                   BLASTX
Method
                   g2760324
NCBI GI
                   322
BLAST score
                   1.0e-29
E value
                   104
Match length
% identity
                   64
NCBI Description
                   (AC002130) F1N21.9 [Arabidopsis thaliana]
Seq. No.
                   5372
                   4817 1.R1040
Contig ID
5'-most EST
                  LIB3040-054-Q1-E1-B9
Seq. No.
                   5373
                   4817 2.R1040
Contig ID
5'-most EST
                  LIB3072-027-Q1-E1-D9
                   5374
Seq. No.
                   4820 1.R1040
Contig ID
5'-most EST
                   leu701147178.h1
Method
                   BLASTX
NCBI GI
                   g4218120
BLAST score
                   1243
E value
                   1.0e-137
Match length
                   356
% identity
                   67
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   5375
Seq. No.
                   4820 2.R1040
Contig ID
5'-most EST
                  wrg700788041.hl
Method
                  BLASTX
NCBI GI
                   g4218120
BLAST score
                   498
E value
                   3.0e-50
Match length
                  122
% identity
                   77
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   5376
Seq. No.
```

4820 3.R1040

BLAST score

```
5'-most EST
                   g4260376
Method
                  BLASTX
NCBI GI
                   q4218120
                   331
BLAST score
                   8.0e-31
E value
                  79
Match length
                   72
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   5377
Seq. No.
                   4823 1.R1040
Contig ID
                   jC-gmro02800040g03d1
5'-most EST
                   5378
Seq. No.
                   4823 2.R1040
Contig ID
                  uxk700672939.h1
5'-most EST
Method
                  BLASTX
                   q3650033
NCBI GI
                   200
BLAST score
                   2.0e-15
E value
Match length
                  81
                   54
% identity
                   (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5379
Seq. No.
Contig ID
                   4823_3.R1040
5'-most EST
                   jC-gmf102220143c10d1
                   5380
Seq. No.
                   4826 1.R1040
Contig ID
5'-most EST
                  LIB3093-007-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                   g3415115
                   498
BLAST score
                   7.0e-50
E value
                   253
Match length
% identity
                   (AF081202) villin 2 [Arabidopsis thaliana]
NCBI Description
                   5381
Seq. No.
                   4827 1.R1040
Contig ID
5'-most EST
                  LIB3028-010-Q1-B1-E6
Method
                   BLASTX
                   g3618316
NCBI GI
BLAST score
                   188
                   4.0e-14
E value
Match length
                   100
                   46
% identity
NCBI Description
                   (AB001886) zinc finger protein [Oryza sativa]
Seq. No.
                   5382
                   4828 1.R1040
Contig ID
5'-most EST
                   wvk700680503.hl
                  BLASTX
Method
                   g4539010
NCBI GI
```

Contig ID

```
1.0e-19
E value
Match length
                   143
% identity
                   48
                   (ALO49481) putative DNA-directed RNA polymerase
NCBI Description
                   [Arabidopsis thaliana]
                   5383
Seq. No.
                   4830 1.R1040
Contig ID
5'-most EST
                   LIB3106-035-Q1-K1-B7
                   BLASTX
Method
NCBI GI
                   g4138916
BLAST score
                   979
E value
                   1.0e-106
Match length
                   242
                   74
% identity
                   (AF059489) expansin precursor [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   5384
                   4830 2.R1040
Contig ID
                   hyd700724977.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4027897
                   452
BLAST score
                   6.0e-45
E value
Match length
                   116
% identity
NCBI Description
                   (AF049353) alpha-expansin precursor [Nicotiana tabacum]
                   5385
Seq. No.
                   4834 1.R1040
Contig ID
                   LIB3138-039-Q1-N1-C11
5'-most EST
Method
                   BLASTX
                   g4468813
NCBI GI
BLAST score
                   748
                   3.0e-79
E value
                   200
Match length
% identity
                   67
NCBI Description
                   (AL035601) putative protein [Arabidopsis thaliana]
                   5386
Seq. No.
Contig ID
                   4836 1.R1040
5'-most EST
                   jC-gmro02910031e04a1
                   5387
Seq. No.
Contig ID
                   4837 1.R1040
5'-most EST
                   LIB3049-053-Q1-E1-E8
Seq. No.
                   5388
Contig ID
                   4837 2.R1040
5'-most EST
                   trc700566031.hl
                   5389
Seq. No.
Contig ID
                   4840 1.R1040
5'-most EST
                  LIB3028-010-Q1-B1-D10
                   5390
Seq. No.
```

4844 1.R1040

BLAST score

```
5'-most EST
                   LIB3028-010-Q1-B1-B9
                   5391
Seq. No.
Contig ID
                   4845 1.R1040
5'-most EST
                   LIB3138-126-Q1-N1-A8
                   5392
Seq. No.
                   4846_1.R1040
Contig ID
5'-most EST
                   uC-gmropic014h09b1
Method
                   BLASTX
NCBI GI
                   q1546702
BLAST score
                   819
E value
                   1.0e-87
Match length
                   248
% identity
                   62
                   (X98809) peroxidase ATP5a [Arabidopsis thaliana]
NCBI Description
                   5393
Seq. No.
                   4846 2.R1040
Contig ID
5'-most EST
                   bth700844765.h1
Method
                   BLASTX
NCBI GI
                   g1546702
BLAST score
                   542
E value
                   2.0e-55
Match length
                   151
                   68
% identity
                   (X98809) peroxidase ATP5a [Arabidopsis thaliana]
NCBI Description
                   5394
Seq. No.
                   4846 3.R1040
Contig ID
                   pmv700893877.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2811262
BLAST score
                   121
E value
                   2.0e-11
Match length
                   75
% identity
                   56
                   (AF043234) ferriprotein porphyrin-containing peroxidase
NCBI Description
                   [Striga asiatica]
                   5395
Seq. No.
Contig ID
                   4848 1.R1040
5'-most EST
                   LIB3028-010-Q1-B1-A9
Method
                   BLASTN
NCBI GI
                   q2746720
BLAST score
                   128
E value
                   2.0e-65
Match length
                   312
% identity
                   85
NCBI Description
                   Capsicum annuum histone H4 mRNA, complete cds
                   5396
Seq. No.
Contig ID
                   4850 1.R1040
5'-most EST
                   g5687831
Method
                   BLASTN
NCBI GI
                   g3127889
```

```
💢 E value
                     0.0e+00
  Match length
                     760
                     89
  % identity
                    Cicer arietinum mRNA for cysteine synthase, partial
  NCBI Description
                     5397
  Seq. No.
                     4850 2.R1040
  Contig ID
  5'-most EST
                     LIB3087-002-Q1-K1-A3
  Method
                     BLASTN
  NCBI GI
                     q3127889
  BLAST score
                     149
                     4.0e-78
  E value
                     193
  Match length
                     94
  % identity
                    Cicer arietinum mRNA for cysteine synthase, partial
  NCBI Description
                     5398
  Seq. No.
                     4856 1.R1040
  Contig ID
                     LIB3106-003-Q1-K1-F1
  5'-most EST
  Method
                     BLASTX
                     q166878
  NCBI GI
                     154
  BLAST score
  E value
                     4.0e-10
  Match length
                     102
                     37
  % identity
  NCBI Description
                     (M95796) St12p protein [Arabidopsis thaliana]
                     5399
  Seq. No.
                     4856 2.R1040
  Contig ID
  5'-most EST
                     LIB3138-014-Q1-N2-H8
  Method
                     BLASTX
  NCBI GI
                     q3785976
  BLAST score
                     206
                     4.0e-16
  E value
  Match length
                     128
  % identity
                     37
                     (AC005560) Sec12p-like protein [Arabidopsis thaliana]
  NCBI Description
                     5400
  Seq. No.
                     4857 1.R1040
  Contig ID
  5'-most EST
                     sat701011352.hl
  Method
                     BLASTX
  NCBI GI
                     q3548802
  BLAST score
                     416
  E value
                     2.0e-40
  Match length
                     168
  % identity
                     50
                     (AC005313) axi 1-like protein [Arabidopsis thaliana]
  NCBI Description
                     >gi 4335769 gb AAD17446 (AC006284) putative axil protein
                     [Nicotiana tabacum] [Arabidopsis thaliana]
  Seq. No.
                     5401
  Contig ID
                     4859 1.R1040
  5'-most EST
                     LIB3093-031-Q1-K1-F6
  Method
                     BLASTX
  NCBI GI
                     g2244924
  BLAST score
                     324
```

```
E value
                  4.0e-30
Match length
                  81
% identity
                  73
NCBI Description
                  (Z97339) glutaredoxin [Arabidopsis thaliana]
Seq. No.
                  5402
Contig ID
                  4859 2.R1040
5'-most EST
                  leu701153189.hl
Method
                  BLASTX
NCBI GI
                  g2244924
                                                          33.
BLAST score
                  226
E value
                  1.0e-18
Match length
                  56
                  73
% identity
NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]
Seq. No.
                  5403
                  4863 1.R1040
Contig ID
5'-most EST
                  uC-gmropic113h06b1
Method
                  BLASTX
NCBI GI
                  g3776084
                  280
BLAST score
E value
                  1.0e-24
Match length
                  85
                  59
% identity
NCBI Description (Y18251) NtN2 [Medicago truncatula]
Seq. No.
                  5404
                  4863 2.R1040
Contig ID
5'-most EST
                  xzm7\overline{0}0763745.h1
Method
                  BLASTX
                  g3776084
NCBI GI
BLAST score
                  188
E value
                  1.0e-18
Match length
                  83
                  58
% identity
NCBI Description (Y18251) NtN2 [Medicago truncatula]
                  5405
Seq. No.
                  4866 1.R1040
Contig ID
5'-most EST
                  LIB3049-015-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  g2136139
BLAST score
                  262
E value
                  2.0e-42
Match length
                  297
% identity
                  15
NCBI Description
                  sds22 protein homolog - human >gi_1085028_emb_CAA90626_
                  (Z50749) yeast sds22 homolog [Homo sapiens]
                  >gi_1585165_prf__2124310A sds22 gene [Homo sapiens]
                  >gi_4506013_ref_NP_002703.1_pPPPP1R7_ protein phosphatase 1,
                  regulatory subunit
Seq. No.
                  5406
Contig ID
                  4867 1.R1040
                  jC-qmst02400009d05d1
5'-most EST
Method
                  BLASTX
```

```
NCBI GI
                  g2673912
BLAST score
                  510
E value
                  2.0e-51
Match length
                  159
                  63
% identity
                  (AC002561) unknown protein [Arabidopsis thaliana]
NCBI Description
                  5407
Seq. No.
                  4867 2.R1040
Contig ID
5'-most EST
                  wvk7\overline{0}0685447.h1
Method
                  BLASTX
                  g2492530
NCBI GI
                  2050
BLAST score
E value
                  0.0e+00
                  531
Match length
                  74
% identity
NCBI Description
                  CHLOROPLAST AMINOPEPTIDASE 1 PRECURSOR (LEUCINE
                  AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE
                  AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi 924630 (U20594)
                  leucine aminopeptidase [Solanum lycopersicum]
Seq. No.
                  5408
                  4867_3.R1040
Contig ID
                  uC-gmropic027e08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2492530
BLAST score
                  588
E value
                  1.0e-60
Match length
                  196
                  61
% identity
                  CHLOROPLAST AMINOPEPTIDASE 1 PRECURSOR (LEUCINE
NCBI Description
                  AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE
                  AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi 924630 (U20594)
                  leucine aminopeptidase [Solanum lycopersicum]
                  5409
Seq. No.
Contig ID
                  4867 4.R1040
5'-most EST
                  uC-gmrominsoy284f02b1
                  5410
Seq. No.
                  4867 5.R1040
Contig ID
5'-most EST
                  jC-gmle01810068e01a1
Method..
                  BLASTX
                  g1483563
NCBI GI
BLAST score
                  485
E value
                  8.0e-49
Match length
                  113
% identity
NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]
Seq. No.
                  5411
Contig ID
                  4867 6.R1040
```

5'-most EST uC-gmropic070c01b1

Method BLASTX
NCBI GI g2673912
BLAST score 421
E value 2.0e-41

==

```
106
Match length
% identity
                  75
NCBI Description
                  (AC002561) unknown protein [Arabidopsis thaliana]
Seq. No.
                  5412
                  4873 1.R1040
Contig ID
5'-most EST
                  LIB3051-043-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  q1408460
BLAST score
                  2168
                  0.0e+00
E value
Match length
                  514
% identity
                  81
                  (U40161) type 2A protein serine/threonine phosphatase 55
NCBI Description
                  kDa B regulatory subunit [Arabidopsis thaliana]
                  5413
Seq. No.
                  4873 2.R1040
Contig ID
5'-most EST
                  jC-gmle01810087b01d1
                  5414
Seq. No.
                  4873_3.R1040
Contig ID
5'-most EST
                  jC-gmro02910046a02d1
                  BLASTX
Method
                  g1408460
NCBI GI
BLAST score
                  341
E value
                  4.0e-32
                  76
Match length
                  88
% identity
NCBI Description
                  (U40161) type 2A protein serine/threonine phosphatase 55
                  kDa B regulatory subunit [Arabidopsis thaliana]
Seq. No.
                  5415
Contig ID
                  4873 4.R1040
                  LIB3028-009-Q1-B1-F11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3421413
BLAST score
                  462
                  2.0e-46
E value
                  125
Match length
% identity
                  73
NCBI Description
                  (AF081922) protein phosphatase 2A 55 kDa B regulatory
                  subunit [Oryza sativa] >gi_3421415 (AF081923) protein
                  phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
Seq. No.
                  5416
Contig ID
                  4875 1.R1040
5'-most EST
                  vzy700750750.hl
Method
                  BLASTX
NCBI GI
                  g3334323
BLAST score
                  966
E value
                  1.0e-105
Match length
                  193
% identity
                  GTP-BINDING PROTEIN SAR1A >gi 1314860 (U56929) Sar1 homolog
NCBI Description
                  [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_
                  (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis
```

thaliana] >gi\_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No. 5417

Contig ID 4875\_2.R1040 5'-most EST asn701138814.h1

Method BLASTX
NCBI GI g3334323
BLAST score 753
E value 8.0e-99
Match length 193
% identity 87

NCBI Description GTP-BINDING PROTEIN SAR1A >gi 1314860 (U56929) Sar1 homolog

[Arabidopsis thaliana] >gi\_2104532\_gb\_AAC78700.1\_

(AF001308) SAR1/GTP-binding secretory factor [Arabidopsis

thaliana]  $>gi_2104550$  (AF001535) AGAA.4 [Arabidopsis

thaliana]

Seq. No. 5418

Contig ID 4875\_3.R1040 5'-most EST ncj700982523.h1

Method BLASTN NCBI GI g2108346

BLAST score 82 E value 4.0e-38 Match length 174 % identity 87

NCBI Description Brassica campestris small GTP-binding protein Bsar1b

(bsar1b) mRNA, complete cds

Seq. No. 5419

Contig ID 4876\_1.R1040 5'-most EST ncj700981385.h1

Method BLASTX
NCBI GI g2194137
BLAST score 321
E value 4.0e-29
Match length 99
% identity 66

NCBI Description (AC002062) ESTs gb\_R29947,gb\_H76702 come from this gene.

[Arabidopsis thaliana]

Seq. No. 5420

Contig ID 4876\_2.R1040 5'-most EST ncj700980838.h1

Seq. No. 5421

Contig ID 4876\_3.R1040

5'-most EST LIB3138-025-Q1-N1-B10

 Method
 BLASTX

 NCBI GI
 g2194137

 BLAST score
 260

 E value
 4.0e-40

 Match length
 126

 % identity
 75

NCBI Description (AC002062) ESTs gb R29947, gb H76702 come from this gene.

[Arabidopsis thaliana]

```
5422
Seq. No.
                   4876 4.R1040
Contig ID
                   epx701106549.h1
5'-most EST
Method
                   BLASTX
                   q2194137
NCBI GI
BLAST score
                   410
                   5.0e-40
E value
                   113
Match length
                   74
% identity
                   (AC002062) ESTs gb_R29947,gb_H76702 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   5423
Seq. No.
                   4878 1.R1040
Contig ID
5'-most EST
                   jsh701066075.hl
                   BLASTX
Method
NCBI GI
                   q4056432
BLAST score
                   1220
                   1.0e-134
E value
                   448
Match length
% identity
                   (AC005990) Similar to gi_2245014 glucosyltransferase
NCBI Description
                   homolog from Arabidopsis thaliana chromosome 4 contig
                   gb Z97341. ESTs gb_T20778 and gb_AA586281 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   5424
                   4878 2.R1040
Contig ID
                   seb700652962.hl
5'-most EST
Seq. No.
                   5425
Contig ID
                   4880 1.R1040
5'-most EST
                   LIB3053-006-Q1-N1-G1
Method
                   BLASTX
NCBI GI
                   g543721
BLAST score
                   169
E value
                   1.0e-11
Match length
                   142
% identity
                   PROTEIN PHOSPHATASE PP2A, 72 KD REGULATORY SUBUNIT (PR72)
NCBI Description
                   >gi_539659_pir__A47114 phosphoprotein phosphatase (EC
                   3.1.3.16) ZA regulatory chain PR72 - human >gi_190222
                   (L12146) protein phosphatase 2A 72 kDa regulatory subunit
                   [Homo sapiens] >gi_4506021_ref_NP_002709.1_pPPP2R3_ protein phosphatase 2 (formerly 2A), regulatory subunit B'' (PR
                   72), alpha isoform and (PR 130), beta isoform
                   5426
Seq. No.
Contig ID
                   4880 2.R1040
5'-most EST
                   uC-gmflminsoy059f03b1
                   5427
Seq. No.
                   4886 1.R1040
Contig ID
                   uC-gmflminsoy058g03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4126403
```

```
BLAST score
                  901
E value
                  4.0e-97
Match length
                  331
                  52
% identity
                  (AB011796) flavonol synthase [Citrus unshiu]
NCBI Description
                  5428
Seq. No.
Contig ID
                  4889 1.R1040
5'-most EST
                  LIB3087-007-Q1-K1-G9
                  5429
Seq. No.
Contig ID
                  4890 1.R1040
5'-most EST
                  fde700874865.hl
Method
                  BLASTX
                  g132717
NCBI GI
BLAST score
                  250
E value
                  3.0e-21
Match length
                  92
                  53
% identity
NCBI Description
                  50S RIBOSOMAL PROTEIN L17 (BL21) >gi 71253 pir R5BS17
                  ribosomal protein L17 - Bacillus stearothermophilus
                  5430
Seq. No.
                  4890 2.R1040
Contig ID
5'-most EST
                  bth700845664.h1
Method
                  BLASTX
NCBI GI
                  q3925782
BLAST score
                  138
E value
                  1.0e-08
Match length
                  49
% identity
                  57
                  (AL034353) putative 60s ribosomal protein
NCBI Description
                  [Schizosaccharomyces pombe]
                  5431
Seq. No.
Contig ID
                  4892 1.R1040
5'-most EST
                  dpv701102209.h1
Method
                  BLASTX
                  g2281102
NCBI GI
BLAST score
                  287
                  2.0e-25
E value
Match length
                  139
% identity
                  52
NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]
                  5432
Seq. No.
Contig ID
                  4894 1.R1040
5'-most EST
                  LIB3039-005-Q1-E1-G11
Method
                  BLASTN
                  q562281
NCBI GI
BLAST score
                  123
E value
                  1.0e-62
Match length
                  247
% identity
                  87
NCBI Description
                  B.oleracea mRNA for PSST subunit of NADH:ubiquinone
                  oxidoreductase
```

```
5433
Seq. No.
                   4894 2.R1040
Contig ID
                  LIB3170-009-Q2-K2-B8
5'-most EST
Method
                  BLASTN
NCBI GI
                   g562281
BLAST score
                   72
                   3.0e-32
E value
                  168
Match length
                  86
% identity
NCBI Description
                  B.oleracea mRNA for PSST subunit of NADH:ubiquinone
                  oxidoreductase
                  5434
Seq. No.
                  4895 1.R1040
Contig ID
5'-most EST
                  LIB3039-033-Q1-E1-C8
Method
                  BLASTX
                  g3193303
NCBI GI
                  261
BLAST score
                   2.0e-22
E value
Match length
                  113
                   46
% identity
                  (AF069298) similar to several proteins containing a tandem
NCBI Description
                  repeat region such as Plasmodium falciparum GGM tandem
                  repeat protein (GB:U27807); partial CDS [Arabidopsis
                  thaliana]
Seq. No.
                  5435
                  4896 1.R1040
Contig ID
                  zhf700961274.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4454042
BLAST score
                  111
                  1.0e-08
E value
                  155
Match length
                  34
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  5436
                  4896 2.R1040
Contig ID
5'-most EST
                  LIB3138-040-Q1-N1-D3
Method
                  BLASTX
NCBI GI
                  g2501555
BLAST score
                  226
                  2.0e-18
E value
Match length
                  140
                  41
% identity
                  POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148)
NCBI Description
                  possible apospory-associated protein [Pennisetum ciliare]
                  5437
Seq. No.
                  4896 3.R1040
Contig ID
                  LIB3\overline{1}09-003-Q1-K1-G7
5'-most EST
Seq. No.
                  5438
                  4899 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy247f03b1
```

```
Seq. No.
                  5439
Contig ID
                   4899 2.R1040
5'-most EST
                  uC-gmronoir009e05b1
Method
                  BLASTX
NCBI GI
                  q130359
BLAST score
                  201
                  9.0e-16
E value
                  75
Match length
                  51
% identity
                  70 KD PEROXISOMAL MEMBRANE PROTEIN (PMP70)
NCBI Description
                  >gi 111319 pir A35723 70K peroxisomal membrane protein -
                  rat >gi 220862 dbj BAA14086 (D90038) PMP70 [Rattus
                  norvegicus]
Seq. No.
                  5440
                  4899 3.R1040
Contig ID
5'-most EST
                  LIB3028-009-Q1-B1-D3
Seq. No.
                  5441
                  4900 1.R1040
Contig ID
5'-most EST
                  LIB3107-010-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4538967
BLAST score
                  237
                  9.0e-20
E value
Match length
                  63
                  39
% identity
NCBI Description
                  (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
                  5442
Seq. No.
Contig ID
                  4902 1.R1040
5'-most EST
                  LIB3051-088-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2984196
                  259
BLAST score
E value
                  4.0e-22
Match length
                  140
% identity
                  41
                  (AE000764) ribosomal protein L11 [Aquifex aeolicus]
NCBI Description
Seq. No.
                  5443
                  4905 1.R1040
Contig ID
5'-most EST
                  zzp700835052.h1
Method
                  BLASTN
NCBI GI
                  g3168839
BLAST score
                  73
E value
                  2.0e-32
Match length
                  145
% identity
NCBI Description
                  Arabidopsis thaliana copper homeostasis factor (CCH) mRNA,
                  complete cds
                  5444
Seq. No.
Contig ID
                  4905 2.R1040
5'-most EST
                  LIB3074-012-Q1-E1-H4
Method
                  BLASTN
```

```
g3168839
NCBI GI
BLAST score
                  71
                  1.0e-31
E value
Match length
                  187
                  84
% identity
                  Arabidopsis thaliana copper homeostasis factor (CCH) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  5445
Contig ID
                  4905 3.R1040
                  LIB3167-078-P1-K2-H5
5'-most EST
Method
                  BLASTN
                  g3168839
NCBI GI
                  42
BLAST score
                  5.0e-14
E value
Match length
                  62
                  92
% identity
                  Arabidopsis thaliana copper homeostasis factor (CCH) mRNA,
NCBI Description
                  complete cds
                  5446
Seq. No.
                  4906 1.R1040
Contig ID
                  jex700906490.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4469008
BLAST score
                  177
E value
                  9.0e-13
                  62
Match length
                  55
% identity
                  (AL035602) UDP rhamnose--anthocyanidin-3-glucoside
NCBI Description
                  rhamnosyltransferase-like protein [Arabidopsis thaliana]
                  5447
Seq. No.
Contig ID
                  4908 1.R1040
                  uC-gmflminsoy058h04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2262116
BLAST score
                  281
E value
                  6.0e-25
Match length
                  135
                  35
% identity
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
                  5448
                  4910 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220057a11d1
                  5449
Seq. No.
Contig ID
                  4911 1.R1040
5'-most EST
                  LIB3093-033-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2285792
BLAST score
                  559
E value
                  4.0e-57
Match length
                  155
% identity
                  70
                  (AB004568) cyanase [Arabidopsis thaliana]
NCBI Description
```

5'-most EST

```
thaliana]
                  5450
Seq. No.
Contig ID
                  4912 1.R1040
5'-most EST
                  jC-gmst02400018d09a1
Method
                  BLASTX
NCBI GI
                  g3643085
BLAST score
                  363
E value
                  3.0e-34
Match length
                  191
% identity
                  41
NCBI Description
                  (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
                  crystallinum]
                  5451
Seq. No.
                  4913_1.R1040
Contig ID
                  uC-qmronoir025d01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3335372
BLAST score
                  409
                  1.0e-39
E value
Match length
                  112
                  65
% identity
NCBI Description
                  (AC003028) putative SRG1 protein [Arabidopsis thaliana]
Seq. No.
                  5452
Contig ID
                  4915 1.R1040
5'-most EST
                  zpv700757869.h1
                  5453
Seq. No.
Contig ID
                  4915 2.R1040
5'-most EST
                  LIB3093-040-Q1-K1-F10
                  5454
Seq. No.
                  4918 1.R1040
Contig ID
5'-most EST
                  g4397125
                                                         . . .
                  5455
Seq. No.
                  4921 1.R1040
Contig ID
5'-most EST
                  LIB3107-059-Q1-K1-B11
Method
                  BLASTN
                  g168498
NCBI GI
BLAST score
                  119
E value
                  3.0e-60
Match length
                  315
                  84
% identity
NCBI Description
                  Corn histone H4 (H4Cl3) gene, complete cds
Seq. No.
                  5456
Contig ID
                  4926 1.R1040
5'-most EST
                  jC-gmro02910066a04a1
Seq. No.
                  5457
Contig ID
                  4926 2.R1040
```

>gi\_3287503\_dbj\_BAA31224\_ (AB015748) cyanase [Arabidopsis

uC-gmflminsoy108e01b1

% identity

88

```
Seq. No.
                   5458
Contig ID
                   4929 1.R1040
                   LIB3\overline{0}92-048-Q1-K1-H11
5'-most EST
                  BLASTX
Method
                   g4220481
NCBI GI
BLAST score
                   515
                   3.0e-52
E value
                   140
Match length
                   67
% identity
NCBI Description
                   (AC006069) unknown protein [Arabidopsis thaliana]
                   5459
Seq. No.
Contig ID
                   4929 2.R1040
5'-most EST
                   uC-gmropic019c09b1
Method
                   BLASTX
NCBI GI
                   g4220481
                   376
BLAST score
E value
                   4.0e-36
                   103
Match length
% identity
                   70
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
                   5460
Seq. No.
                   4929 3.R1040
Contig ID
5'-most EST
                   uC-gmropic106f02b1
Method
                   BLASTX
                  g4220481
NCBI GI
BLAST score
                   242
                   2.0e-29
E value
Match length
                   139
                   52
% identity
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
                   5461
Seq. No.
                   4929 4.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy105b11b1
Seq. No.
                   5462
                   4937 1.R1040
Contig ID
5'-most EST
                   dpv701099233.h1
Method
                   BLASTX
NCBI GI
                  g1418990
BLAST score
                   701
E value
                   6.0e-74
Match length
                   203
% identity
NCBI Description
                  (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                   5463
Contig ID
                   4937_2.R1040
                  LIB3107-065-Q1-K1-G11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                   487
                   4.0e-49
E value
Match length
                  101
```

Match length

80

```
NCBI Description
                      (Z75524) unknown [Lycopersicon esculentum]
                      5464
Seq. No.
                      4937 3.R1040
Contig ID
5'-most EST
                      LIB3028-008-Q1-B1-F5
                      BLASTX
Method
NCBI GI
                      q1418990
BLAST score
                      282
E value
                      3.0e-44
Match length
                      103
% identity
                      86
                      (Z75524) unknown [Lycopersicon esculentum]
NCBI Description
Seq. No.
Contig ID
                      4939 1.R1040
5'-most EST
                      pxt700944780.h1
Method
                      BLASTN
NCBI GI
                      q434342
BLAST score
                      144
E value
                      8.0e-75
Match length
                      464
% identity
                      83
NCBI Description
                     A.thaliana (C24) mRNA for S18 ribosomal protein
                      5466
Seq. No.
Contiq ID
                      4939 2.R1040
5'-most EST
                     LIB3040-048-01-E1-H12
Method
                     BLASTX
NCBI GI
                      q464707
BLAST score
                      677
E value
                      3.0e-71
Match length
                      152
% identity
                      86
NCBI Description
                      40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
                     protein S18.A - Arabidopsis thaliana
                     >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                      [Arabidopsis thaliana] \ge gi_434343_emb_CAA82273_ (Z28701)
                      S18 ribosomal protein [Arabidopsis thaliana]
                     >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                      S18 ribosomal protein [Arabidopsis thaliana]
                     >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                     gb_R30430 come from this gene. [Arabidopsis thaliana]
                     >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                     protein [Arabidopsis thaliana]
Seq. No.
                     5467
                      4939 3.R1040
Contig ID
5'-most EST
                     ncj7\overline{0}0983777.h1
Method
                     BLASTX
NCBI GI
                     q3746064
BLAST score
                     146
E value
                     2.0e-09
```

```
% identity
                   42
NCBI Description
                   (AC005311) unknown protein [Arabidopsis thaliana]
                   5468
Seq. No.
Contig ID
                   4939 6.R1040
                   leu7\overline{0}1150769.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g434344
BLAST score
                   76
E value
                   8.0e-35
                   172
Match length
                   86
% identity
                   A.thaliana (Columbia) mRNA for S18 ribosomal protein
NCBI Description
                   (641bp)
                   5469
Seq. No.
                   4940 1.R1040
Contig ID
5'-most EST
                   jex700904203.h1
                   BLASTX
Method
                   g2961384
NCBI GI
BLAST score
                   612
                   1.0e-63
E value
                   189
Match length
                   59
% identity
NCBI Description
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
                   thaliana]
                   5470
Seq. No.
                   4941 1.R1040
Contig ID
5'-most EST
                   LIB3051-071-Q1-K1-G8
                   5471
Seq. No.
                   4943_1.R1040
Contig ID
5'-most EST
                   LIB3028-008-Q1-B1-E4
                   BLASTX
Method
NCBI GI
                   g1707480
BLAST score
                   195
E value
                   2.0e-29
Match length
                   153
% identity
                   45
                   (Y08614) CRM1 [Homo sapiens]
NCBI Description
Seq. No.
                   5472
                   4944 1.R1040
Contig ID
5'-most EST
                   LIB3170-050-Q1-J1-E7
Method
                   BLASTX
NCBI GI
                   g2244906
BLAST score
                   257
E value
                   4.0e-22
Match length
                   122
                   43
% identity
NCBI Description
                   (Z97339) indole-3-acetate beta-glucosyltransferase
```

Seq. No. 5473

Contig ID 4945 1.R1040

5'-most EST LIB3049-019-Q1-E1-H6

[Arabidopsis thaliana]

NCBI GI

```
Method
                   BLASTX
NCBI GI
                   g1871184
BLAST score
                   157
                   2.0e-10
E value
Match length
                   66
% identity
                   59
                   (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5474
Seq. No.
Contig ID
                   4947_1.R1040
                   jC-gmro02800035g06a1
5'-most EST
Method
                   BLASTX
                   g2213783
NCBI GI
BLAST score
                   258
E value
                   3.0e-29
Match length
                   104
% identity
                   67
                   (U89256) Pti5 [Lycopersicon esculentum]
NCBI Description
                   5475
Seq. No.
Contig ID
                   4949 1.R1040
5'-most EST
                   LIB3028-008-Q1-B1-F12
                   5476
Seq. No.
Contig ID
                   4951 1.R1040
5'-most EST
                   LIB3094-069-Q1-K1-H3
Method
                   BLASTX
                   g20020
NCBI GI
BLAST score
                   370
E value
                   2.0e-35
Match length
                   83
% identity
                   92
                  (X62368) ribosomal protein L12-la [Nicotiana tabacum]
NCBI Description
                   5477
Seq. No.
                   4951 2.R1040
Contig ID
5'-most EST
                   LIB3106-098-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g548655
BLAST score
                   215
E value
                   4.0e-17
Match length
                   137
% identity
                   39
                   50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)
NCBI Description
                   >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast
                   - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046)
                   ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                   5478
Contig ID
                   4952 1.R1040
5'-most EST
                   uC-gmropic087e09b1
Seq. No.
                   5479
Contig ID
                   4957 1.R1040
                   leu7\overline{0}1147618.h1
5'-most EST
Method
                   BLASTX
```

g1050849

```
242
BLAST score
E value
                   1.0e-19
                   210
Match length
                   32
% identity
                   (X83742) MAP kinase phosphatase [Xenopus laevis]
NCBI Description
                   5480
Seq. No.
                   4958 1.R1040
Contig ID
5'-most EST
                   LIB3170-069-Q1-J1-D12
                   5481
Seq. No.
                   4958 2.R1040
Contig ID
5'-most EST
                   LIB3028-008-Q1-B1-C9
Method
                   BLASTN
                   g1150683
NCBI GI
BLAST score
                   592
                   0.0e + 00
E value
                   720
Match length
                   97
% identity
                  V.radiata atpB, rbcL and trnK genes
NCBI Description
                   5482
Seq. No.
                   4959 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220067g01a1
Method
                   BLASTX
                   g2829863
NCBI GI
BLAST score
                   459
                   9.0e-56
E value
                   211
Match length
                   56
% identity
                   (AC002396) Putative peroxidase [Arabidopsis thaliana]
NCBI Description
                   5483
Seq. No.
                   4961 1.R1040
Contig ID
                   xpa700795669.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1946365
BLAST score
                   401
                   9.0e-39
E value
                   99
Match length
                   73
% identity
                   (U93215) glutaredoxin isolog [Arabidopsis thaliana]
NCBI Description
                   5484
Seq. No.
                   4961 2.R1040
Contig ID
5'-most EST
                   LIB3065-009-Q1-N1-A10
Method
                   BLASTX
                   g1946365
NCBI GI
BLAST score
                   404
                   3.0e-39
E value
                   99
Match length
% identity
NCBI Description
                   (U93215) glutaredoxin isolog [Arabidopsis thaliana]
                   5485
Seq. No.
                   4961 3.R1040
Contig ID
```

 $wrg7\overline{0}0786730.h2$ 

5'-most EST

```
5486
Seq. No.
Contig ID
                   4962 1.R1040
                   LIB3109-022-Q1-K1-A4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3063706
BLAST score
                   467
                   2.0e-46
E value
                   131
Match length
% identity
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   5487
Seq. No.
                   4964 1.R1040
Contig ID
                   jC-gmro02910067f08a1
5'-most EST
Method
                   BLASTN
                   g2565418
NCBI GI
BLAST score
                   153
                   2.0e-80
E value
                   385
Match length
                   85
% identity
                  Onobrychis viciifolia histone H3 mRNA, complete cds
NCBI Description
                   5488
Seq. No.
                   4964 2.R1040
Contig ID
5'-most EST
                   leu701155595.h1
                   BLASTN
Method
NCBI GI
                   g166383
BLAST score
                   104
                   2.0e-51
E value
                   240
Match length
                   86
% identity
                  Alfalfa histone H3 (H3-1.1) gene, complete cds
NCBI Description
                   5489
Seq. No.
                   4965 1.R1040
Contig ID
                   fC-gmro700845991a2
5'-most EST
                   5490
Seq. No.
Contig ID
                   4965 2.R1040
                   uC-gmropic020h10b1
5'-most EST
                   5491
Seq. No.
Contig ID
                   4967 1.R1040
                   LIB3028-008-Q1-B1-A9
5'-most EST
                   BLASTN
Method
NCBI GI
                   g11571
BLAST score
                   380
E value
                   0.0e + 00
Match length
                   401
                   98
% identity
                  Soybean chloroplast rps12 and rps7 genes
NCBI Description
Seq. No.
                   5492
                   4968_1.R1040
Contig ID
5'-most EST
                   LIB3029-011-Q1-B1-C12
```

1047

BLASTX

Method

% identity

67

```
g3241945
NCBI GI .
BLAST score
                   437
                   5.0e-43
E value
Match length
                   132
                   58
% identity
                   (AC004625) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5493
Seq. No.
                   4968 2.R1040
Contig ID
5'-most EST
                   jex700904823.h1
                   5494
Seq. No.
Contig ID
                   4969 1.R1040
5'-most EST
                   LIB3028-008-Q1-B1-B10
                   5495
Seq. No.
                   4971 1.R1040
Contig ID
5'-most EST
                   wvk700682772.h1
                   BLASTX
Method
NCBI GI
                   g4469012
BLAST score
                   311
                   1.0e-28
E value
                   88
Match length
                   76
% identity
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5496
                   4972 1.R1040
Contig ID
                   jC-qmf102220106a08a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2804278
BLAST score
                   1861
                   0.0e + 00
E value
Match length
                   414
                   83
% identity
NCBI Description
                   (AB003516) squalene epoxidase [Panax ginseng]
Seq. No.
                   5497
                   4972_2.R1040
Contig ID
                   jC-gmf102220086d06a1
5'-most EST
Method
                   BLASTX
                   g2804278
NCBI GI
BLAST score
                   698
                   2.0e-75
E value
                   179
Match length
% identity
                   (AB003516) squalene epoxidase [Panax ginseng]
NCBI Description
Seq. No.
                   5498
                   4973 1.R1040
Contig ID
5'-most EST
                   qsv701050692.hl
Method
                   BLASTX
NCBI GI
                   a4262228
BLAST score
                   424
E value
                   7.0e-53
Match length
                   161
```

NCBI Description

```
NCBI Description
                   (AC006200) putative receptor protein kinase [Arabidopsis
                   thaliana]
                   5499
Seq. No.
                   4974 1.R1040
Contig ID
5'-most EST
                   LIB3040-003-Q1-E1-F10
                   5500
Seq. No.
Contig ID
                   4975 1.R1040
5'-most EST
                   epx7\overline{0}1105965.h1
                                                                            1.0
                   5501
Seq. No.
Contig ID
                   4975 2.R1040
5'-most EST
                   LIB3092-029-Q1-K1-F1
                   5502
Seq. No.
                   4980 1.R1040
Contig ID
5'-most EST
                   k117\overline{0}1214527.h1
                   5503
Seq. No.
Contig ID
                   4980 2.R1040
5'-most EST
                   LIB3139-047-P1-N1-D1
                   BLASTX
Method
NCBI GI
                   g729486
BLAST score
                   180
E value
                   4:0e-13
Match length
                   102
% identity
                   41
NCBI Description
                   PRE-RRNA PROCESSING PROTEIN FHL1 >gi_626950_pir__$43738
                   transcription activator FHL1 - yeast (Saccharomyces
                   cerevisiae) >gi_454255_emb_CAA82202_ (Z28348) Fhl1p
                   [Saccharomyces cerevisiae] >gi_914975 (U32445) Pre-rRNA
                   processing protein Fhll (Swiss Prot. accession number
                   P39521) [Saccharomyces cerevisiae]
                   5504
Seq. No.
Contig ID
                   4983_1.R1040
5'-most EST
                   jC-gmf102220079h05a1
Method
                   BLASTX
NCBI GI
                   g577301
BLAST score
                   188
E value
                   6.0e-14
Match length
                   108
% identity
NCBI Description
                   (D42044) The ha3523 gene product is related to S.cerevisiae
                   gene product located in chromosome III. [Homo sapiens]
Seq. No.
                   5505
Contig ID
                   4985 1.R1040
5'-most EST
                   zpv700758101.hl
Method
                   BLASTX
NCBI GI
                   q4510425
BLAST score
                   620
E value
                   2.0e-64
Match length
                   140
% identity
```

(AC006929) unknown protein [Arabidopsis thaliana]

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```
5506
Seq. No.
Contig ID
                   4986 1.R1040
                   jex700907662.hl
5'-most EST
Method
                   BLASTX
                   g1458245
NCBI GI
                   397
BLAST score
E value
                   4.0e-38
Match length
                   254
% identity
                   (U64834) coded for by C. elegans cDNA cm17a1; coded for by
NCBI Description
                   C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                   CEMSE26F; similar to methyltransferases [Caenorhabditis
                   elegans]
Seq. No.
                   5507
                   4987 1.R1040
Contig ID
5'-most EST
                   awf700838030.hl
                   BLASTX
Method
NCBI GI
                   g2623299
BLAST score
                   306
                   5.0e-28
E value
Match length
                   127
                   50
% identity
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5508
Seq. No.
                   4989 1.R1040
Contig ID
5'-most EST
                   LIB3139-043-P1-N1-D2
Method
                   BLASTX
NCBI GI
                   g2191129
BLAST score
                   489
E value
                   6.0e-49
Match length
                   129
                   74
% identity
NCBI Description
                   (AF007269) similar to SPF1 DNA-binding protein [Arabidopsis
                   thaliana]
                   5509
Seq. No.
                   4997 1.R1040
Contig ID
                   leu701145678.hl
5'-most EST
Seq. No.
                   5510
                   4997 2.R1040
Contig ID
                   asn7\overline{0}1136067.h1
5'-most EST
Seq. No.
                   5511
Contig ID
                   4999 1.R1040
                   LIB3\overline{0}28-007-Q1-B1-F6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g544110
BLAST score
                   212
E value
                   5.0e-17
                   59
Match length
% identity
                   68
NCBI Description
                   COLD SHOCK-LIKE PROTEIN CSPE >qi 1363394 pir S49050 CspE
```

protein - Escherichia coli >gi 471099\_dbj\_BAA05856\_

(D28497) CspE (MsmC) [Escherichia coli] >gi\_833769 (L29054) gicA gene product [Escherichia coli] >gi\_1651256\_dbj\_BAA35266 (D90703) CspE protein [Escherichia coli] >gi\_1786841 (AE000167) cold shock protein [Escherichia coli] >gi\_3851642 (AF098260) unknown [Vibrio cholerae]

Seq. No. 5512

Contig ID 5000 1.R1040

5'-most EST LIB3028-007-Q1-B1-F8

Seq. No. 5513

Contig ID 5002 1.R1040

5'-most EST LIB3028-007-Q1-B1-G10

Method BLASTX
NCBI GI g2347195
BLAST score 198
E value 3.0e-15

Match length 67 % identity 54

NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5514

Contig ID 5003\_1.R1040 5'-most EST bth700846021.h1

Method BLASTX
NCBI GI g3790581
BLAST score 316
E value 1.0e-28
Match length 175
% identity 39

NCBI Description (AF079179) RING-H2 finger protein RHB1a [Arabidopsis

thaliana]

Seq. No. 5515

Contig ID 5003 2.R1040

5'-most EST LIB3028-007-Q1-B1-G2

Seq. No. 5516

Contig ID 5006 1.R1040

5'-most EST LIB3028-007-Q1-B1-G7

Seq. No. 5517

Contig ID 5007\_1.R1040

5'-most EST LIB3028-007-Q1-B1-G9

Method BLASTX
NCBI GI g1888357
BLAST score 497
E value 4.0e-50
Match length 189
% identity 54

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 5518

Contig ID 5008 1.R1040

```
5'-most EST
                   fua701039005.h1
                   BLASTX
Method
NCBI GI
                   g3560264
BLAST score
                   367
                   1.0e-34
E value
                   219
Match length
                   42
% identity
                   (ALO31535) soll family protein [Schizosaccharomyces pombe]
NCBI Description
                   5519
Seq. No.
                   5008 2.R1040
Contig ID
                   hyd7\overline{0}0729250.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q731737
BLAST score
                   155
                   5.0e-10
E value
                   129
Match length
                   33
% identity
                   SOL3 PROTEIN >gi_626676_pir__S48903 SOL3 protein - yeast
NCBI Description
                   (Saccharomyces cerevisiae) >gi_458904 (U00027) Sol3p
                   [Saccharomyces cerevisiae] >gi 1184943 (U46560) Sol3p
                   [Saccharomyces cerevisiae]
                   5520
Seq. No.
                   5009 1.R1040
Contig ID
                   jC-gmle01810043g06d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1653626
                   182
BLAST score
                   3.0e-13
E value
                   84
Match length
                   44
% identity
                   (D90915) hypothetical protein [Synechocystis sp.]
NCBI Description
                   5521
Seq. No.
                   5010 1.R1040
Contig ID
5'-most EST
                   epx701106413.hl
                   BLASTX
Method
                   g4455787
NCBI GI
                   332
BLAST score
                   8.0e-31
E value
                   147
Match length
% identity
                   43
                   (AL035536) putative DNA polymerase accessory protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   5522
Seq. No.
Contig ID
                   5011_1.R1040
5'-most EST
                   LIB3028-007-Q1-B1-D8
                   BLASTX
Method
NCBI GI
                   g4263710
BLAST score
                   455
E value
                   3.0e-45
Match length
                   173
                   36
% identity
NCBI Description
                   (AC006223) putative pur-alpha transcriptional activator
                   protein [Arabidopsis thaliana]
```

```
5523
Seq. No.
                  5012 1.R1040
Contig ID
5'-most EST
                  taw700660051.hl
                  BLASTX
Method
                  g400198
NCBI GI
                  199
BLAST score
                  3.0e-15
E value
                  101
Match length
                  50
% identity
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
NCBI Description
                   (LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)
                  >gi_99604_pir__S21023 hypothetical protein - upland cotton
                  >gi_1361978_pir__A57500 photosystem II protein psbT -
                  upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown
                  reading frame [Gossypium hirsutum]
Seq. No.
                  5524
                  5012 2.R1040
Contig ID
                  jC-qmst02400063f12a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g400198
                  190
BLAST score
                  5.0e-14
E value
                  104
Match length
% identity
                  43
NCBI Description
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
                  (LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)
                  >gi 99604 pir S21023 hypothetical protein - upland cotton
                  >gi 1361978_pir __A57500 photosystem II protein psbT -
                  upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown
                  reading frame [Gossypium hirsutum]
Seq. No.
                  5525
Contig ID
                  5012 3.R1040
                  LIB3074-004-Q1-K1-E8
5'-most EST
Method
                  BLASTX
                  g400198
NCBI GI
BLAST score
                  192
                  2.0e-14
E value
                  103
Match length
% identity
NCBI Description
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
                  (LIGHT-REGULATED UNKNOWN 11 KD PROTEIN)
                  >gi_99604_pir__S21023 hypothetical protein - upland cotton
                  >gi_1361978_pir__A57500 photosystem II protein psbT -
                  upland cotton >gi_18512_emb_CAA38027_ (X54092) unknown
                  reading frame [Gossypium hirsutum]
                  5526
Seq. No.
                  5013_1.R1040
Contig ID
5'-most EST
                  g4313283
Method
                  BLASTX
                  q4262250
NCBI GI
BLAST score
                  1690
E value
                  0.0e + 00
Match length
                  382
```

342

```
% identity
                   86
                   (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   5527
Seq. No.
                   5013 2.R1040
Contig ID
                   uC-gmropic010g08b1
5'-most EST
                   BLASTX
Method
                   g4262250
NCBI GI
BLAST score
                   502
                   9.0e-51
E value,
                   145
Match length
                   74
% identity
NCBI Description
                   (AC006200) putative aldolase [Arabidopsis thaliana]
                   5528
Seq. No.
                   5013 3.R1040
Contig ID
                   seb7\overline{0}0653622.h1
5'-most EST
                   5529
Seq. No.
                   5018 1.R1040
Contig ID
5'-most EST
                   uaw7\overline{0}0666311.h1
                   5530
Seq. No.
                   5021 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910014e08a1
                   BLASTX
Method
NCBI GI
                   g1769887
BLAST score
                   2015
                   0.0e + 00
E value
Match length
                   471
                   78
% identity
NCBI Description
                   (X95736) amino acid permease 6 [Arabidopsis thaliana]
                   5531
Seq. No.
                   5021 3.R1040
Contig ID
5'-most EST
                   rca700996181.hl
Method
                   BLASTX
NCBI GI
                   g1769887
BLAST score
                   292
E value
                   2.0e-26
Match length
                   72
                   85
% identity
                   (X95736) amino acid permease 6 [Arabidopsis thaliana]
NCBI Description
                   5532
Seq. No.
Contig ID
                   5024 1.R1040
5'-most EST
                   seb7\overline{0}0651789.h1
Method
                   BLASTX
NCBI GI
                   g3128168
BLAST score
                   1075
                   1.0e-117
E value
                   253
Match length
% identity
                   72
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
```

5533

Seq. No.

Method

BLASTN

```
Contig ID
                   5025 1.R1040
5'-most EST
                   uC-gmflminsoy118b03b1
Method
                   BLASTX
NCBI GI
                   g4567235
BLAST score
                   150
                   9.0e-10
E value
                   81
Match length
                   47
% identity
                   (AC007119) putative phosphatidylinositol/phophatidylcholine
NCBI Description
                   transfer protein [Arabidopsis thaliana]
                   5534
Seq. No.
Contig ID
                   5026 1.R1040
                   LIB3093-014-Q1-K1-G6
5'-most EST
Seq. No.
                   5535
                   5026 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810089h07a1
                   5536
Seq. No.
                   5028 1.R1040
Contig ID
5'-most EST
                   gsv701046547.hl
                   BLASTX
Method
                   g2398829
NCBI GI
BLAST score
                   302
                   2.0e-27
E value
Match length
                   72
                   39
% identity
                   (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                   tuberosum]
                   5537
Seq. No.
                   5029 1.R1040
Contig ID
5'-most EST
                   vzy700753080.hl
Method
                   BLASTX
NCBI GI
                   g1946329
BLAST score
                   1014
E value
                   1.0e-110
Match length
                   278
% identity
                   (U69154) prohibitin [Nicotiana tabacum]
NCBI Description
Seq. No.
                   5538
                   5029 2.R1040
Contig ID
5'-most EST
                   LIB3\overline{1}67-027-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1946329
BLAST score
                   420
E value
                   3.0e-41
Match length.
                   111
                   72
% identity
NCBI Description
                   (U69154) prohibitin [Nicotiana tabacum]
Seq. No.
                   5539
Contig ID
                   5033 1.R1040
5'-most EST
                   LIB3138-031-Q1-N1-D11
```

NCBI Description

```
NCBI GI
                   g1370147
BLAST score
                   317
E value
                   1.0e-178
Match length
                   529
                   91
% identity
                   L.japonicus mRNA for small GTP-binding protein, RAB11D
NCBI Description
                   5540
Seq. No.
                   5033 2.R1040
Contig ID
5'-most EST
                   pmv700891967.hl
Method
                   BLASTN
                   g1370149
NCBI GI
BLAST score
                   127
                   7.0e-65
E value
Match length
                   203
% identity
                   91
                   L. japonicus mRNA for small GTP-binding protein, RAB11E
NCBI Description
                   5541
Seq. No.
                   5035 1.R1040
Contig ID
                   ssr7\overline{0}0553580.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g343022
BLAST score
                   191
                   1.0e-103
E value
                   500
Match length
                   91
% identity
                   Pea chloroplast photosystem II gene encoding the D2 and
NCBI Description
                   44kd chlorophyll a-binding proteins, complete cds
                   5542
Seq. No.
                   5036 1.R1040
Contig ID
5'-most EST
                   LIB3030-007-Q1-B1-D2
                   5543
Seq. No.
                   5041 1.R1040
Contig ID
                   LIB3028-007-Q1-B1-A5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1143511
BLAST score
                   1630
E value
                   0.0e + 00
Match length
                   303
                   99
% identity
NCBI Description
                   (Z47076) Ser/Thr protein phosphatase homologous to PPX
                   [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein
                   phosphatase [Malus domestica]
                   5544
Seq. No.
Contig ID
                   5041 3.R1040
5'-most EST
                   LIB3170-019-Q1-K1-H10
Method
                   BLASTN
NCBI GI
                   g1143510
                   154
BLAST score
                   4.0e-81
E value
Match length
                   350
% identity
```

M.domestica Borkh mRNA for serine/threonine protein

## phosphatase (PPX) Seq. No. 5545 Contig ID 5041 5.R1040 LIB3170-059-Q1-K1-A7 5'-most EST Method BLASTN NCBI GI g1143510 BLAST score 139 3.0e-72 E value 291 Match length 87 % identity NCBI Description M.domestica Borkh mRNA for serine/threonine protein phosphatase (PPX) Seq. No. 5546 Contig ID 5041 6.R1040 pcp700989770.hl 5'-most EST Method BLASTN NCBI GI q1143510 BLAST score 67 E value 2.0e-29 Match length 131 % identity 88 M.domestica Borkh mRNA for serine/threonine protein NCBI Description phosphatase (PPX) 5547 Seq. No. Contig ID 5042 1.R1040 5'-most EST uC-gmropic090g05b1 Method BLASTX NCBI GI g1881585 BLAST score 361 6.0e-34 E value Match length 124 % identity 58 (U72489) remorin [Solanum tuberosum] NCBI Description 5548 Seq. No. Contig ID 5044 1.R1040 $ncj7\overline{0}0983465.h1$ 5'-most EST Method BLASTX g1402878 NCBI GI BLAST score 1075 1.0e-117 E value Match length 444 % identity (X98130) unknown [Arabidopsis thaliana] NCBI Description 5549 Seq. No. Contig ID 5044 2.R1040 jC-gmf102220132aa06d1 5'-most EST Method BLASTX NCBI GI g3367522 BLAST score 272 E value 9.0e-24 83 Match length

57

% identity

5'-most EST

```
(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   5550
Seq. No.
                   5044 3.R1040
Contig ID
                   jC-gmle01810042e08d1
5'-most EST
                   BLASTX
Method
                   g3367522
NCBI GI
                   492
BLAST score
                   2.0e-49
E value
                   196
Match length
                   47
% identity
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   5551
Seq. No.
                   5044 4.R1040
Contig ID
                   LIB3170-066-Q1-K1-H5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1402878
BLAST score
                   253
                   1.0e-21
E value
                   94
Match length
                   50
% identity
NCBI Description (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                   5552
                   5044 5.R1040
Contig ID
                   zzp7\overline{0}0833553.h1
5'-most EST
                   BLASTX
Method
                   g3367522
NCBI GI
BLAST score
                   311
                   4.0e-28
E value
                   186
Match length
                   45
% identity
                   (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   5553
Seq. No.
                   5044 9.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1157040.h1
Seq. No.
                   5554
                   5045 1.R1040
Contig ID
5'-most EST
                   LIB3138-042-Q1-N1-E1
                   5555
Seq. No.
Contig ID
                   5046 2.R1040
5'-most EST
                   LIB3139-064-P1-N1-H8
                   5556
Seq. No.
                   5048 1.R1040
Contig ID
5'-most EST
                   asj700967448.hl
                   5557
Seq. No.
                   5049 1.R1040
Contig ID
```

LIB3106-019-Q1-K1-F2

Method BLASTX NCBI GI g1655653 BLAST score 223 9.0e-18 E value 149 Match length 36 % identity (Z81368) hypothetical protein Rv2406c [Mycobacterium NCBI Description tuberculosis] 5558 Seq. No. 5049 2.R1040 Contig ID 5'-most EST g4313995 5559 Seq. No. 5049 4.R1040 Contig ID 5'-most EST awf700843120.hl

5'-most EST awf700843120.h1

Seq. No. 5560
Contig ID 5051\_1.R1040
5'-most EST LIB3106-110-Q1-K1-C3
Method BLASTX

Method BLASTX
NCBI GI g2828280
BLAST score 1020
E value 1.0e-111
Match length 206
% identity 93

NCBI Description (AL021687) putative protein [Arabidopsis thaliana] >gi\_2832633\_emb\_CAA16762\_ (AL021711) putative protein

[Arabidopsis thaliana]

Seq. No. 5561 Contig ID 5051\_2.R1040

5'-most EST zzp700835746.h1
Method BLASTX

NCBI GI g2828280
BLAST score 156
E value 2.0e-10
Match length 33
% identity 88

NCBI Description (AL021687) putative protein [Arabidopsis thaliana] >gi\_2832633\_emb\_CAA16762\_ (AL021711) putative protein

[Arabidopsis thaliana]

Seq. No. 5562

Contig ID 5055 1.R1040

5'-most EST uC-gmflminsoy045h04b1

Method BLASTX
NCBI GI g3860250
BLAST score 1604
E value 1.0e-179
Match length 398
% identity 80

NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 5563

Contig ID 5055\_2.R1040

```
5'-most EST
                   uC-gmropic111d07b1
                   BLASTN
Method
                   g2351064
NCBI GI
BLAST score
                   35
E value
                   4.0e-10
Match length
                   47
                   94
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDJ22, complete sequence [Arabidopsis thaliana]
                   5564
Seq. No.
                   5057 1.R1040
Contig ID
5'-most EST
                   LIB3028-006-Q1-B1-H10
Method
                   BLASTX
                   g4559398
NCBI GI
BLAST score
                   796
                   6.0e-85
E value
                   229
Match length
                   66
% identity
                   (AC006526) putative mitochondrial carrier protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   5565
                   5060 1.R1040
Contig ID
5'-most EST
                   LIB3139-101-P1-N1-B4
Method
                   BLASTX
                   g3451068
NCBI GI
BLAST score
                   471
E value
                   4.0e-47
Match length
                   159
                   64
% identity
NCBI Description
                   (AL031326) putative protein [Arabidopsis thaliana]
                   5566
Seq. No.
                   5060_2.R1040
Contig ID
5'-most EST
                   LIB3028-008-Q1-B1-F3
                   BLASTX
Method
                   g3451067
NCBI GI
BLAST score
                   306
E value
                   6.0e-28
Match length
                   99
% identity
NCBI Description
                   (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   5567
                   5060_3.R1040
Contig ID
5'-most EST
                   LIB3106-087-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g3451067
BLAST score
                   137
E value
                   5.0e-15
Match length
                   82
% identity
                   59
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   5568
Seq. No.
```

5060\_4.R1040

Contig ID

```
5'-most EST
                  LIB3106-076-Q1-K1-G6
Method
                   BLASTX
                   g3451067
NCBI GI
BLAST score
                   373
E value
                   1.0e-35
                   99
Match length
                   75
% identity
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   5569
Seq. No.
                   5060 5.R1040
Contig ID
5'-most EST
                   leu701155251.h1
Seq. No.
                   5570
                   5062 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy067f01b1
Method
                   BLASTX
NCBI GI
                   g4204267
BLAST score
                   639
                   1.0e-66
E value
Match length
                   201
% identity
                   67
                   (AC005223) 55585 [Arabidopsis thaliana]
NCBI Description
                   5571
Seq. No.
                   5063 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy045f06b1
Method
                   BLASTX
                   g1351856
NCBI GI
BLAST score
                   1789
                   0.0e+00
E value
Match length
                   375
                   90
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                   [Cucurbita sp.]
Seq. No.
                   5572
                   5063_2.R1040
Contig ID
5'-most EST
                  LIB3028-001-Q1-B1-D1
Method
                   BLASTX
NCBI GI
                   g1351856
BLAST score
                   432
E value
                   2.0e-42
Match length
                   106
% identity
                   79
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                   [Cucurbita sp.]
                   5573
Seq. No.
Contig ID
                   5065 1.R1040
5'-most EST
                   leu7\overline{0}1149686.h1
Method
                   BLASTN
NCBI GI
                   g710349
BLAST score
                   445
```

0.0e+00

E value

```
757
Match length
                   90
% identity
                  Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
NCBI Description
                  complete cds
                  5574
Seq. No.
                   5065 2.R1040
Contig ID
                  seb700648557.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  g710349
                  302
BLAST score
                  1.0e-169
E value
Match length
                  546
                  89
% identity
                  Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
NCBI Description
                  complete cds
                  5575
Seq. No.
                  5065 4.R1040
Contig ID
                  LIB3139-117-P1-N1-H12
5'-most EST
                  BLASTN
Method
                  g558922
NCBI GI
                  216
BLAST score
                  1.0e-118
E value
                   352
Match length
                  90
% identity
                  Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
NCBI Description
                  complete cds
                   5576
Seq. No.
                   5069 1.R1040
Contig ID
5'-most EST
                   zhf700955726.h1
                   5577
Seq. No.
                   5073 1.R1040
Contig ID
                  LIB3039-018-Q1-E1-B5
5'-most EST
                  BLASTX
Method
                   g3860308
NCBI GI
                   357
BLAST score
                   2.0e-33
E value
                   132
Match length
% identity
                   (AJ012681) hypothetical protein [Cicer arietinum]
NCBI Description
                   5578
Seq. No.
                   5073_2.R1040
Contig ID
                   LIB3039-010-Q1-E1-D4
5'-most EST
                   BLASTX
Method
                   g3860308
NCBI GI
BLAST score
                   375
                   1.0e-35
E value
                   122
Match length
                   69
% identity
                   (AJ012681) hypothetical protein [Cicer arietinum]
NCBI Description
                   5579
Seq. No.
                   5077 1.R1040
Contig ID
```

5'-most EST

```
BLASTX
Method
NCBI GI
                  q1730328
BLAST score
                  825
                  3.0e-88
E value
                  210
Match length
% identity
                  73
                   (U78100) unknown protein 038 [Phalaenopsis sp. 'hybrid
NCBI Description
                  SM9108']
                  5580
Seq. No.
                  5079 1.R1040
Contig ID
                  LIB3073-020-Q1-K1-D10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1255954
BLAST score
                  451
                  1.0e-44
E value
Match length
                  106
% identity
                  78
                  (Z70677) thioredoxin [Ricinus communis]
NCBI Description
Seq. No.
                  5581
Contig ID
                  5079 2.R1040
                  LIB3072-054-Q1-E1-F1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g267124
BLAST score
                  424
E value
                  1.0e-41
Match length
                  105
                  75
% identity
                  THIOREDOXIN H-TYPE 1 (TRX-H1) >gi_100387_pir__S16590
NCBI Description
                  thioredoxin h1 - common tobacco >gi_20047_emb_CAA41415_
                   (X58527) thioredoxin [Nicotiana tabacum]
                   5582
Seq. No.
                   5080 1.R1040
Contig ID
                  trc700567583.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3123295
BLAST score
                   408
E value
                   1.0e-39
Match length
                  136
                   38
% identity
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169
NCBI Description
                   (AF026473) calmodulin-related protein [Arabidopsis
                  thaliana]
                   5583
Seq. No.
                   5083 1.R1040
Contig ID
                  LIB3138-128-Q1-N1-B11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2494140
BLAST score
                  192
                  2.0e-14
E value
Match length
                  80
% identity
                   47
                   (AC003002) R29515 1 [Homo sapiens] >gi 3068727 (AF058918)
NCBI Description
```

:

LIB3030-001-Q1-B1-D10

Match length

95

## 5584 Seq. No. 5083 2.R1040 Contig ID jsh701064323.h1 5'-most EST BLASTX Method q2494140 NCBI GI 350 BLAST score 1.0e-32 E value 135 Match length 52 % identity (AC003002) R29515 1 [Homo sapiens] >gi 3068727 (AF058918) NCBI Description unknown [Homo sapiens] 5585 Seq. No. 5088 1.R1040 Contig ID 5'-most EST jC-qmst02400076e12a1 Method BLASTX g1362490 NCBI GI 284 BLAST score 5.0e-25 E value Match length 159 41 % identity hypothetical protein YFR024c-a - yeast (Saccharomyces NCBI Description cerevisiae) Seq. No. 5586 Contig ID 5089 1.R1040 LIB3139-005-P1-N1-H5 5'-most EST BLASTN Method g2736287 NCBI GI BLAST score 191 E value 1.0e-103 427 Match length 86 % identity NCBI Description Camptotheca acuminata isopentenyl diphosphate isomerase II (IPI2) mRNA, complete cds 5587 Seq. No. 5089 2.R1040 Contig ID LIB3138-121-Q1-N1-E9 5'-most EST Method BLASTN g1695182 NCBI GI ... 118 BLAST score E value 1.0e-59 210 Match length 89 % identity NCBI Description N.tabacum mRNA for isopentenyl pyrophosphate isomerase 5588 Seq. No. 5090 1.R1040 Contig ID 5'-most EST jex700904292.h1Method BLASTX NCBI GI g4522008 BLAST score 307 E value 4.0e-28

unknown [Homo sapiens]

Method

```
% identity
                   (AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   5091 1.R1040
5'-most EST
                   uC-gmrominsoy178h09b1
Seq. No.
                   5590
                   5100 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy099c12b1
                   BLASTX
Method
NCBI GI
                   g2224901
BLAST score
                   162
                   5.0e-11
E value
                   41
Match length
% identity
                   (U67134) PcMYB1 protein [Petroselinum crispum]
NCBI Description
Seq. No.
                   5591
                   5103 1.R1040
Contig ID
                   LIB3039-010-Q1-E1-A5
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3236237
BLAST score
                   852
                   1.0e-91
E value
Match length
                   270
% identity
                   (AC004684) putative ribotol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   5592
Seq. No.
Contig ID
                   5104 1.R1040
5'-most EST
                   LIB3093-016-Q1-K2-E5
                   BLASTX
Method
NCBI GI
                   g2281627
BLAST score
                   370
E value
                   4.0e-35
Match length
                   127
                   61
% identity
NCBI Description
                   (AF003094) AP2 domain containing protein RAP2.1
                   [Arabidopsis thaliana]
                   5593
Seq. No.
                   5104 2.R1040
Contig ID
5'-most EST
                   LIB3093-016-Q1-K2-F6
Method
                   BLASTX
                   g2464890
NCBI GI
BLAST score
                   283
                   5.0e-25
E value
Match length
                   60
% identity
                   85
                   (Z99707) TINY-like protein [Arabidopsis thaliana]
NCBI Description
                   5594
Seq. No.
                   5113 1.R1040
Contig ID
5'-most EST
                   LIB3170-083-Q1-K1-H1
                   BLASTX
```

Method

BLASTN

```
NCBI GI
                   q2827656
BLAST score
                   282
                   6.0e-25
E value
Match length
                   73
% identity
                   71
                   (AL021637) DAG-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5113 2.R1040
Contig ID
5'-most EST
                   LIB3109-034-Q1-K1-G5
                   5596
Seq. No.
Contig ID
                   5113 3.R1040
5'-most EST
                   bth700846831.h1
Seq. No.
Contig ID
                   5115 1.R1040
5'-most EST
                  LIB3049-044-Q1-E1-H9
Method
                   BLASTX
                   q130271
NCBI GI
                   543
BLAST score
                   3.0e-55
E value
                   165
Match length
% identity
                   PLASTOCYANIN PRECURSOR >qi 100238 pir S05303 plastocyanin
NCBI Description
                   precursor - tomato >gi 193\overline{0}0 emb \overline{C}AA3\overline{21}21 (X13934)
                  pre-plastocyanin (AA -64 to 106) [Lycopersicon esculentum]
Seq. No.
                   5598
Contig ID
                   5115 2.R1040
                   g5677250
5'-most EST
Method
                   BLASTX
NCBI GI
                   q130265
BLAST score
                   467
E value
                   1.0e-46
Match length
                   99
% identity
                  PLASTOCYANIN >gi 65834 pir CUVM plastocyanin - field
NCBI Description
                   pumpkin
                   5599
Seq. No.
Contig ID
                   5115 3.R1040
5'-most EST
                   LIB3040-007-Q1-E1-B6
                   BLASTX
Method
NCBI GI
                   q130271
BLAST score
                   518
E value
                   2.0e-52
Match length
                   167
                   64
% identity
                   PLASTOCYANIN PRECURSOR >qi 100238 pir S05303 plastocyanin
NCBI Description
                  precursor - tomato >gi 19300 emb CAA32121 (X13934)
                  pre-plastocyanin (AA -64 to 106) [Lycopersicon esculentum]
Seq. No.
                   5600
Contig ID
                   5115 4.R1040
5'-most EST
                   LIB3073-006-Q1-K1-F9
```

```
q20845
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
Match length
                  74
% identity
                  86
                  Pea gene for plastocyanin
NCBI Description
Seq. No.
Contig ID
                  5119 1.R1040
5'-most EST
                  fde700873747.h1
                  BLASTX
Method
NCBI GI
                  q4539423
BLAST score
                  704
                  2.0e-74
E value
                  164
Match length
% identity
NCBI Description
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                   [Arabidopsis thaliana]
Seq. No.
Contig ID
                  5120 1.R1040
5'-most EST
                  LIB3053-001-Q1-B1-C5
                  BLASTX
Method
NCBI GI
                  g1352245
BLAST score
                  512
                  8.0e-52
E value
Match length
                  226
% identity
                  FATTY ALDEHYDE DEHYDROGENASE (ALDEHYDE DEHYDROGENASE,
NCBI Description
                  MICROSOMAL) (CLASS 3) >qi 687254 (U14390) aldehyde
                  deydrogenase [Mus musculus]
                  5603
Seq. No.
Contig ID
                  5121 1.R1040
5'-most EST
                  zsg701129386.hl
Method
                  BLASTX
                  g4325282
233
NCBI GI
BLAST score
E value
                  2.0e-19
Match length
                  57
% identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                  >gi 4325286 gb AAD17314 (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                  5604
Seq. No.
                  5121 2.R1040
Contig ID
                  uC-gmflminsoy029b08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4325282
                  578
BLAST score
                  1.0e-59
E value
Match length
                  148
% identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                  >gi 4325286 gb AAD17314 (AF123311) NAC domain protein NAM
```

[Arabidopsis thaliana]

BLAST score

333

```
5605
Seq. No.
                   5122 1.R1040
Contig ID
                   LIB3106-068-P1-K1-E6
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3860330
BLAST score,
                   155
                   2.0e-81
E value
                   387
Match length
                   85
% identity
                  Cicer arietinum mRNA for hypothetical protein, clone Can106
NCBI Description
                   5606
Seq. No.
Contig ID
                   5122 2.R1040
                   kl1701207777.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3860330
BLAST score
                   112
                   5.0e-56
E value
                   236
Match length
                   87
% identity
                  Cicer arietinum mRNA for hypothetical protein, clone Can106
NCBI Description
                   5607
Seq. No.
Contig ID
                   5132 1.R1040
                   fua7\overline{0}1038545.h1
5'-most EST
Seq. No.
                   5608
                   5133 1.R1040
Contig ID
5'-most EST
                   LIB3138-057-Q1-N1-D4
Method
                   BLASTX
                   g2129517
NCBI GI
BLAST score
                   1719
                   0.0e+00
E value
Match length
                   359
% identity
                   24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis
NCBI Description
                   thaliana
                   5609
Seq. No.
                   5133 2.R1040
Contig ID
5'-most EST
                   uC-gmropic067d03b1
Method
                   BLASTX
NCBI GI
                   g2129517
BLAST score
                   557
                   3.0e-57
E value
                   124
Match length
                   80
% identity
                  24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis
NCBI Description
                   thaliana
                   5610
Seq. No.
                   5133 4.R1040
Contig ID
5'-most EST
                  LIB3092-030-Q1-K1-H5
Method
                  BLASTX
                   g2129517
NCBI GI
```

```
E value
                   4.0e-31
                   153
Match length
% identity
                   76
                   24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis
NCBI Description
                   thaliana
                   5611
Seq. No.
                   5134 1.R1040
Contig ID
5'-most EST
                   g5175390
                   BLASTX
Method
                   g464981
NCBI GI
BLAST score
                   789
                   4.0e-84
E value
Match length
                   148
                   99
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                   ubiquitin carrier protein [Lycopersicon esculentum]
                   5612
Seq. No.
                   5134 2.R1040
Contig ID
                   pmv7\overline{0}0890042.h1
5'-most EST
Method
                   BLASTX
                   g464981
NCBI GI
                   781
BLAST score
                   2.0e-83
E value
Match length
                   148
                   97
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                   ubiquitin carrier protein [Lycopersicon esculentum]
                   5613
Seq. No.
                   5134 3.R1040
Contig ID
                   zhf7\overline{0}0961505.h1
5'-most EST
                   BLASTN
Method
                   g456567
NCBI GI
                   80
BLAST score
E value
                   7.0e-37
Match length
                   200
                   85
% identity
                   Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                   5614
Seq. No.
                   5134 4.R1040
Contig ID
                   uC-gmflminsoy056g03b1
5'-most EST
                   BLASTX
Method
                   g441457
NCBI GI
BLAST score
                   216
                   2.0e-17
E value
Match length
                   44
                   91
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                   esculentum]
```

5615

Seq. No.

BLAST score

405

```
5134 5.R1040
Contig ID
5'-most EST
                  LIB3093-022-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q464981
BLAST score
                  757
                  2.0e-80
E value
                  148
Match length
% identity
                  95
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >qi 388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  5616
                  5134 6.R1040
Contig ID
                  trc700561374.hl
5'-most EST
                  BLASTN
Method
                  q456567
NCBI GI
BLAST score
                  48
E value
                  4.0e-18
                  80
Match length
                  90
% identity
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
Seq. No.
                  5617
                  5135 2.R1040
Contig ID
5'-most EST
                  jC-gmf102220050a07a1
                  BLASTN
Method
NCBI GI
                  q861154
BLAST score
                  130
                  8.0e-67
E value
Match length
                  294
                  86
% identity
NCBI Description
                  V.faba VFCWINV1 mRNA for cell wall invertase I
                  5618
Seq. No.
Contig ID
                  5136 1.R1040
5'-most EST
                  asn701139401.h1
Method
                  BLASTX
NCBI GI
                  q3023651
BLAST score
                  182
E value
                  1.0e-13
Match length
                  121
% identity
NCBI Description
                  D-LACTATE DEHYDROGENASE [CYTOCHROME] PRECURSOR (D-LACTATE
                  FERRICYTOCHROME C OXIDOREDUCTASE) (D-LCR)
                  >gi 1076962 pir S51528 D-lactate dehydrogenase
                  (cytochrome) (EC 1.1.2.4) - yeast (Kluyveromyces marxianus
                  var. lactis) >gi 602029 emb CAA50635 (X71628) D-lactate
                  dehydrogenase (cytochrome) [Kluyveromyces lactis]
                  5619
Seq. No.
Contig ID
                  5138 1.R1040
                  wvk700682539.h2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3298441
```

Seq. No.

5627

```
2.0e-39
E value
Match length
                   140
                   62
% identity
NCBI Description
                   (AB010879) chloroplast ribosomal protein L10 [Nicotiana
                   tabacum]
                   5620
Seq. No.
Contig ID
                   5138 2.R1040
                   uxk700670986.h1
5'-most EST
                   BLASTX
Method
                   g329844.1
NCBI GI
BLAST score
                   230
                   2.0e-19
E value
                   80
Match length
                   62
% identity
                   (AB010879) chloroplast ribosomal protein L10 [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   5621
                   5140 1.R1040
Contig ID
                   LIB3051-078-Q1-K1-D12
5'-most EST
                   5622
Seq. No.
Contig ID
                   5144 1.R1040
5'-most EST
                   LIB3028-005-Q1-B1-G7
                   5623
Seq. No.
                   5145 1.R1040
Contig ID
5'-most EST
                   LIB3028-005-Q1-B1-G8
Method
                   BLASTX
NCBI GI
                   q1076288
BLAST score
                   355
                   1.0e-33
E value
Match length
                   104
% identity
                   62
                   amino acid permease AAP3 - Arabidopsis thaliana
NCBI Description
                   5624
Seq. No.
Contig ID
                   5149 1.R1040
5'-most EST
                   ssr700559066.hl
                   BLASTX
Method
NCBI GI
                   q4105794
BLAST score
                   442
E value
                   2.0e-43
Match length
                   140
% identity
                   57
                   (AF049928) PGP224 [Petunia x hybrida]
NCBI Description
                   5625
Seq. No.
Contig ID
                   5152 1.R1040
5'-most EST
                   LIB3028-005-Q1-B1-E11
Seq. No.
                   5626
                   5152 2.R1040
Contig ID
                   wrg700787541.hl
5'-most EST
```

```
Contig ID
                   5154 1.R1040
5'-most EST
                   LIB3028-005-Q1-B1-E3
                   5628
Seq. No.
                   5159 1.R1040
Contig ID
                   asn701139905.hl
5'-most EST
Method
                   BLASTX
                   g3283996
NCBI GI
BLAST score
                   1094
                   1.0e-120
E value
Match length
                   240
% identity
                   71
                   (AF072908) calcium-dependent protein kinase [Nicotiana
NCBI Description
                   tabacum]
                   5629
Seq. No.
                   5162 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy310b03b1
                   5630
Seq. No.
                   5162 2.R1040
Contig ID
                   LIB3138-071-P1-N1-D2
5'-most EST
Method
                   BLASTX
                   g2708532
NCBI GI
                   256
BLAST score
                   8.0e-22
E value
                   145
Match length
% identity
                   (AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
                   5631
Seq. No.
                   5163 1.R1040
Contig ID
5'-most EST
                   zhf700955007.h1
Method
                   BLASTX
                   g4567262
NCBI GI
BLAST score
                   1083
                   1.0e-118
E value
Match length -
                   258
% identity
                   79
                   (AC006841) putative ubiquitin [Arabidopsis thaliana]
NCBI Description
                   5632
Seq. No.
                   5164 1.R1040
Contig. ID
5'-most EST
                   LIB3109-007-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g2708737
BLAST score
                   718
E value
                   9.0e-76
                   295
Match length
% identity
                   (AC003952) putative nuclear protein [Arabidopsis thaliana]
NCBI Description
```

5633 Seq. No. 5164 2.R1040 Contig ID

5'-most EST LIB3049-044-Q1-E1-B12

Method BLASTX NCBI GI g2708737

```
BLAST score
                   248
                   3.0e-21
E value
Match length
                   54
% identity
                   36
                   (AC003952) putative nuclear protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5634
                   5166 1.R1040
Contig ID
                   jC-qmst02400009a02a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3080433
BLAST score
                   558
                   3.0e-57
E value
                   196
Match length
% identity
                   50
                   (AL022605) putative gamma-glutamyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   5635
Seq. No.
                   5171 1.R1040
Contig ID
                   zhf700962664.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455337
BLAST score
                   155
                   3.0e-10
E value
                   100
Match length
                   40
% identity
NCBI Description
                   (AL035525) pectinesterase-like protein [Arabidopsis
                   thaliana]
                   5636
Seq. No.
                   5172 1.R1040
Contig ID
                   gsv701052361.hl
5'-most EST
                   5637
Seq. No.
                   5173 1.R1040
Contig ID
                   vwf700675859.h1
5'-most EST
Seq. No.
                   5638
Contig ID
                   5175 1.R1040
                   xpa700796134.hl
5'-most EST
                   BLASTN
Method
                   q557693
NCBI GI
BLAST score
                   48
                   7.0e-18
E value
                   80
Match length
                   90
% identity
                   Arabidopsis thaliana Columbia GTP binding protein beta
NCBI Description
                   subunit (AGB1) mRNA, complete cds
                   5639
Seq. No.
Contig ID
                   5175 2.R1040
                   pxt700944124.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1346106
BLAST score
                   196
```

4.0e-15

E value

```
Match length
                  39
                  90
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi 557694
NCBI Description
                   (U12232) GTP binding protein beta subunit [Arabidopsis
                  thaliana] >gi 3096915 emb CAA18825.1 (AL023094) GTP
                  binding protein beta subunit [Arabidopsis thaliana]
Seq. No.
                  5640
                  5176 1.R1040
Contig ID
                  uC-gmrominsoy103c05b1
5'-most EST
Seq. No.
                  5641
                  5180 1.R1040
Contig ID
                  hrw7\overline{0}1059233.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g169295
BLAST score
                  173
E value
                  3.0e-92
Match length
                  471
% identity
                  Pharbitis nil heat shock protein 83 (Hsp83) gene, complete
NCBI Description
                  5642
Seq. No.
                  5181 1.R1040
Contig ID
                  LIB3139-110-P1-N1-E5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g951449
BLAST score
                  1060
                  1.0e-116
E value
Match length
                  324
% identity
                   (L46681) aspartic protease precursor [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  5643
                   5184 1.R1040
Contig ID
                  uC-gmrominsoy128c08b1
5'-most EST
Method
                  BLASTX
                  g2244849
NCBI GI
BLAST score
                   417
                  1.0e-40
E value
                  174
Match length
% identity
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5644
Seq. No.
                   5188 1.R1040
Contig ID
                   zhf700953137.hl
5'-most EST
Method
                  BLASTX
                   g266567
NCBI GI
BLAST score
                   845
E value
                   1.0e-90
Match length
                   265
```

MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR

(ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)

65

% identity

NCBI Description

```
(EC 3.4.99.41) alpha chain precursor - potato
                  >gi_21493_emb_CAA46990 (X66284) mitochondrial processing
                  peptidase [Solanum tuberosum]
                  5645
Seq. No.
Contig ID
                  5188 2.R1040
                  LIB3170-015-Q1-J1-C9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g266567
                                                    BLAST score
                  242
                  3.0e-20
E value
Match length
                  60
                  78
% identity
                  MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
NCBI Description
                  (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
                  >gi_421956_pir__S23558 mitochondrial processing peptidase
                  (EC 3.4.99.41) alpha chain precursor - potato
                  >qi 21493 emb CAA46990 (X66284) mitochondrial processing
                  peptidase [Solanum tuberosum]
                  5646
Seq. No.
Contig ID
                  5190 1.R1040
5'-most EST
                  LIB3028-005-Q1-B1-B3
                  5647
Seq. No.
Contig ID
                  5191 1.R1040
5'-most EST
                  uC-qmrominsoy131b04b1
Method
                  BLASTX
NCBI GI
                  q4128197
BLAST score
                  199
E value
                  2.0e-15
Match length
                  103
% identity
                  (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
NCBI Description
                  5648
Seq. No.
                  5191 2.R1040
Contig ID
5'-most EST
                  cf1700863652.h1
Method
                  BLASTX
NCBI GI
                  q4128197
BLAST score
                  147
E value
                  3.0e-09
Match length
                  86
% identity
                  (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5649
                  5192 1.R1040
Contig ID
5'-most EST
                  uC-gmropic010d01b1
Method
                  BLASTX
NCBI GI
                  g602292
BLAST score
                  555
E value
                  5.0e-57
Match length
                  162
% identity
                  (U17987) RCH2 protein [Brassica napus]
NCBI Description
```

>gi 421956 pir S23558 mitochondrial processing peptidase

```
5650
Seq. No.
Contig ID
                   5193 1.R1040
                  jC-qmf102220086f03a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1771162
BLAST score
                  752
                   5.0e-80
E value
Match length
                   206
% identity
                  _70
                   (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                  >qi 3687307 emb CAA07000 (AJ006379) subtilisin-like
                  protease [Lycopersicon esculentum]
Seq. No.
                   5651
Contig ID
                   5200 1.R1040
5'-most EST
                   vwf700675653.hl
                  BLASTX
Method
NCBI GI
                  q2832672
BLAST score
                   623
E value
                   1.0e-64
Match length
                  148
% identity
                  82
                   (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   5200 2.R1040
5'-most EST
                  LIB3074-004-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2832672
BLAST score
                   629
                  2.0e-65
E value
Match length
                  153
% identity
                   (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                   5653
Seq. No.
                   5202 1.R1040
Contig ID
5'-most EST
                   fde700870929.hl
Method
                  BLASTX
                  g3064045
NCBI GI
BLAST score
                   493
                   7.0e-50
E value
Match length
                  111
% identity
                  81
                   (AF054449) adenylosuccinate lyase [Mesembryanthemum
NCBI Description
                  crystallinum]
                  5654
Seq. No.
Contig ID
                   5213 1.R1040
                  LIB3065-008-Q1-N1-H4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1352681
BLAST score
                  269
                  3.0e-23
E value
Match length
                  112
```

50

% identity

```
NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457
                   phosphoprotein phosphatase (EC 3.\overline{1}.3.16) \overline{2}C - Arabidopsis
                   thaliana >gi 633028 dbj BAA07287_ (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                   5213 2.R1040
Contiq ID
                   sat701007474.h2
5'-most EST
                   BLASTX
Method
                   g1352681
NCBI GI
BLAST score
                   975
                   1.0e-106
E value
Match length
                   345
                   59
% identity
                   PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457
NCBI Description
                   phosphoprotein phosphatase (EC \overline{3.1.3.16}) \overline{2C} - Arabidopsis
                   thaliana >qi 633028 dbj BAA07287 (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                   5213 3.R1040
Contig ID
                   LIB3039-048-Q1-E1-A11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1352681
BLAST score
                   196
                   6.0e-15
E value
                   128
Match length
                   43
% identity
                   PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457
NCBI Description
                   phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
                   thaliana >qi 633028 dbj BAA07287 (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
                   5657
Seq. No.
Contig ID
                   5214 1.R1040
                   zhf7\overline{0}0958201.h1
5'-most EST
                   BLASTX
Method
                   q1778015
NCBI GI
BLAST score
                   209
                   2.0e-16
E value
Match length
                   99
% identity
                   (U59508) osmotic stress-induced proline dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   5658
                   5216 1.R1040
Contig ID
                   pmv700890843.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1945611
BLAST score
                   920
                   4.0e-99
E value
Match length
                   435
% identity
                   (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                   >qi 4506221 ref NP 002807.1_pPSMD12_ proteasome (prosome,
```

macropain) 26S subunit, non-ATPase,

NCBI Description

```
5659
Seq. No.
                  5216 2.R1040
Contig ID
                  jC-gmf102220051h08a1
5'-most EST
                  BLASTX
Method
                  g4432854
NCBI GI
BLAST score
                  239
                  3.0e-19
E value
                  208
Match length
                  18
% identity
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  5660
Seq. No.
                  5216 3.R1040
Contig ID
                   zsg701119349.h1
5'-most EST
Method
                  BLASTX
                  q1945611
NCBI GI
BLAST score
                  169
                   1.0e-11
E value
Match length
                   66
                   48
% identity
                   (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                  >gi 4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
                   5661
Seq. No.
                   5220 1.R1040
Contig ID
5'-most EST
                   uC-gmropic011h01b1
Method
                   BLASTX
                   q3193298
NCBI GI
                   176
BLAST score
                   3.0e-12
E value
                   122
Match length
% identity
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
NCBI Description
                   5662
Seq. No.
                   5220 2.R1040
Contig ID
                   LIB3040-041-Q1-E1-C5
5'-most EST
Method
                   BLASTX
                   q3193298
NCBI GI
                   158
BLAST score
                   2.0e-10
E value
Match length
                   87
% identity
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
NCBI Description
                   5663
Seq. No.
                   5226 1.R1040
Contig ID
                   LIB3028-004-Q1-B1-G11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3287696
                   257
BLAST score
                   3.0e-22
E value
                   79
Match length
% identity
                   (AC003979) Strong similarity to phosphoribosylanthranilate
```

% identity

70

```
transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
```

```
Seq. No.
                   5664
                   5229 1.R1040
Contig ID
                   hrw701058845.h1
5'-most EST
Method
                   BLASTX
                   a3860321
NCBI GI
BLAST score
                   1018
                   1.0e-111
E value '
Match length
                   223
% identity
                   (AJ012687) beta-galactosidase [Cicer arietinum]
NCBI Description
Seq. No.
Contig ID
                   5233 1.R1040
5'-most EST
                   leu701147642.h1
Method
                   BLASTX
                   q4469023
NCBI GI
                   1492
BLAST score
                   1.0e-166
E value
                   387
Match length
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   5666
Seq. No.
                   5233 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220051d01a1
Method
                   BLASTX
NCBI GI
                   q4469023
BLAST score
                   744
                   6.0e-79
E value
Match length
                   199
% identity
                   73
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   5667
Seq. No.
Contig ID
                   5235 1.R1040
5'-most EST
                   LIB3107-057-Q1-K1-F4
                   BLASTX
Method
NCBI GI
                   q2739365
BLAST score
                   801
E value
                   2.0e-85
Match length
                   188
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5668
Contig ID
                   5235 2.R1040
5'-most EST
                   g4276997
Method
                   BLASTX
NCBI GI
                   q3201969
BLAST score
                   299
                   6.0e-27
E value
Match length
                   71
```

Contig ID

5'-most EST

```
NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]
                   5669
Seq. No.
Contig ID
                   5235 4.R1040
5'-most EST
                   LIB3028-047-Q1-B1-A10
                   BLASTX
Method
                   q2739365
NCBI GI
BLAST score
                   423
                   9.0e-42
E value
Match length
                   101
                   72
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5670.
Seq. No.
                   5239 1.R1040
Contig ID
5'-most EST
                   q4396664
Method
                   BLASTX
NCBI GI
                   q3135264
BLAST score
                   359
                   3.0e-34
E value
Match length
                   117
% identity
                   (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5671
Seq. No.
                   5240 1.R1040
Contig ID
5'-most EST
                   trc700563942.h1
                   BLASTX
Method
NCBI GI
                   g585338
BLAST score
                   1079
                   1.0e-118
E value
Match length
                   225
                   92
% identity
                   ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                   >qi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                   sativa]
                   5672
Seq. No.
Contig ID
                   5240 2.R1040
5'-most EST
                   zzp700831593.hl
                   BLASTX
Method
NCBI GI
                   q585338
BLAST score
                   419
E value
                   3.0e-41
Match length
                   89
% identity
                   ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                   >gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza
                   sativa]
                   5673
Seq. No.
                   5242 1.R1040
Contig ID
                   k117\overline{0}1211937.h1
5'-most EST
                   5674
Seq. No.
```

5243\_1.R1040 pmv700893482.h1

BLAST score

371

```
Method
                   BLASTX
NCBI GI
                   q3860251
BLAST score
                   1050
                   1.0e-115
E value
Match length
                   272
% identity
                   73
                   (AC005824) putative permease [Arabidopsis thaliana]
NCBI Description
                   5675
Seq. No.
                   5244 1.R1040
Contig ID
                   uC-gmflminsoy029b03b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1280434
BLAST score
                   274
E value
                   1.0e-23
Match length
                   306
% identity
                   31
NCBI Description
                   (U42014) hemomucin [Drosophila melanogaster]
Seq. No.
Contig ID
                   5245 1.R1040
5'-most EST
                   leu701150315.h1
Seq. No.
                   5677
Contig ID
                   5246 1.R1040
                   sat7\overline{0}1009292.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4455338
BLAST score
                   910
                   4.0e-98
E value
Match length
                   272
% identity
                   (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   5678
Seq. No.
                   5250 1.R1040
Contig ID
5'-most EST
                   hyd700727832.h1
Seq. No.
                   5679
Contig ID
                   5255 1.R1040
5'-most EST
                   epx701106273.h1
Method
                   BLASTX
NCBI GI
                   g1176658
BLAST score
                   405
E value
                   2.0e-60
Match length
                   256
% identity
                   52
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                   >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
                   5680
Seq. No.
                   5255 2.R1040
Contig ID
                   kmv700738802.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1176658
```

```
E value
                   6.0e-35
Match length
                   155
                   47
% identity
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                   >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
Seq. No.
                   5681
                   5255 3.R1040
Contig ID
                   jC-gmf102220071a03a1
5'-most EST
                   5682
Seq. No.
                   5255 4.R1040
Contig ID
5'-most EST
                   LIB3051-034-Q1-K1-E12
                   5683
Seq. No.
Contig ID
                   5256 1.R1040
                   LIB3107-021-Q1-K1-G4
5'-most EST
Seq. No.
                   5684
                   5256 2.R1040
Contig ID
                   LIB3092-030-Q1-K1-A12
5'-most EST
Seq. No.
                   5685
                   5259 1.R1040
Contig ID
                   LIB3028-003-Q1-B1-H6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3659909
BLAST score
                   281
                   5.0e-25
E value
                   80
Match length
% identity
                   (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   5686
Seq. No.
                   5261 1.R1040
Contig ID
                                                                       . . .
                   r1r700898683.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2832696
BLAST score
                   718
E value
                   6.0e-76
                   235
Match length
                   60
% identity
                   (ALO21713) putative protein [Arabidopsis thaliana]
NCBI Description
                   5687
Seq. No.
                   5262 1.R1040
Contig ID
                   zpv700759945.hl
5'-most EST
Seq. No.
                   5688
                   5264 1.R1040
Contig ID
                   smc7\overline{0}0748955.h1
5'-most EST
                   5689
Seq. No.
                   5265 1.R1040
Contig ID
                   LIB3106-101-Q1-K1-G2
5'-most EST
```

BLASTX

Method

E value

4.0e-48

```
g2465923
NCBI GI
BLAST score
                   1068
                   1.0e-125
E value
Match length
                   461
                   54
% identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   5690
Seq. No.
                   5265 3.R1040
Contig ID
                   g5057646
5'-most EST
Seq. No.
                   5691
                   5266 1.R1040
Contig ID
                   LIB3107-010-Q1-K1-H3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3292829
                   1081
BLAST score
E value
                   1.0e-118
Match length
                   458
                   62
% identity
                   (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   5692
Seq. No.
                   5266 2.R1040
Contig ID
5'-most EST
                   LIB3030-002-Q1-B1-G9
Method
                   BLASTX
                   g2697129
NCBI GI
BLAST score
                   426
E value
                   4.0e-41
                   415
Match length
% identity
                   (AF025654) mRNA capping enzyme [Homo sapiens]
NCBI Description
                   >gi 4506563 ref NP 003791.1 pRNGTT UNKNOWN
Seq. No.
Contig ID
                   5269 1.R1040
5'-most EST
                   leu701156667.hl
                   BLASTX
Method
NCBI GI
                   g2245020
BLAST score
                   184
E value
                   4.0e-13
Match length
                   195
% identity
NCBI Description
                   (Z97341) growth regulator homolog [Arabidopsis thaliana]
Seq. No.
                   5694
Contig ID
                   5269 2.R1040
5'-most EST
                   uaw700666916.hl
Seq. No.
                   5695
Contig ID
                   5271 1.R1040
5'-most EST
                   dpv701096923.h1
Method
                   BLASTX
NCBI GI
                   q3820614
BLAST score
                   480
```



Match length 189 % identity 55

NCBI Description (AF094516) E1-like protein [Homo sapiens]

Seq. No. 5696

Contig ID 5272 1.R1040

5'-most EST jC-gmro02910016d05a1

Method BLASTX
NCBI GI 94539371
BLAST score 410
E value 1.0e-39
Match length 199
% identity 50

NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 5697

Contig ID 5272 2.R1040

5'-most EST jC-gmle01810005e04a1

Seq. No. 5698

Contig ID 5276 1.R1040

5'-most EST jC-gmle01810082c09a1

Method BLASTX
NCBI GI g3043529
BLAST score 292
E value 3.0e-26

Match length 92 % identity 58

NCBI Description (AJ002204) polyamine oxidase [Zea mays]

Seq. No. 5699

Contig ID 5277 1.R1040 5'-most EST hrw701063235.h1

Method BLASTX
NCBI GI 94063751
BLAST score 145
E value 2.0e-13
Match length 118
% identity 47

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi\_4510409\_gb\_AAD21495.1\_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 5700

Contig ID 5279 1.R1040

5'-most EST uC-gmflminsoy079g08b1

Method BLASTX
NCBI GI g2288997
BLAST score 286
E value 1.0e-25
Match length 69
% identity 80

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5701

Contig ID 5280 1.R1040

5'-most EST LIB3049-002-Q1-E1-F7

```
Method
                   BLASTX
                   g2632252
NCBI GI
BLAST score
                   558
                   4.0e-57
E value
Match length
                   186
% identity
                   (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   5702
Sea. No.
                   5280 2.R1040
Contig ID
                   jC-gmst02400056c02a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2632252
BLAST score
                   586
                   2.0e-60
E value
Match length
                   195
% identity
                   61
                   (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   5703
Seq. No.
                   5284 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910060c10d1
                   5704
Seq. No.
Contig ID
                   5289 1.R1040
                   LIB3094-023-Q1-K1-B2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3142331
BLAST score
                   237
                   2.0e-19
E value
Match length
                   178
% identity
                   33
                   (U97327) calcyclin binding protein [Mus musculus]
NCBI Description
                   5705
Seq. No.
                   5289 2.R1040
Contig ID
                   k11701206226.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3122258
BLAST score
                   916
E value
                   6.0e-99
                   245
Match length
                   73
% identity
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) (B4
NCBI Description
                   INTEGRIN INTERACTOR) (CAB) >gi 2809383 (AF022229)
                   translation initiation factor \overline{6} [Homo sapiens]
                   >gi_2910997_emb_CAA72243_ (Y11435) b4 integrin interactor
                   [Homo sapiens] >gi 3335506 (AF047433) b(2)gcn homolog [Homo
                   sapiens] >gi 4504771 ref NP 002203.1_pITGB4BP_ integrin
                   beta 4 binding protein
                   5706
Seq. No.
                   5289 3.R1040
Contig ID
                   zhf700956194.hl
5'-most EST
                   BLASTX
Method
                   q3355311
NCBI GI
```

564

BLAST score

```
E value
                   5.0e-58
Match length
                   128
% identity
                   85
                   (AJ009737) eukaryotic translation initiation factor 6 [Beta
NCBI Description
                   vulgaris]
Seq. No.
                   5707
                   5289 5.R1040
Contig ID
                   LIB3040-055-Q1-E1-H11
5'-most EST
Method
                   BLASTX
                   g3355311
NCBI GI
BLAST score
                   278
                   7.0e-25
E value
                   59
Match length
% identity
                   92
NCBI Description
                   (AJ009737) eukaryotic translation initiation factor 6 [Beta
                   5708
Seq. No.
                   5289 10.R1040
Contiq ID
                   smc7\overline{0}0750180.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3355310
BLAST score
                   45
E value
                   3.0e-16
                   93
Match length
                   87
% identity
NCBI Description
                   Beta vulgaris mRNA for eukaryotic translation initiation
                   factor 6, partial
                   5709
Seq. No.
                   5290 1.R1040
Contig ID
                   LIB3028-003-Q1-B1-E3
5'-most EST
Method
                   BLASTX
                   g2252830
NCBI GI
BLAST score
                   829
E value
                   1.0e-88
Match length
                   289
% identity
                   57
NCBI Description
                   (AF013293) weak similarity to receptor protein kinase
                   [Arabidopsis thaliana]
                   5710
Seq. No.
                   5301 1.R1040
Contig ID
5'-most EST
                   LIB3170-013-Q1-K1-D5
Method
                   BLASTX
                   q4006872
NCBI GI
BLAST score
                  .994
                   1.0e-108
E value
Match length
                   283
```

Seq. No. 5711

% identity

NCBI Description

Contig ID 5302\_1.R1040 5'-most EST wrg700789428.h2

65

thaliana]

(299707) methionyl aminopeptidase-like protein [Arabidopsis]

```
Method
                   BLASTX
                   g2829910
NCBI GI
BLAST score
                   523
                   1.0e-53
E value
                   114
Match length
                   21
% identity
                   (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                   5712
Seq. No.
                   5304 1.R1040
Contig ID
                   pxt700944576.hl
5'-most EST
                   BLASTX
Method
                   q2129496
NCBI GI
BLAST score
                   1529
E value
                   0.0e+00
                   424
Match length
                   81
% identity
                   acetolactate synthase (EC 4.1.3.18) precursor (clone A19) -
NCBI Description
                   upland cotton
                   5713
Seq. No.
Contig ID
                   5305 1.R1040
                   LIB3028-003-Q1-B1-F8
5'-most EST
Seq. No.
                   5714
                   5308 1.R1040
Contig ID
5'-most EST
                   zhf700954109.hl
Method
                   BLASTN
                   g3617740
NCBI GI
BLAST score
                   37
                   7.0e-11
E value
                   157
Match length
 % identity
                   Arabidopsis thaliana BAC F1I21 from chromosome 1, near 59
NCBI Description
                   cM, complete sequence [Arabidopsis thaliana]
                   5715
Seq. No.
Contig ID
                   5308 2.R1040
                   LIB3051-088-Q1-K1-C3
 5'-most EST
Method
                   BLASTN
                   g2281636
NCBI GI
                   37
BLAST score
                   3.0e-11
E value
Match length
                   157
 % identity
                   Arabidopsis thaliana AP2 domain containing protein RAP2.6
NCBI Description
                   mRNA, partial cds
 Seq. No.
                   5716
                   5308 3.R1040
 Contig ID
                   jC-gmf102220089g10a1
 5'-most EST
                   5717
 Seq. No.
                   5313 1.R1040
Contig ID
                   jex700904162.hl
 5'-most EST
```

BLASTX

Method

5'-most EST

```
NCBI GI
                   q2149640
BLAST score
                   1365
E value
                   1.0e-151
Match length
                   316
% identity
                  84
                   (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5718
                   5313 2.R1040
Contig ID
                   uC-gmflminsoy026c06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2149640
                   931
BLAST score
                   1.0e-101
E value
Match length
                   206
% identity
                   (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                   5719
Seq. No.
                   5313 3.R1040
Contig ID
                  LIB3107-014-Q1-K1-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2149640
BLAST score
                   1754
                   0.0e + 00
E value
Match length
                   393
% identity
                   86
                   (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5720
                   5313 4.R1040
Contig ID
                   ish701069173.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2149640
BLAST score
                   175
                   3.0e-22
E value
                   75
Match length
% identity
NCBI Description
                   (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                   5721
                   5315 1.R1040
Contig ID
                   wrq700786111.h2
5'-most EST
                   BLASTX
Method
                   q1710401
NCBI GI
                   594
BLAST score
                   1.0e-90
E value
                   189
Match length
                   87
% identity
                  RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
NCBI Description
                   (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                   >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase
                   R2 [Nicotiana tabacum]
Seq. No.
                   5722
                   5317 1.R1040
Contig ID
```

LIB3028-003-Q1-B1-D8

NCBI Description

```
Method
                   BLASTX
NCBI GI
                   q466158
BLAST score
                   219
                   2.0e-23
E value
Match length
                   74
                   70
% identity
                   HYPOTHETICAL 9.3 KD PROTEIN ZK652.1 IN CHROMOSOME III
NCBI Description
                   >qi 630768 pir S44901 ZK652.1 protein - Caenorhabditis
                   elegans >gi 289767 (L14429) putative [Caenorhabditis
                   elegans]
                   5723
Seq. No.
Contig ID
                   5318 1.R1040
                   ncj7\overline{0}0987601.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3510539
BLAST score
                   291
E value
                   1.0e-162
Match length
                   591
                   87
% identity
                   Prunus armeniaca expansin (Exp2) mRNA, complete cds
NCBI Description
Seq. No.
                   5724
Contig ID
                   5319 1.R1040
5'-most EST
                   bth700849223.h1
                   5725
Seq. No.
Contig ID
                   5320 1.R1040
5'-most EST
                   LIB3028-003-Q1-B1-E10
Seq. No.
                   5726
                   5324 1.R1040
Contig ID
                   zsq701122415.h1
5'-most EST
                   5727
Seq. No.
                   5326 1.R1040
Contig ID
                   ncj7\overline{0}0983837.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2960216
BLAST score
                   1563
E value
                   1.0e-174
Match length
                   382
% identity
                   77
                   (AJ223384) 26S proteasome regulatory ATPase subunit 10b
NCBI Description
                   (S10b) [Manduca sexta]
                   5728
Seq. No.
                   5326 2.R1040
Contig ID
                   jsh7\overline{0}1064850.h1
5'-most EST
Method
                   BLASTN
                   g3236477
NCBI GI
BLAST score
                   123
E value
                   1.0e-62
Match length
                   227
                   89
% identity
                   Gossypium hirsutum 26S protease regulatory subunit (PRA2)
```

mRNA, partial cds

5'-most EST

Method

```
Seq. No.
                    5729
 Contig ID
                    5329 2.R1040
 5'-most EST
                    smc700744869.hl
                    5730
 Seq. No.
 Contig ID
                    5330 1.R1040
 5'-most EST
                    LIB3028-003-Q1-B1-B4
Seq. No.
                    5332 1.R1040
 Contig ID
 5'-most EST
                    gsv7\overline{0}1054195.h1
 Method
                    BLASTX
                    g4454469
 NCBI GI
 BLAST score
                    636
                    1.0e-66
 E value
 Match length
                    151
 % identity
                    (AC006234) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    5732
 Seq. No.
                    5338 1.R1040
 Contig ID
                    LIB3073-003-Q1-K1-A7
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q3608481
 BLAST score
                    621
                    1.0e-64
 E value
 Match length
                    147
 % identity
                    80
                    (AF088913) ribosomal protein L27a [Petunia x hybrida]
 NCBI Description
                    5733
 Seq. No.
 Contig ID
                    5338 2.R1040
 5'-most EST
                    LIB3049-034-Q1-E1-H7
 Method
                    BLASTX
 NCBI GI
                    g3608481
 BLAST score
                    590
 E value
                    6.0e-61
 Match length
                    142
 % identity
 NCBI Description
                    (AF088913) ribosomal protein L27a [Petunia x hybrida]
 Seq. No.
                    5734
                    5348 1.R1040
 Contig ID
 5'-most EST
                    qsv7\overline{0}1055090.h1
 Method
                    BLASTX
 NCBI GI
                    g2583117
 BLAST score
                    220
 E value
                    2.0e-17
 Match length
                    193
                    32
 % identity
                    (AC002387) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    5735
                    5348 2.R1040
 Contig ID
```

1090

uC-gmropic100f03b1

BLASTX

```
NCBI GI
                   g2827551
BLAST score
                   202
E value
                   2.0e-15
Match length
                   133
% identity
                   42
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5736
                   5350 1.R1040
Contig ID
                   jC-gmro02800032c07a1
5'-most EST
                   BLASTX-
Method
NCBI GI
                   g3445201
BLAST score
                   246
                   2.0e-20
E value
Match length
                   154
                   40
% identity
                   (AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
                   5737
Seq. No.
                   5351 1.R1040
Contig ID
5'-most EST
                   q5677092
Seq. No.
                   5738
                   5351 2.R1040
Contig ID
                   pcp700992609.h1
5'-most EST
                   5739
Seq. No.
Contig ID
                   5351 3.R1040
5'-most EST
                   hyd700725439.h1
                   5740
Seq. No.
                   5357 1.R1040
Contig ID
                   uC-gmrominsoy194a10b1
5'-most EST
                   5741
Seq. No.
                   5359 1.R1040
Contig ID
                   LIB3028-002-Q1-B1-F7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3269292
BLAST score
                   280
E value
                   1.0e-24
                   72
Match length
                   65
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   5742
Seq. No.
                   5362 1.R1040
Contig ID
                   LIB3028-002-Q1-B1-G1
5'-most EST
                   BLASTX
Method
                   g2979556
NCBI GI
BLAST score
                   127
                   9.0e-12
E value
                   157
Match length
% identity
                   (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
```

5743

Seq. No.

```
Contig ID
                   5363 1.R1040
                   txt700732041.h1
5'-most EST
                   BLASTX
Method
                   g2352492
NCBI GI
BLAST score
                   310
                   4.0e-28
E value
Match length
                   127
% identity
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
                   5744
Seq. No.
                   5363 2.R1040
Contig ID
                   dpv7\overline{0}1097370.h1
5'-most EST
Method
                   BLASTX
                   g2352492
NCBI GI
BLAST score
                   309
                   3.0e-28
E value
                   123
Match length
                   50
% identity
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
                   5745
Seq. No.
                   5363 3.R1040
Contig ID
5'-most EST
                   qsv7\overline{0}1046587.h1
Method
                   BLASTX
                   q4262147
NCBI GI
                   148
BLAST score
                   9.0e-10
E value
Match length
                   44
% identity
                   (AC005275) putative homolog of transport inhibitor response
NCBI Description
                   1 [Arabidopsis thaliana]
                   5746
Seq. No.
Contig ID
                   5364 1.R1040
5'-most EST
                   q5508964
Method
                   BLASTN
                   g21103
NCBI GI
BLAST score
                   72
                   4.0e-32
E value
                   180
Match length
% identity
                   R.sativus mRNA for HMG-COA reductase (clone cRS8)
NCBI Description
                   5747
Seq. No.
                   5364 2.R1040
Contig ID
5'-most EST
                   zhf700954225.hl
                   BLASTN
Method
                   q21103
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
                   180
Match length
```

83

% identity

24.

```
NCBI Description R.sativus mRNA for HMG-COA reductase (clone cRS8)
Seq. No.
                  5748
                  5365 1.R1040
Contig ID
                  LIB3028-002-Q1-B1-G12
5'-most EST
Seq. No.
                  5749
                  5367 1.R1040
Contig ID
                  LIB3028-002-Q1-B1-B6
5'-most EST
                  BLASTX
Method
                  q3914006
NCBI GI
BLAST score
                  552
                  2.0e-67
E value
Match length
                  242
                   61
% identity
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1816588
NCBI Description
                   (U85495) LON2 [Zea mays]
                  5750
Seq. No.
                   5372 1.R1040
Contig ID
                  LIB3094-054-Q1-K1-B6
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3023728
                  290
BLAST score
                   2.0e-25
E value
Match length
                   246
                   31
% identity
                  EXOSTOSIN-2 (PUTATIVE TUMOUR SUPPRESSOR PROTEIN EXT2)
NCBI Description
                   (MULTIPLE EXOSTOSES PROTEIN 2) >gi 1619954 (U72141)
                  multiple exostosis 2 protein [Mus musculus]
Seq. No.
                   5373 1.R1040
Contig ID
                   k11701214081.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539335
BLAST score
                   1454
                   1.0e-176
E value
Match length
                   486
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   5752
Seq. No.
                   5374 1.R1040
Contig ID
5'-most EST
                   LIB3109-034-Q1-K1-B1
                   5753
Seq. No.
                   5375 1.R1040
Contiq ID
                   LIB3028-002-Q1-B1-D9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2499570
BLAST score
                   394
E value
                   4.0e-49
Match length
                   147
% identity
                   68
                   PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE
NCBI Description
                   (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN
```

```
L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) >gi_414332 (L07941) L-isoaspartyl methyltransferase [Triticum aestivum]
```

```
5754
Seq. No.
                   5377 1.R1040
Contig ID
                   leu7\overline{0}1147682.h1
5'-most EST
                   BLASTX
Method
                   g2879867
NCBI GI
BLAST score
                   415
E value
                   3.0e-40
Match length
                   134
% identity
                   62
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
                   5755
Seq. No.
Contig ID
                   5377 2.R1040
5'-most EST
                   LIB3170-005-Q1-K1-E3
Method
                   BLASTX
                   g2879867
NCBI GI
BLAST score
                   420
E value
                   6.0e-41
Match length
                   134
% identity
                   63
NCBI Description
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
                   5756
Seq. No.
                   5377 3.R1040
Contig ID
                   LIB3040-026-Q1-E1-D1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2618605
BLAST score
                   110
                   1.0e-54
E value
Match length
                   262
                   85
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUK11, complete sequence [Arabidopsis thaliana]
                   5757
Seq. No.
                   5377 4.R1040
Contig ID
5'-most EST
                   LIB3049-054-Q1-E1-G3
Method
                   BLASTN
                   g2618605
NCBI GI
BLAST score
                   89
E value
                   2.0e-42
Match length
                   305
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No. 5758

% identity

Contig ID 5380 1.R1040 5'-most EST leu701148742.h1

82

Method BLASTX NCBI GI g228403

5'-most EST

```
BLAST score
                  1676
                  0.0e+00
E value
Match length
                  371
% identity
                  89
NCBI Description glycolate oxidase [Lens culinaris]
Seq. No.
                  5759
                  5380 2.R1040
Contig ID
                  LIB3093-032-Q1-K1-G8
5'-most EST
Method
                  BLASTN
                  g3435305
NCBI GI
BLAST score
                  94
E value
                  4.0e-45
Match length
                  266
                  84
% identity
                  Medicago sativa glycolate oxidase mRNA, partial cds
NCBI Description
Seq. No.
                  5760
                  5382 1.R1040
Contig ID
                  LIB3053-005-Q1-N1-G12
5'-most EST
                  BLASTN
Method
NCBI GI
                  g508303
BLAST score
                  83
                  2.0e-38
E value
Match length
                  243
                  84
% identity
NCBI Description Alfalfa bimodular protein (corC) mRNA, complete cds
Seq. No.
                  5761
                  5382 2.R1040
Contig ID
                  LIB3106-043-Q1-K1-D1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q508303
BLAST score
                  81
E value
                  1.0e-37
Match length
                  185
                  86
% identity
                  Alfalfa bimodular protein (corC) mRNA, complete cds
NCBI Description
Seq. No.
                  5762
Contig ID
                  5383 1.R1040
5'-most EST
                  LIB3049-051-Q1-E1-D6
Seq. No.
                  5763
                  5384 1.R1040
Contig ID
                  LIB3028-009-Q1-B1-E3
5'-most EST
Method
                  BLASTN
NCBI GI
                  g563328
BLAST score
                  120
E value
                  1.0e-60
Match length
                  316
                  86
% identity
NCBI Description
                  A.officinalis mRNA for histone 2B
                  5764
Seq. No.
Contig ID
                  5384 2.R1040
```

LIB3040-058-Q1-E1-C11

NCBI GI

```
a a
```

```
Method
                    BLASTN
 NCBI GI
                    q2935449
 BLAST score
                    114
                    4.0e-57
 E value
 Match length
                    278
                    85
 % identity
                    Malus domestica histone H2B mRNA, partial cds
 NCBI Description
                    5765
 Seq. No.
                    5384 3.R1040
 Contig ID
                    LIB3170-001-Q1-K1-D10
 5'-most EST
 Method
                    BLASTN
                    g563328
 NCBI GI
 BLAST score
                    138
 E value
                    2.0e-71
 Match length
                    310
                    88
 % identity
                    A.officinalis mRNA for histone 2B
 NCBI Description
                    5766
 Seq. No.
                    5384 4.R1040
 Contig ID
                    LIB3040-032-Q1-E1-F8
 5'-most EST
 Method
                    BLASTN
                    g563328
 NCBI GI
 BLAST score
                    136
                    4.0e-70
 E value
 Match length
                    280
 % identity
                    87
                    A.officinalis mRNA for histone 2B
 NCBI Description
                    5767
 Seq. No.
                    5384 5.R1040
 Contig ID
 5'-most EST
                    LIB3106-014-Q1-K1-D4
 Method
                    BLASTN
 NCBI GI
                    g2558961
                    129
 BLAST score
                    6.0e-66
 E value
. Match length
                    265
 % identity
                    87
                    Gossypium hirsutum histone H2B1 mRNA, complete cds
 NCBI Description
                    5768
 Seq. No.
                    5384 6.R1040
 Contig. ID
                    jC-gmro02910069a02a1
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    g563328
 BLAST score
                    127
                    8.0e-65
 E value
 Match length
                    315
                    87
 % identity
 NCBI Description
                    A.officinalis mRNA for histone 2B
                    5769
 Seq. No.
 Contig ID
                    5384 7.R1040
                    LIB3039-012-Q1-E1-E7
 5'-most EST
                    BLASTN
 Method
```

g2935449

```
2.0e-62
E value
                  279
Match length
                  86
% identity
NCBI Description Malus domestica histone H2B mRNA, partial cds
                  5770
Seq. No.
                  5384 8.R1040
Contig ID
                  LIB3039-047-Q1-E1-H1
5'-most EST
                  BLASTN
Method
                  g2558961
NCBI GI
BLAST score
                  120
                  1.0e-60
E value
                  276
Match length
                  86
% identity
                  Gossypium hirsutum histone H2B1 mRNA, complete cds
NCBI Description
Seq. No.
                  5771
                  5384 10.R1040
Contig ID
                  LIB3049-040-Q1-E1-F7
5'-most EST
                  BLASTN
Method
                  g2935449
NCBI GI
                  82
BLAST score
                  3.0e-38
E value
                  114
Match length
                   93
% identity
                  Malus domestica histone H2B mRNA, partial cds
NCBI Description
                   5772
Seq. No.
                   5384 11.R1040
Contig ID
                  LIB3106-033-Q1-K1-F3
5'-most EST
                   BLASTN
Method
                   g2935449
NCBI GI
                   88
BLAST score
                   8.0e-42
E value
                   160
Match length
                   89
% identity
                  Malus domestica histone H2B mRNA, partial cds
NCBI Description
                   5773
Seq. No.
                   5384 12.R1040
Contig ID
                   LIB3170-002-Q1-K1-G8
5'-most EST
                   BLASTN
Method.
                   g4309679
NCBI GI
                   75
BLAST score
                   5.0e-34
E value
                   207
Match length
                   43
% identity
                   Arabidopsis thaliana phosphoribosylanthranilate isomerase
NCBI Description
                   (PAI1) and (PAI4) genes, complete cds
                   5774
Seq. No.
                   5385 1.R1040
Contig ID
                   vzy700755223.hl
5'-most EST
                   BLASTX
Method
```

123

BLAST score

g2529707

430

NCBI GI BLAST score

NCBI Description

```
2.0e-42
E value
Match length
                  148
                  55
% identity
                  (AF001434) Hpast [Homo sapiens]
NCBI Description
                  5775
Seq. No.
                  5387_1.R1040
Contig ID
                  vwf700677464.hl
5'-most EST
                  BLASTX
Method
                  g1762436
                                         . .
NCBI GI
                  1379
BLAST score
                  1.0e-153
E value
                  353
Match length
                  72
% identity
                   (U60277) acyl-acyl carrier protein desaturase [Asclepias
NCBI Description
                  syriaca]
                  5776
Seq. No.
                  5390 1.R1040
Contig ID
                  LIB3138-017-Q1-N1-C12
5'-most EST
                  BLASTX
Method
                  g3451078
NCBI GI
BLAST score
                   306
                   2.0e-27
E value
                  282
Match length
                  33
% identity
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                   5777
Seq. No.
                   5390 2.R1040
Contig ID
                   LIB3051-102-Q1-K1-H1
5'-most EST
                   5778
Seq. No.
                   5395 1.R1040
Contig ID
                   sat701014384.hl
5'-most EST
                   BLASTX
Method
                   g4204281
NCBI GI
                   338
BLAST score
E value
                   2.0e-31
                   175
Match length
                   39
% identity
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5779
Seq. No.
                   5395 2.R1040
Contig ID
                   LIB3051-091-Q1-K1-G11
5'-most EST
                   5780
Seq. No.
                   5412 1.R1040
Contig ID
                   LIB3094-090-Q1-K1-D2
5'-most EST
                   BLASTX
Method
                   g2827551
NCBI GI
                   456
BLAST score
                   2.0e-45
E value
                   115
Match length
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
```

```
5781
Seq. No.
                  5414 1.R1040
Contig ID
                  crh7\overline{0}0854530.h1
5'-most EST
                  BLASTX
Method
                  q1944518
NCBI GI
                  1142
BLAST score
                  1.0e-125
E value
                   303
Match length
                  73
% identity
                   (Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana]
NCBI Description
                  >qi 3047105 (AF058919) protein kinase [Arabidopsis
                  thaliana]
                   5782
Seq. No.
                   5419 1.R1040
Contig ID
                  LIB3039-039-Q1-E1-D5
5'-most EST
Method
                   BLASTX
                   q3201623
NCBI GI
BLAST score
                   1864
                   0.0e+00
E value
                   380
Match length
% identity
                   91
                   (AC004669) shaggy-like kinase dzeta [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5783
                   5419 2.R1040
Contig ID
5'-most EST
                   LIB3093-036-Q1-K1-E5
Method
                   BLASTX
                   g1877397
NCBI GI
BLAST score
                   306
                   1.0e-27
E value
                   102
Match length
% identity
                   (Y11591) shaggy-like kinase [Ricinus communis]
NCBI Description
                   5784
Seq. No.
                   5419 4.R1040
Contig ID
5'-most EST
                   LIB3170-006-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   q2129738
BLAST score
                   484
                   1.0e-48
E value
Match length
                   117
% identity
                   81
                   shaggy-like kinase dzeta - Arabidopsis thaliana
NCBI Description
                   >gi 1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
                   [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)
                   serine/threonine kinase [Arabidopsis thaliana]
                   5785
Seq. No.
                   5419 5.R1040
Contig ID
                   LIB3109-041-Q1-K1-G7
5'-most EST
Method
                   BLASTN
                   q1877396
NCBI GI
BLAST score
                   106
```

1.0e-52

E value



64

81

Match length % identity

NCBI Description

```
Match length
                   274
% identity
                   85
                   R.communis mRNA for shaggy-like kinase, partial
NCBI Description
                   5786
Seq. No.
                   5419 6.R1040
Contig ID
                   zhf7\overline{0}0953024.h1
5'-most EST
                   BLASTN
Method
                   g1161509
NCBI GI
                   5.6
BLAST score
                   1.0e-22
E value
Match length
                   140
                   85
% identity
                   A.thaliana mRNA for shaggy-like kinase dzeta
NCBI Description
Seq. No.
                   5787
                   5425 1.R1040
Contig ID
5'-most EST
                   LIB3028-001-Q1-B1-H3
                   5788
Seq. No.
                   5427 1.R1040
Contig ID
                   fua701038054.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2982311
BLAST score
                   867
                   4.0e-93
E value
                   238
Match length
% identity
NCBI Description
                   (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
                   mariana]
                   5789
Seq. No.
                   5429 1.R1040
Contig ID
5'-most EST
                   LIB3056-004-Q1-N1-H3
                   5790
Seq. No.
                   5431 1.R1040
Contig ID
                   ncj7\overline{0}0975521.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2160166
BLAST score
                   631
                   2.0e-65
E value
                   243
Match length
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   5791
Seq. No.
                   5434 1.R1040
Contig ID
                   LIB3049-003-Q1-E1-F11
5'-most EST
Method
                   BLASTX
                   g3850582
NCBI GI
BLAST score
                   281
E value
                   9.0e-25
```

(AC005278) F15K9.14 [Arabidopsis thaliana]